

# **SUPPORTING INFORMATION**

## **Nucleotide Excision Repair and Impact of Site-Specific 5',8-Cyclopurine and Bulky DNA Lesions on Physical Properties of Nucleosomes**

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**Synthesis of 147 bp Fragments of the 601 Widom DNA Containing Single 5',8-Cyclopurine Lesions and Cy3 and Cy5 Dyes.** These lesions were embedded in the 17-mer sequences 5'- CCACCAAC $X^{cP}$ CTACCACC with the following modifications of the neighboring sequences (Figure S1):

**“Out” rotational setting of the lesion  
Modified strand (sequence 2)**

***a* : 17-mer sequence**

5'- CCACCAAC $X^{cP}$ CTACCACC,  $X^{cP}$  = cdA or cdG

***b* : 57-mer sequence**

5'- CACAGGATGTATATATCTGACACGTGCCTGGA $Y$ ACTAGGGAGTAATCCCCTTGGCGG,  
 $Y$  = G or Cy3

***c* : 73-mer sequence,**

5'-  
GCGCGTACGTGCGTTTAAGCGGTGCTAGAGCTGTCTACGACCAATTGAGCGGCCTCGGCACC  
GGGATTCTCCA

***d* : 49-mer scaffold strand**

5'- CACCGCTTAAACGCACGTACGCGCGGTGGTAGCGTTGGTGGCCGCCAAG

**Complementary strand (sequence 1)**

***e* : 49-mer sequence (Left)**

5'- TGGAGAATCCCGGTGCCGAGGCCGCTCAATTGGT $Z$ GTAGACAGCTCTAG  
 $Z$  = C or Cy5

***f* : 49-mer sequence (Middle),**

5'- CACCGCTTAAACGCACGTACGGTGGTAGCGTTGGTGGTTAACCGCCAAG

***g* : 49-mer sequence (Right),**

5'- GGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCCTGTG

***h* : 20-mer scaffold strand**

5'-GAGTAATCCCCTTGGCGGCC

***i* : 20-mer scaffold strand**

5'- TTAAGCGGTGCTAGAGCTGT

**“In” rotational setting of the lesion  
Modified strand (sequence 2)**

***a* : 17-mer sequence**

5'- CCACCAAC $X^{cP}$ CTACCACC,  $X^{cP}$  = cdA or cdG

***b* : 61-mer sequence**

5'-  
CACAGGATGTATATATCTGACACGTGCCTGGAYACTAGGGAGTAATCCCCTTGGCGGTAA  
Y = G or Cy3

***c* : 69-mer sequence,**

5'-  
GTACGTGCGTTTAAGCGGTGCTAGAGCTGTCTACGACCAATTGAGCGGCCTCGGCACCGGGA  
TTCTCCA

***d* : 49-mer scaffold strand**

5'- CACCGCTTAAACGCACGTACGGTGGTAGCGTTGGTGGTTAACCGCCAAG

**Complementary strand (sequence 1)**

***e* : 49-mer sequence (Left)**

5'- TGGAGAATCCCGGTGCCGAGGCCGCTCAATTGGTZGTAGACAGCTCTAG  
Z = C or Cy5

***f* : 49-mer sequence (Middle),**

5'- CACCGCTTAAACGCACGTACGGTGGTAGCGTTGGTGGTTAACCGCCAAG

***g* : 49-mer sequence (Right),**

5'- GGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCCTGTG

***h* : 20-mer scaffold strand**

5'-GAGTAATCCCCTTGGCGGCC

***i* : 20-mer scaffold strand**

5'- TTAAGCGGTGCTAGAGCTGT

**Synthesis of 147 bp Fragments of the 601 Widom DNA Containing Single BP-**

**dGLesions and Cy3 and Cy5 Dyes.** These lesions were embedded in the 11-mer sequences 5'-

CCATCG<sup>G<sup>BP</sup></sup>CTACC with the following modifications of the neighboring sequences (Figure

S1):

**“Out” rotational setting of the lesion**

**Modified strand (sequence 2)**

***a* : 11-mer sequence**

5'-CCATCG<sup>G<sup>BP</sup></sup>CTACC, <sup>G<sup>BP</sup></sup> = *cis*- or *trans*-BPDE-G

***b* : 60-mer sequence**

5'- CACAGGATGTATATATCTGACACGTGCCTGGA<sup>Y</sup>ACTAGGGAGTAATCCCCTTGGCGG,  
<sup>Y</sup> = G or Cy3

**c : 76-mer sequence,**

5'-  
GCGCGTACGTGCGTTTAAGCGGTGCTAGAGCTGTCTACGACCAATTGAGCGGCCTCGGCACC  
GGGATTCTCCA

**d : 49-mer scaffoldstrand**

5'- CACCGCTTAAACGCACGTACGCGCGGTGGTAGCGTTGGTGGCCGCCAAG

**Complementary strand (sequence 1)**

**e : 49-mer sequence (Left)**

5'- TGGAGAATCCCGGTGCCGAGGCCGCTCAATTGGT<sup>Z</sup>GTAGACAGCTCTAG  
<sup>Z</sup> = C or Cy5

**f : 49-mer sequence (Middle),**

5'- CACCGCTTAAACGCACGTACGGTGGTAGCGTTGGTGGTTAACCGCCAAG

**g : 49-mer sequence (Right),**

5'- GGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCCTGTG

**h : 20-mer scaffold strand**

5'-GAGTAATCCCCTTGGCGGCC

**i : 20-mer scaffold strand**

5'- TTAAGCGGTGCTAGAGCTGT

**“In” rotational setting of the lesion**

**Modified strand (sequence 2)**

**a : 11-mer sequence**

5'-CCATC<sup>G<sup>BP</sup></sup>CTACC, <sup>G<sup>BP</sup></sup> = *cis*- or *trans*-BPDE-G

**b : 64-mer sequence**

5'-  
CACAGGATGTATATATCTGACACGTGCCTGGA<sup>Y</sup>ACTAGGGAGTAATCCCCTTGGCGGTAA  
<sup>Y</sup> = G or Cy3

**c : 72-mer sequence,**

5'-  
GTACGTGCGTTTAAGCGGTGCTAGAGCTGTCTACGACCAATTGAGCGGCCTCGGCACCGGGA  
TTCTCCA

**d : 49-mer scaffold strand**

5'- CACCGCTTAAACGCACGTACGGTGGTAGCGTTGGTGGTTAACCGCCAAG

**Complementary strand (sequence 1)**

***e* : 49-mer sequence (Left)**

5' - TGGAGAATCCCGGTGCCGAGGCCGCTCAATTGGT**Z**GTAGACAGCTCTAG  
**Z = C or Cy5**

***f* : 49-mer sequence (Middle),**

5' - CACCGCTTAAACGCACGTACGGTGGTAGCGTTGGTGGTTAACCGCCAAG

***g* : 49-mer sequence (Right),**

5' - GGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCCTGTG

***h* : 20-mer scaffold strand**

5' - GAGTAATCCCCTTGGCGGCC

***i* : 20-mer scaffold strand**

5' - TTAAGCGGTGCTAGAGCTGT

**FIGURES**

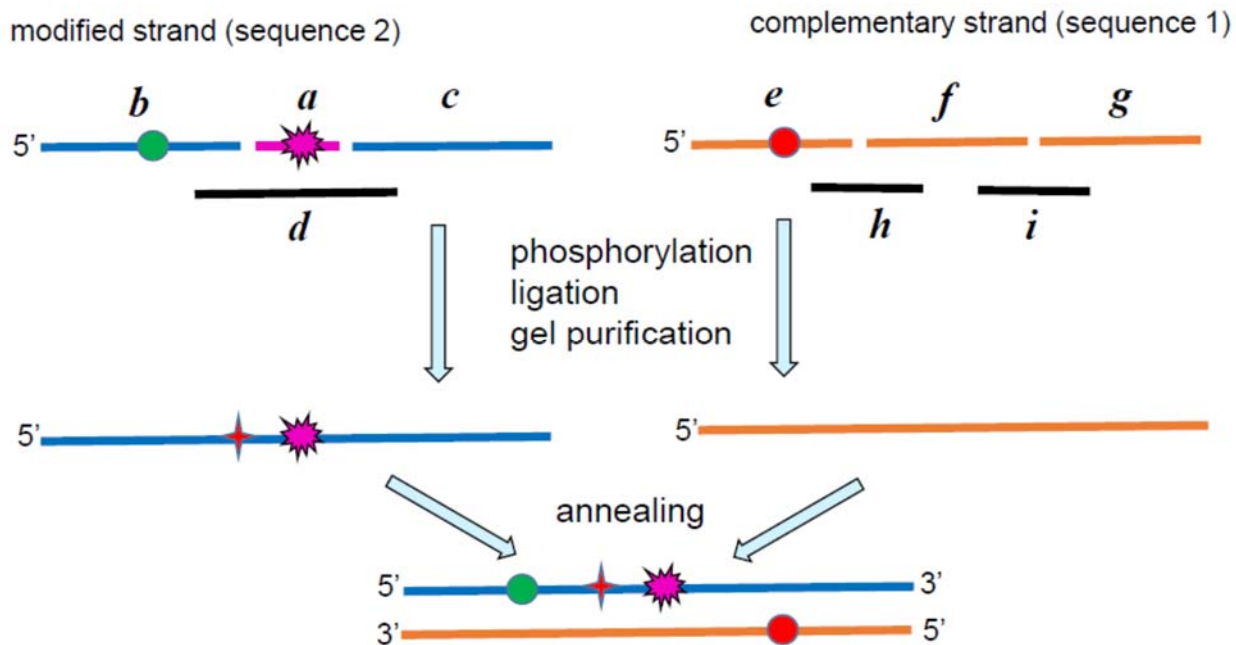
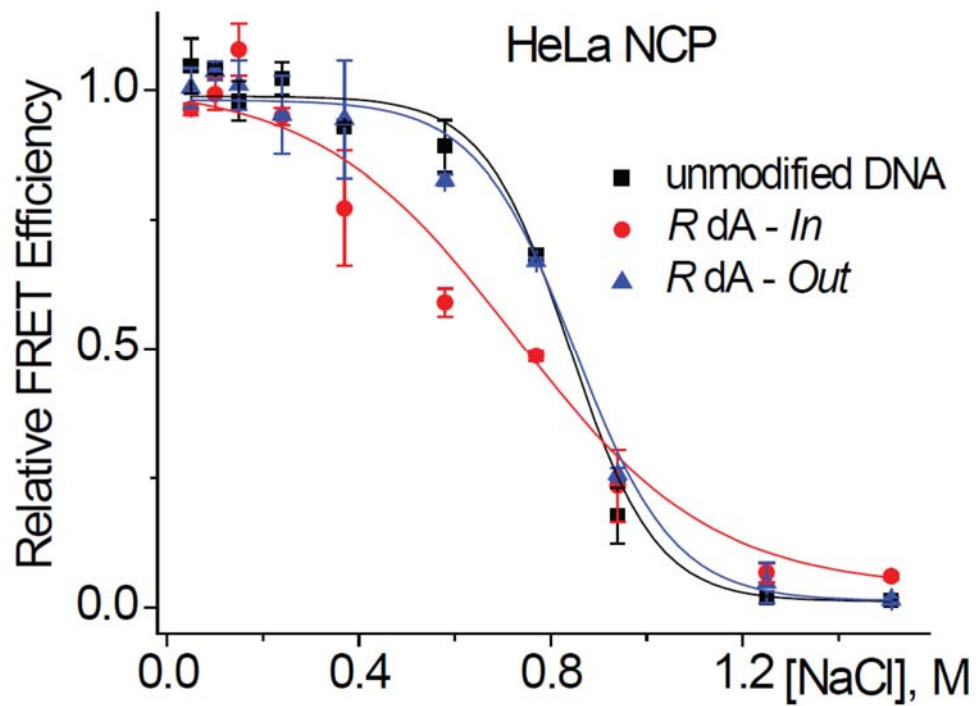


Figure S1. Construction of the <sup>32</sup>P-internally labeled (✦) 147 bp fragments of 601 Widom sequence containing single 5',8-cyclopurine lesion (✱) for NER experiments. The 5'-<sup>32</sup>P-endlabeled modified strands were used in the hydroxyl radical footprinting and competitive reconstruction experiments. The Cy3 (●) and Cy5 (●) were incorporated for the FRET studies.



**Figure S2.** Relative FRET signals measured at 670 nm of HeLa histone nucleosomes with *R cdA* lesions as a function of NaCl concentrations; the sigmoidal curves are plots of Eq. 3.