SUPPLEMENTAL DATA

Structural and Kinetic Analysis of Miscoding Opposite the DNA Adduct 1,N^6-Ethenodeoxyadenosine by Human Translesion DNA Polymerase η

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FIGURE S1. **Steady-state kinetics of incorporation of individual dNTPs opposite 1,N^6-εdA (Substrate C) by hpol η.** *A*, dATP; *B*, dCTP; *C*, dGTP; *D*, dTTP. See Table 3 for estimated parameters.

Substrate C

```
5′-(FAM)GTT CTA GCG TGT AGG TAT          -3′
     3′-CAA GAT CGC ACA TCC ATA (εdA)CT CC-5′
```

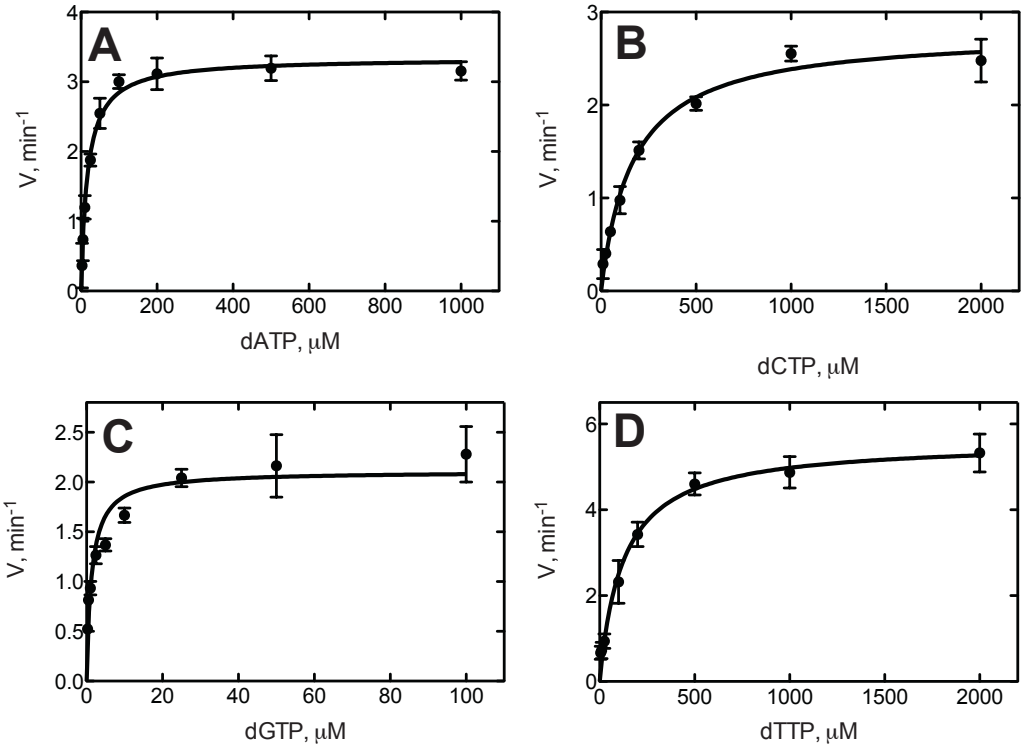

FIGURE S2. **Pre-steady-state kinetics of incorporation of individual dNTPs opposite 1,N^6-εdA (Substrate A) by hpol η.** *A*, dATP; *B*, dGTP; *C*, dCTP; *D*, dTTP.

Substrate A

```
5´-(FAM)TCG TAA GCG TCA T          -3´
     3´-AGC ATT CGC AGT A(εdA)C ACT-5´
```

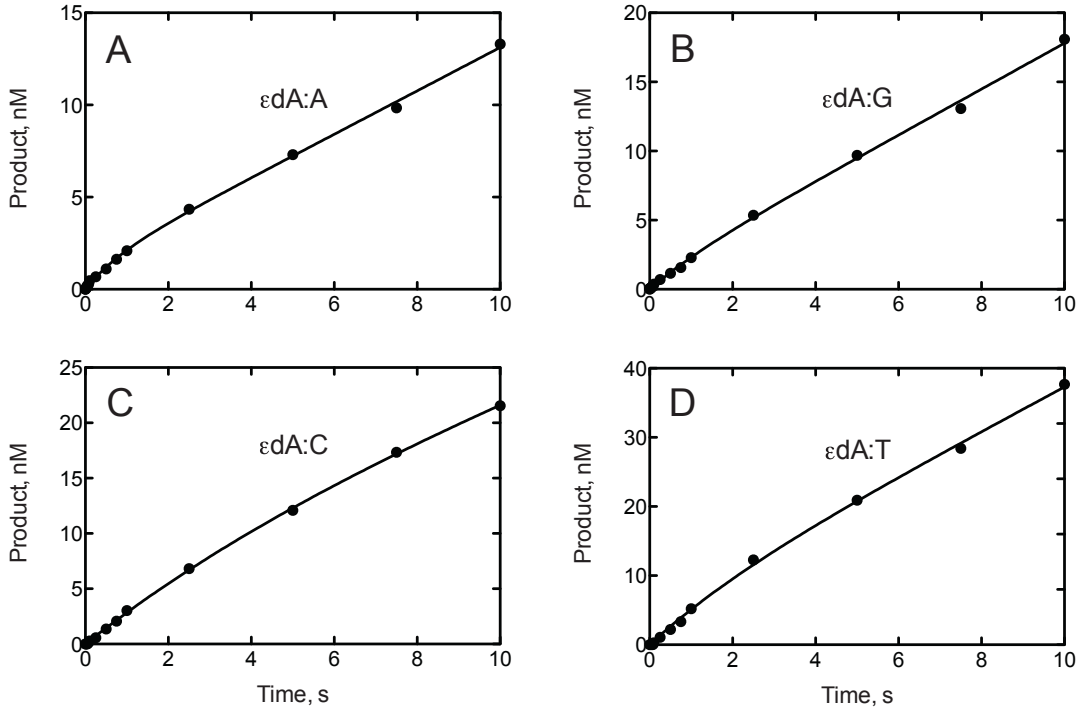

FIGURE S3. **LC-MS analysis of extension products.** See Table 5 for calculated results.

```
Substrate A–U  5´-(FAM)TCG TAA GCG TCU T          -3´
                     3´-AGC ATT CGC AGT A(εdA)C ACT-5´
```

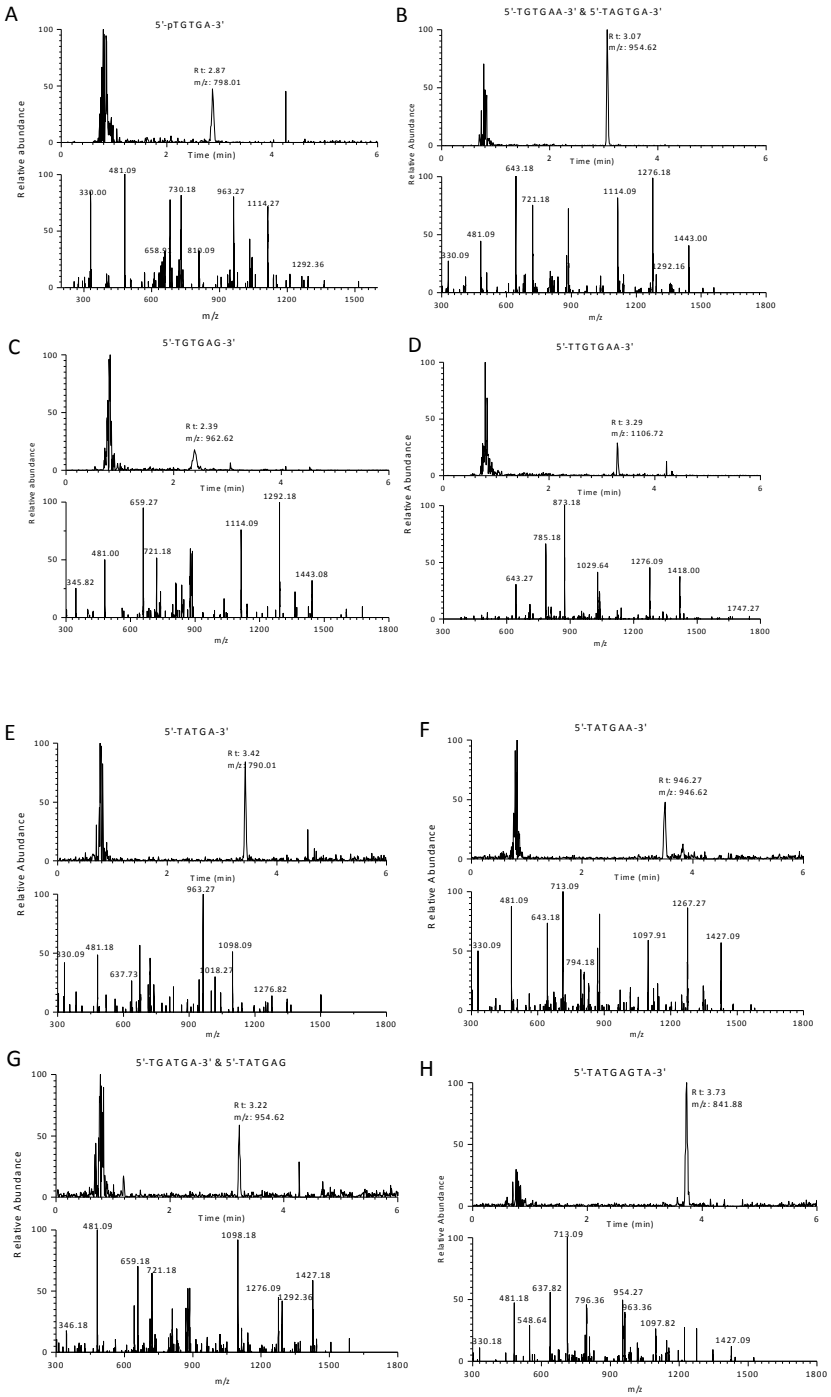

Table S1. Predicted CID fragment ions of frameshift product (pAT_GAGG) from hpol η extension of the 18-mer primer sequence.

LC-MS analysis of products of extension of primer (opposite template 1,N^6-εdA, Substrate C-U, Table 1) by hpol η in the presence of all four dNTPs. (Underscore indicates a deletion in product.) See Fig. 1*B*.

n	Charge	*m*/*z*, a-B ion	*m*/*z*, w ion
1	-1		346.21
2	-1	490.29	675.42
	-2	244.64	337.21
3	-1	794.48	988.64
	-2	396.74	493.81
4	-1	1123.69	1317.85
	-2	561.34	658.42
5	-1	1436.9	1622.04
	-2	717.95	810.52