

Supporting Information for

“In-vitro Replication Studies on O²-Methylthymidine and O⁴-Methylthymidine”

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Figure S1. Product-ion spectrum of the $[M-4H]^4$ ion (m/z 1300.4) of the 17-mer ODN d(CCATGGCAXGAGAATTC), where “X” is O^2 -MdT (A) and O^4 -MdT (B). Shown in the inset is the negative-ion ESI-MS for the ODNs.

Figure S2. Calibration curves for the ratios of unextended primer d(AATTCTC) to d(AATTCTCATGC) (i.e., 11A) (A); d(AATTCTCA) (i.e., 8A) to 11A (B); d(AATTCTCG) (i.e., 8G) to 11A (C); d(AATTCTCTGC) (i.e., 10Del) to 11A (D); d(AATTCTCCTGC) (i.e., 11C) to 11A (E); d(AATTCTCTTGC) (i.e., 11T) to 11A (F); d(AATTCTCGTGC) (i.e., 11G) to 11A (G).

Figure S3. Representative gel images for steady-state kinetic assays measuring nucleotide incorporation opposite undamaged dT (A), O^2 -MdT (B), and O^4 -MdT (C) with Kf⁻ (0.7-7 nM). Reactions were conducted in the presence of individual dNTPs with the highest concentrations indicated in the figures. The ratios of dNTP concentrations were 0.5-0.6 between neighboring lanes.

Figure S4. Representative gel images for steady-state kinetic assays measuring nucleotide incorporation opposite undamaged dT (A), O^2 -MdT (B), and O^4 -MdT (C) with human DNA polymerase κ (1-5 nM). Reactions were conducted in the presence of individual dNTPs with the highest concentrations indicated in the figures. The concentration ratios of dNTP between neighboring lanes were 0.5-0.6.

Figure S5. Representative gel images for steady-state kinetic assays measuring nucleotide incorporation opposite undamaged dT (A), O^2 -MdT (B), and O^4 -MdT (C) with yeast polymerase η (7.5 nM). Reactions were conducted in the presence of individual dNTPs with the highest concentrations indicated in the figures. The concentration ratios of dNTP between neighboring lanes were 0.5-0.6.

Figure S6. (A) The total-ion chromatogram derived from the LC-MS/MS analysis of the human pol κ -induced replication products of O^2 -MdT-containing substrates that have been treated with two restriction enzymes, NcoI and EcoRI plus shrimp alkaline phosphatase. (B) ESI-MS averaged from the peaks eluting in 18.5-20.5 min in part (A), where ‘T*’ designates the remnant of the digested template containing the damaged site, i.e., d(CATGGCAXGAG), where ‘X’ is O^2 -MdT, and ‘P*’ designates the 5’ portion of the digested primer, i.e., d(GCTAGGATCATAG)

Figure S7. Analysis of the unextended primer and +1 extension products from the human pol κ -induced replication reaction arising from replication of O^2 -MdT-containing substrates that have been treated with two restriction enzymes, NcoI and EcoRI, and shrimp alkaline phosphatase. Product-ion spectra of the ESI-produced $[M-2H]^2$ ion of: the 7mer, d(AATTCTC) (precursor ion m/z 1026.2) (A); 8A, d(AATTCTCA) (precursor ion m/z 1182.7) (B); 8G, d(AATTCTCG) (precursor ion m/z 1190.7) (C); 10Del, d(AATTCTCTGC) (precursor ion m/z 1487.3) (D). In this and the following MS/MS figures, the arrow indicates the fragmentation process, and the solid and open circles represent the precursor ion and fragment ions, respectively.

Figure S8. Analysis of full-length extension products from the human pol κ -induced replication reaction arising from replication of O^2 -MdT-containing substrates that have been treated with

two restriction enzymes, NcoI and EcoRI, and shrimp alkaline phosphatase. Product-ion spectra of the ESI-produced $[M-2H]^{2-}$ ions of: 11C, d(AATTCTCCTGC) (precursor ion m/z 1631.8) (A); 11T, d(AATTCTCTTGC) (precursor ion m/z 1639.3) (B); 11A, d(AATTCTCATGC) (precursor ion m/z 1643.8) (C); 11G, d(AATTCTCGTGC) (precursor ion m/z 1651.7) (D).

Figure S9. The selected-ion chromatograms (SICs) derived from the LC-MS/MS analysis of the replication mixture of the substrate containing dT with: Klenow fragment exo^- (A), yeast pol η (B), and human pol κ (C).

Figure S10. The SICs derived from the LC-MS/MS analysis of the replication mixture of the substrate containing O^2 -MdT with: Klenow fragment exo^- (A), and yeast pol η (B).

Figure S11. The SICs derived from the LC-MS/MS analysis of the replication mixture of the substrate containing O^4 -MdT with: Klenow fragment exo^- (A), yeast pol η (B), and human pol κ (C).

Figure S12. LC-MS/MS for monitoring possible demethylation of O^2 -MdT-containing template following primer extension with human pol κ and restriction digestion. Shown are the SICs derived from ultra-zoom scans monitoring the $[M-3H]^{3-}$ ions from the unmethylated and O^2 -MdT 12mer arising from the digestion of the original O^2 -MdT-containing template.

Figure S13. LC-MS/MS for monitoring possible demethylation of O^2 -MdT-containing templates following primer extension with human pol κ . Shown are the product-ion spectra of the ESI-produced $[M-3H]^{3-}$ ions of: unmethylated 12mer, d(CATGGCCATGAG) (precursor ion m/z 1221.9) (A); original 12mer, d(CATGGCCA[O^2 -MdT]GAG) (precursor ion m/z 1226.5) (B).

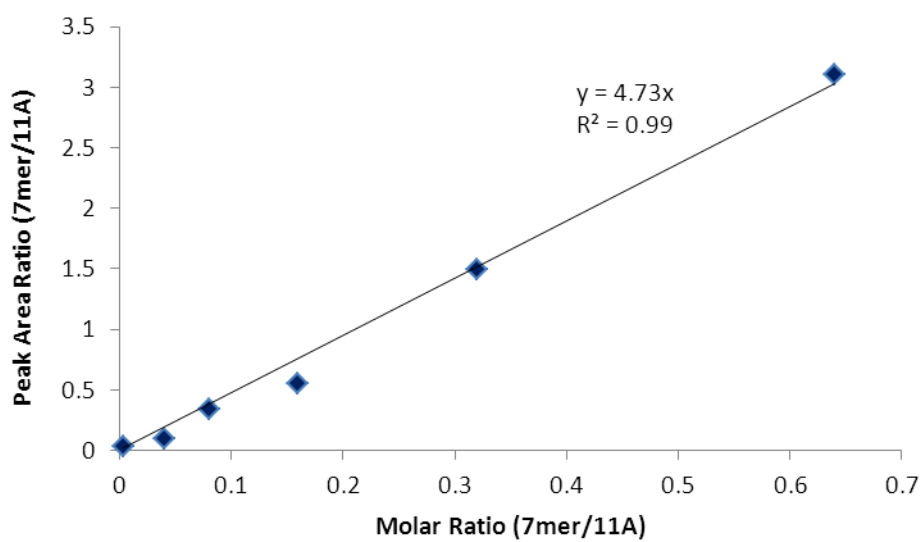
Figure S14. The SICs derived from the LC-MS/MS analysis of the replication mixture of the substrate containing O^4 -MdT with yeast pol η : low dNTPs (A), 6 hr (B).

Figure S15. Representative gel images for steady-state kinetic assays measuring extension past undamaged dT (A), O^2 -MdT (B), and O^4 -MdT (C) with the base opposite the lesion indicated in the figure. Reactions were conducted with human polymerase κ (1-5 nM) in the presence of individual dNTPs with the highest concentrations indicated in the figures. The concentration ratios of dNTP between neighboring lanes were 0.5-0.6.

Table S1. Summary of the percentages of replication products produced for O^4 -MdT-containing substrates by yeast pol η as determined by LC-ESI-MS/MS experiments. Reactions were conducted under two separate conditions: (1) low dNTPs concentrations (50 μ M each) at 37°C overnight; (2) 1 mM dNTPs at 37°C for 6 hr. The template was d(CCATGGCA X GAGAATTCTATGATCCTAG), where ' X ' represents O^4 -MdT.

Table S2. Efficiency and fidelity of human polymerase κ -mediated nucleotide extension with dATP and dGTP opposite undamaged dT, O^2 -MdT and O^4 -MdT as determined by steady-state kinetic measurements.

(A)



(B)

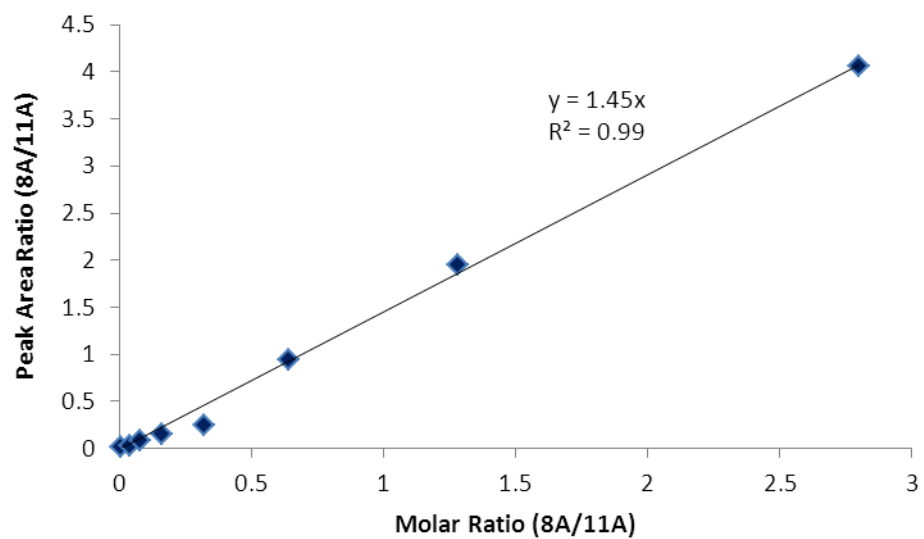
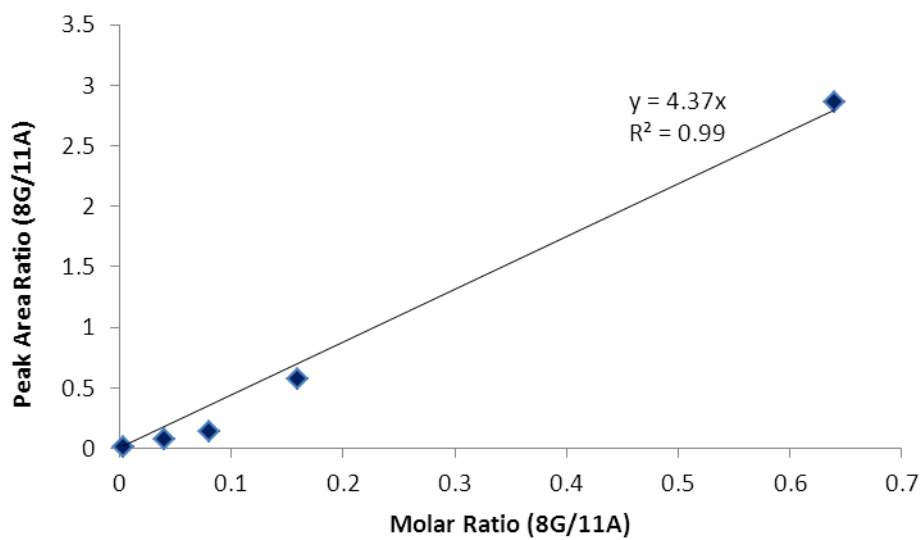


Figure S2.

(C)



(D)

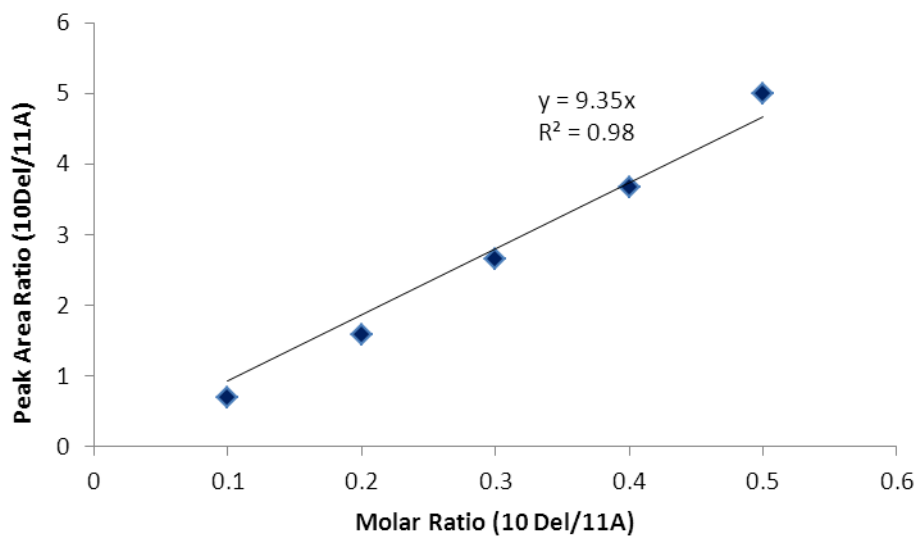
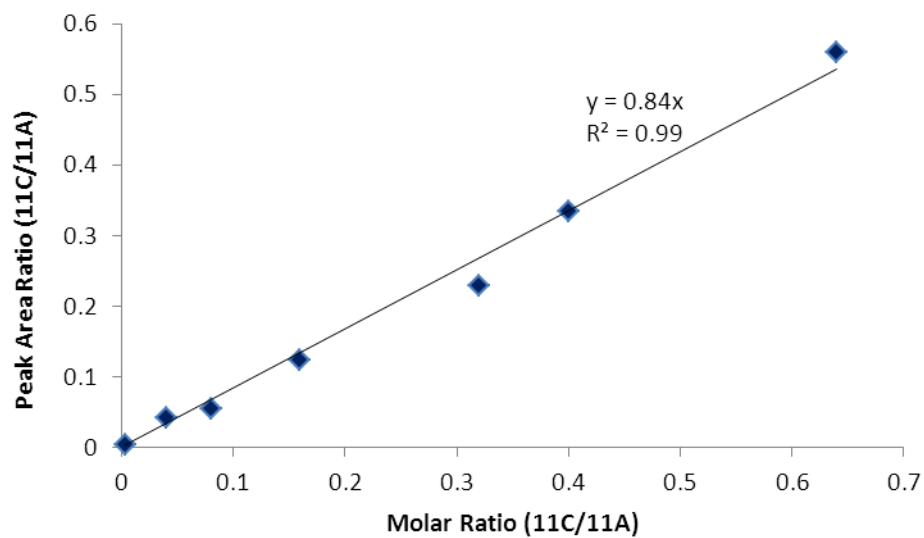


Figure S2.

(E)



(F)

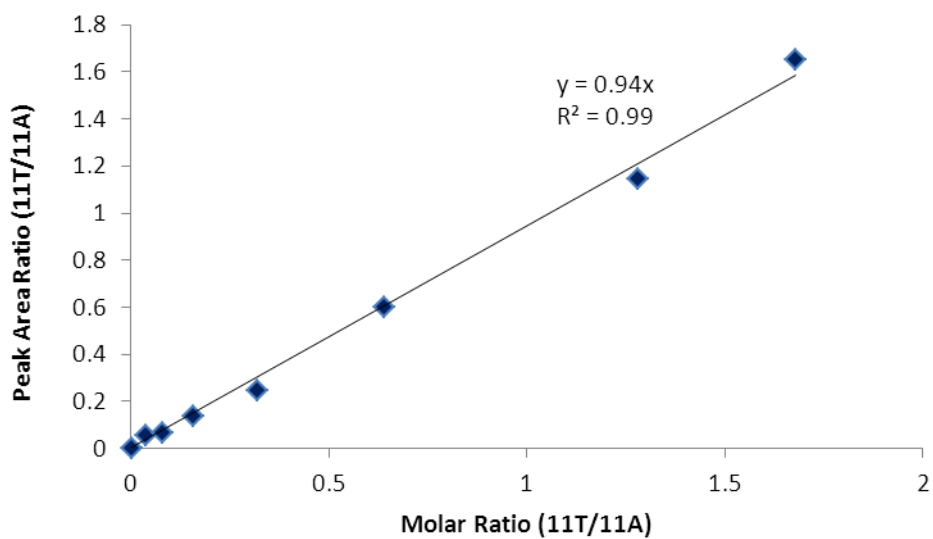


Figure S2.

(G)

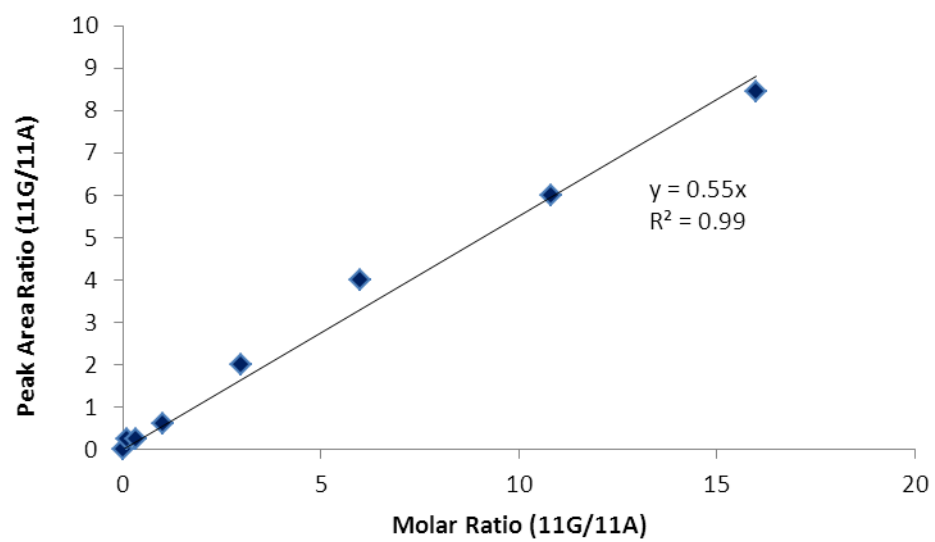
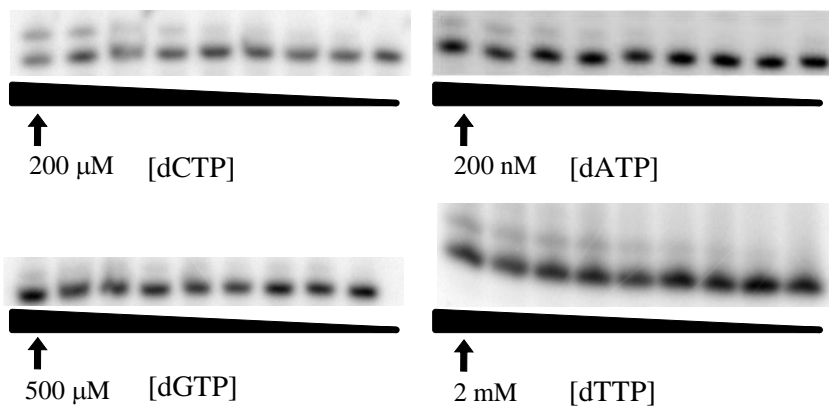


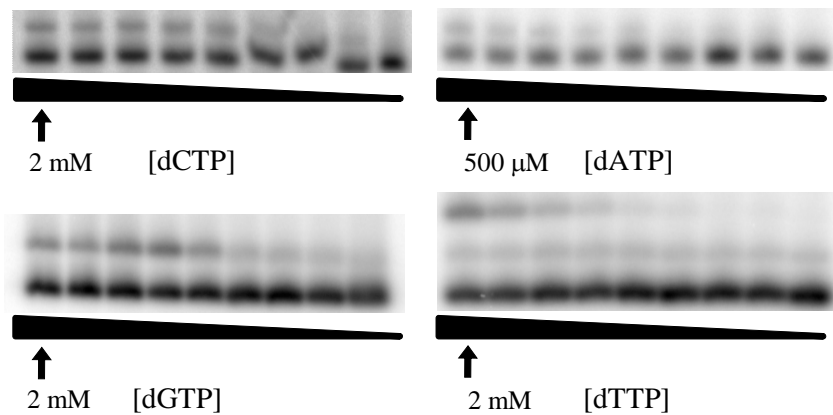
Figure S2.

Primer: 5'- ³²P GCTAGGATCATAGAATTCTC ↙ dNTP incorporation
 Template: 3'- GATCCTAGTATCTTAAGAG[X]ACGGTACC - 5'

(A) X = dT



(B) X = [*O*²-MdT]



(C) X = [*O*⁴-MdT]

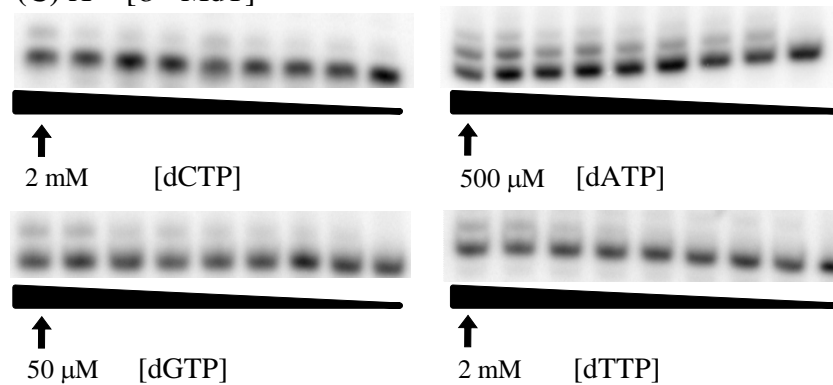
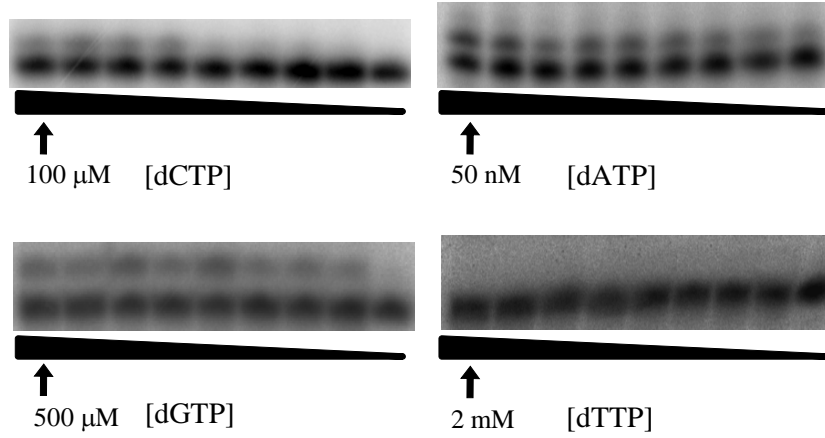


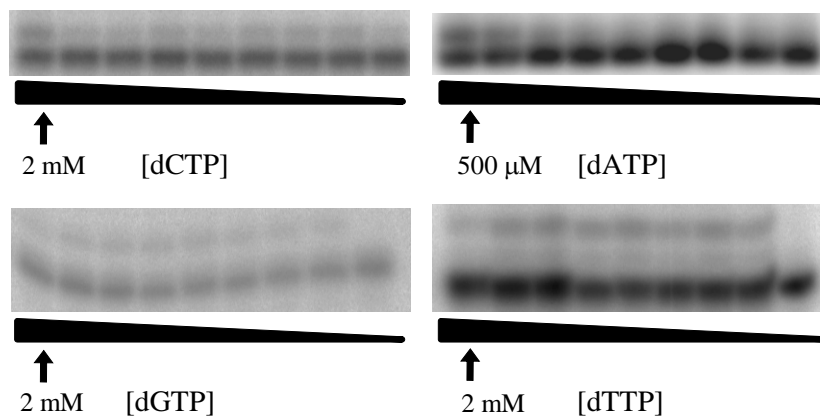
Figure S3.

Primer: 5' - ³²PGCTAGGATCATAGAATTCTC ↙
 Template: 3' - GATCCTAGTATCTTAAGAG[X]ACGGTACC - 5'

(A) X = dT



(B) X = [O²-MdT]



(C) X = [O⁴-MdT]

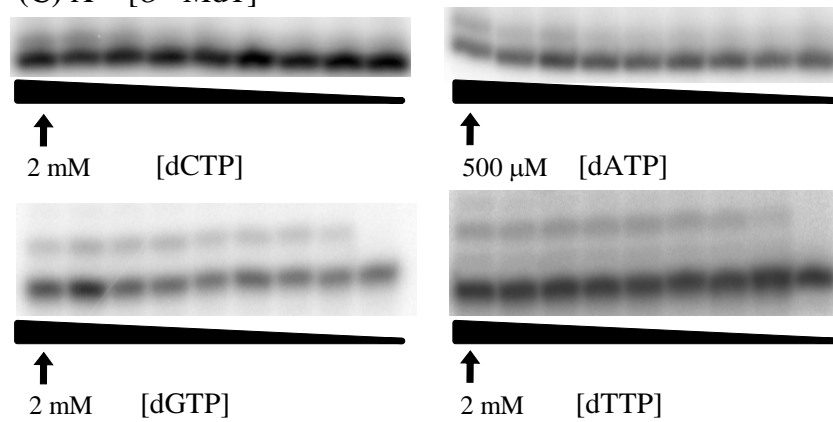


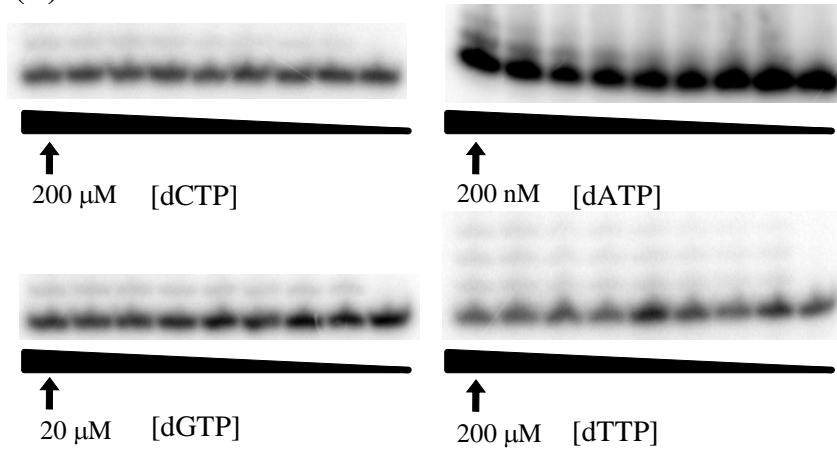
Figure S4.

dNTP incorporation

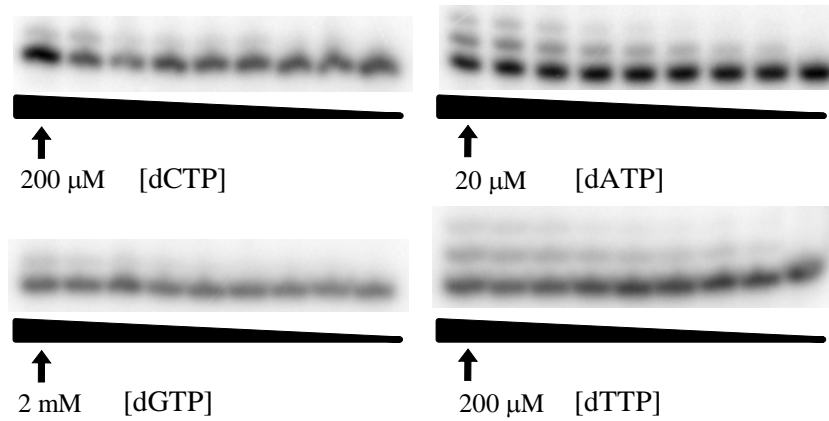
Primer: 5' - ³²P GCTAGGATCATAGAATTCTC

Template: 3' - GATCCTAGTATCTTAAGAG[X]ACGGTACC - 5'

(A) X = dT



(B) X = [*O*²-MdT]



(C) X = [*O*⁴-MdT]

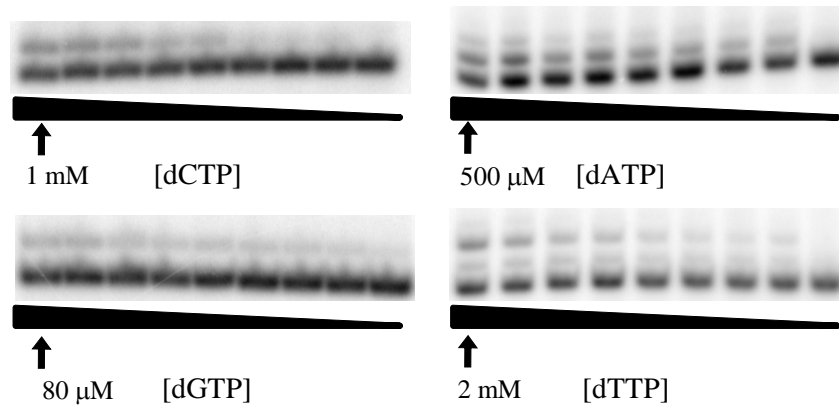
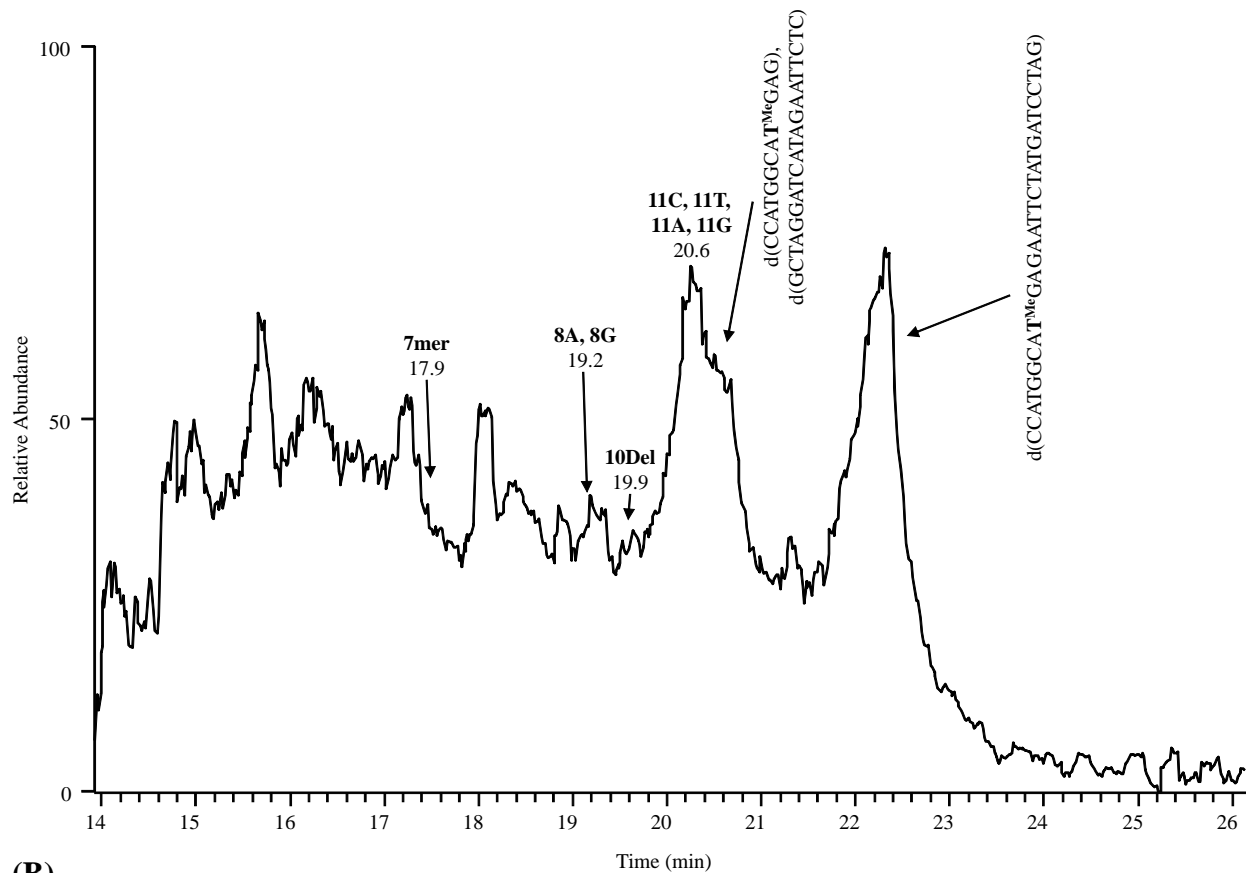


Figure S5.

(A)



(B)

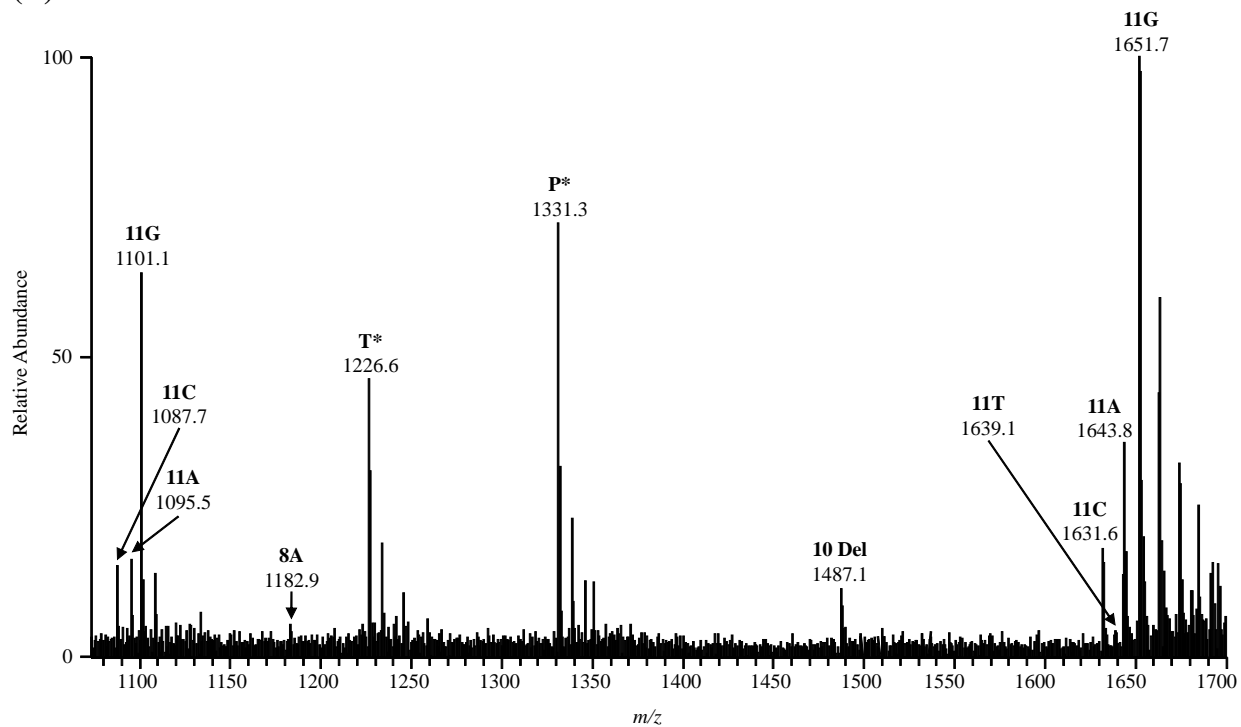


Figure S6.

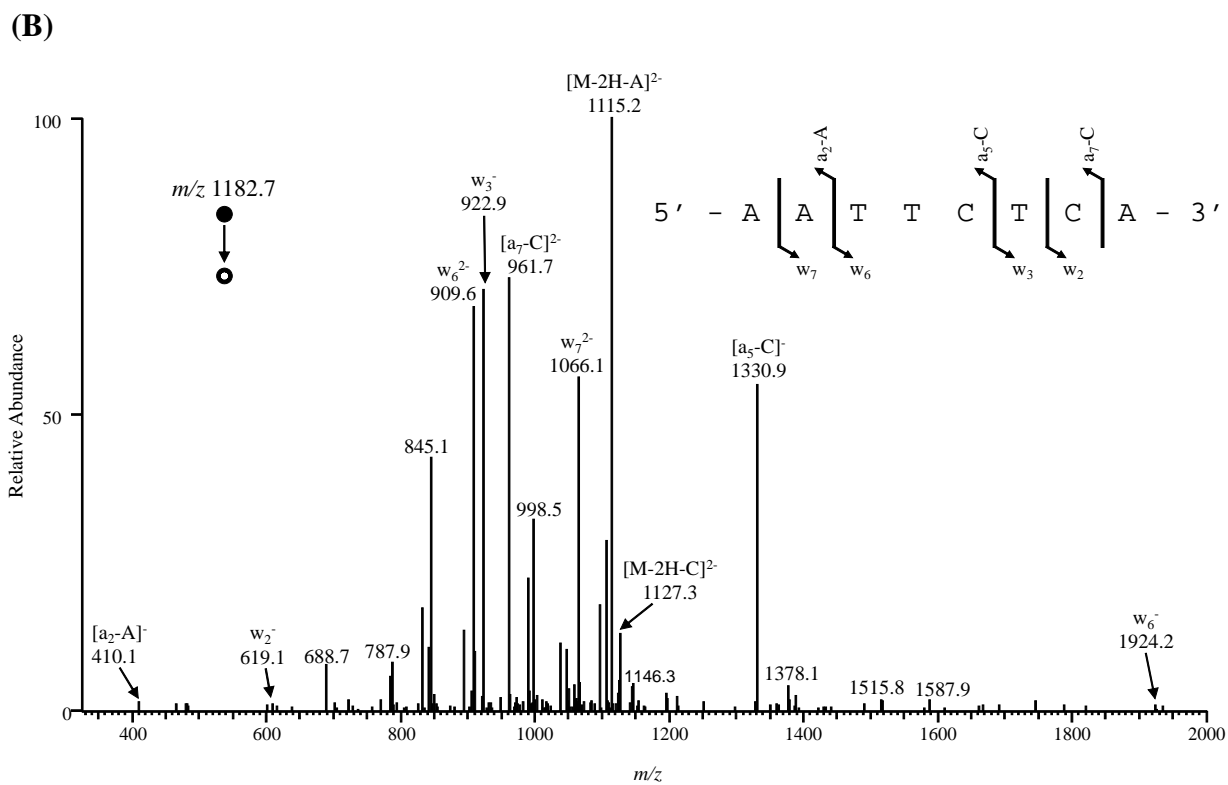
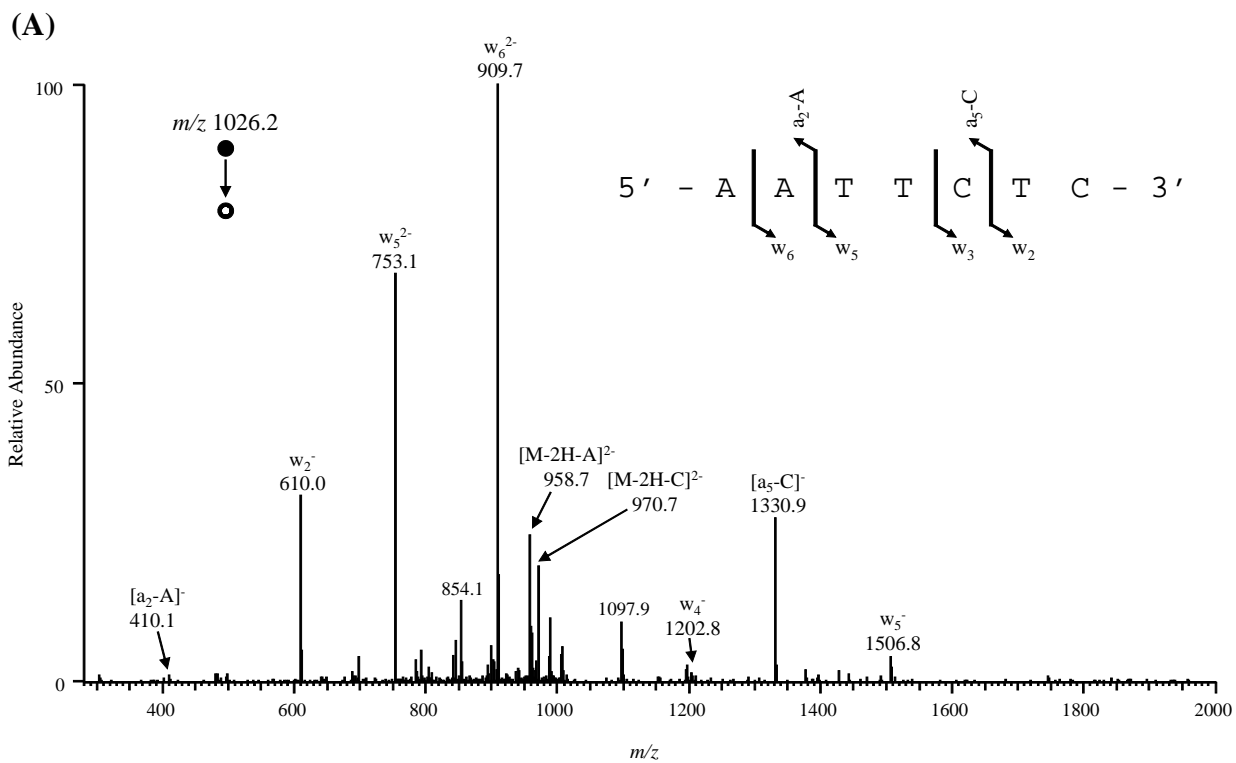


Figure S7.

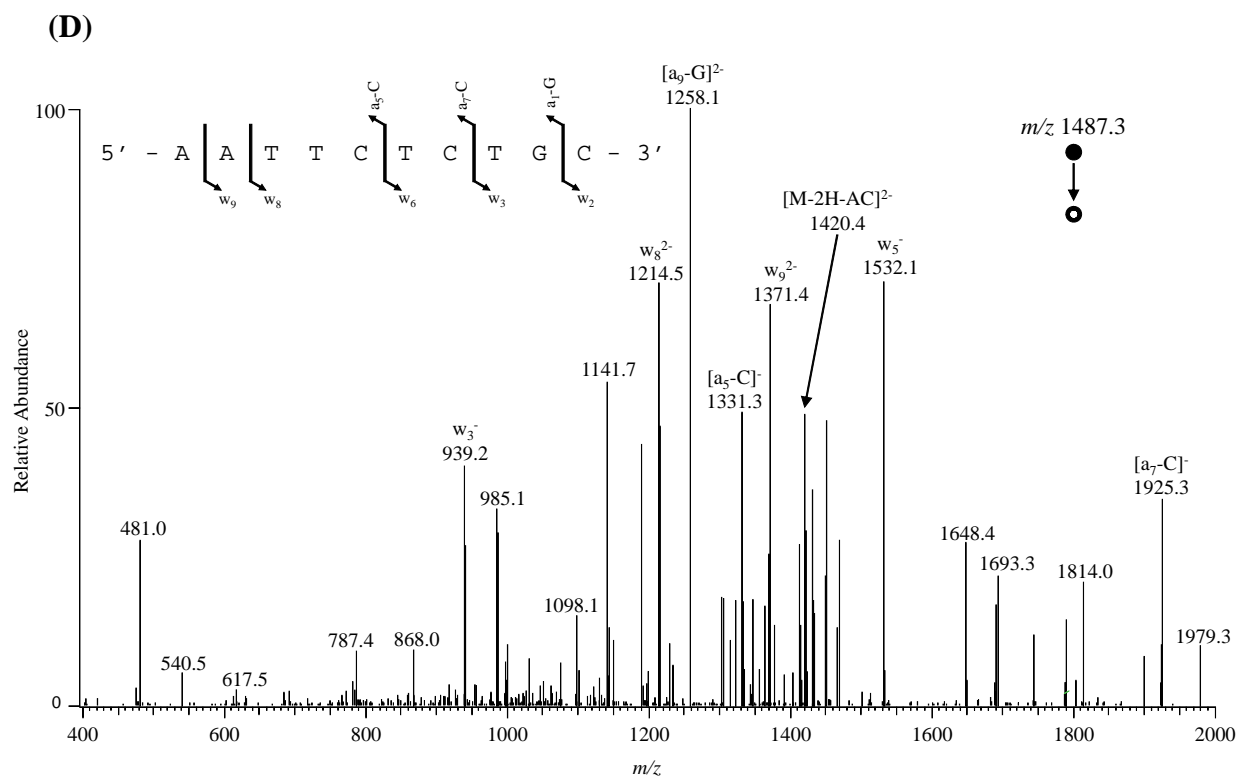
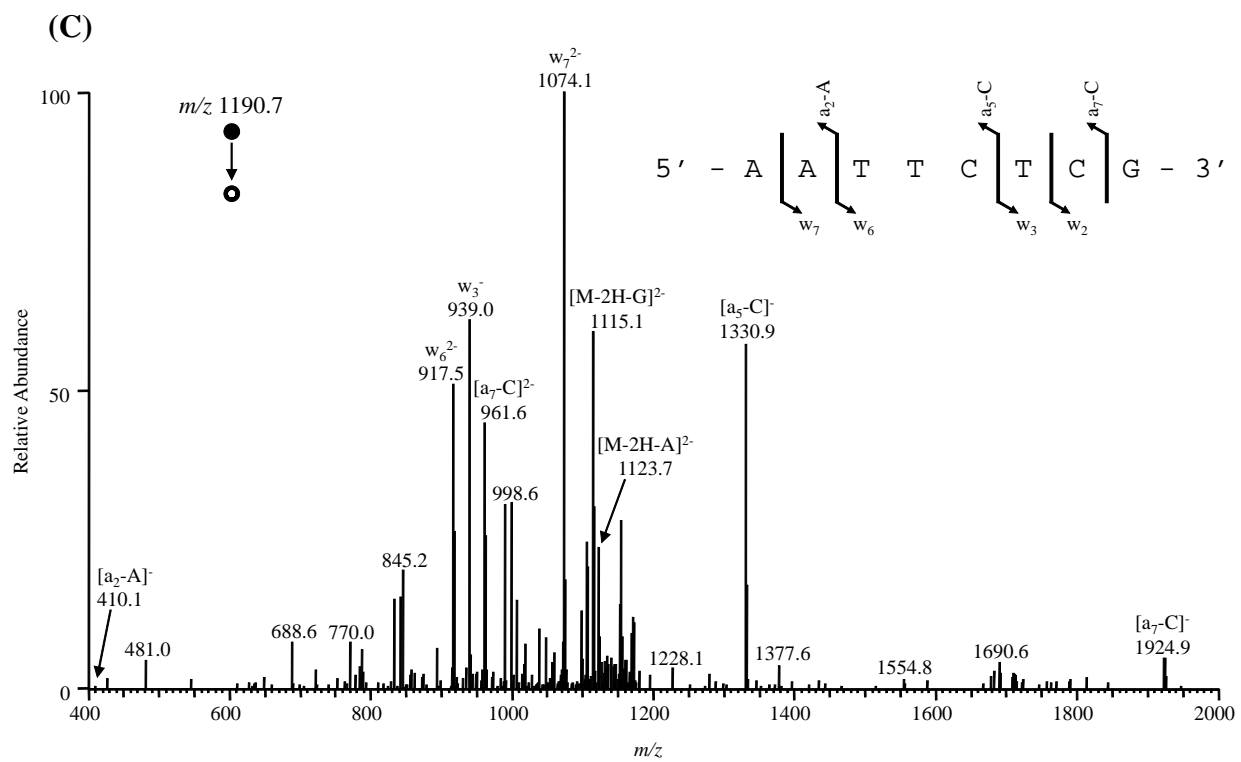


Figure S7.

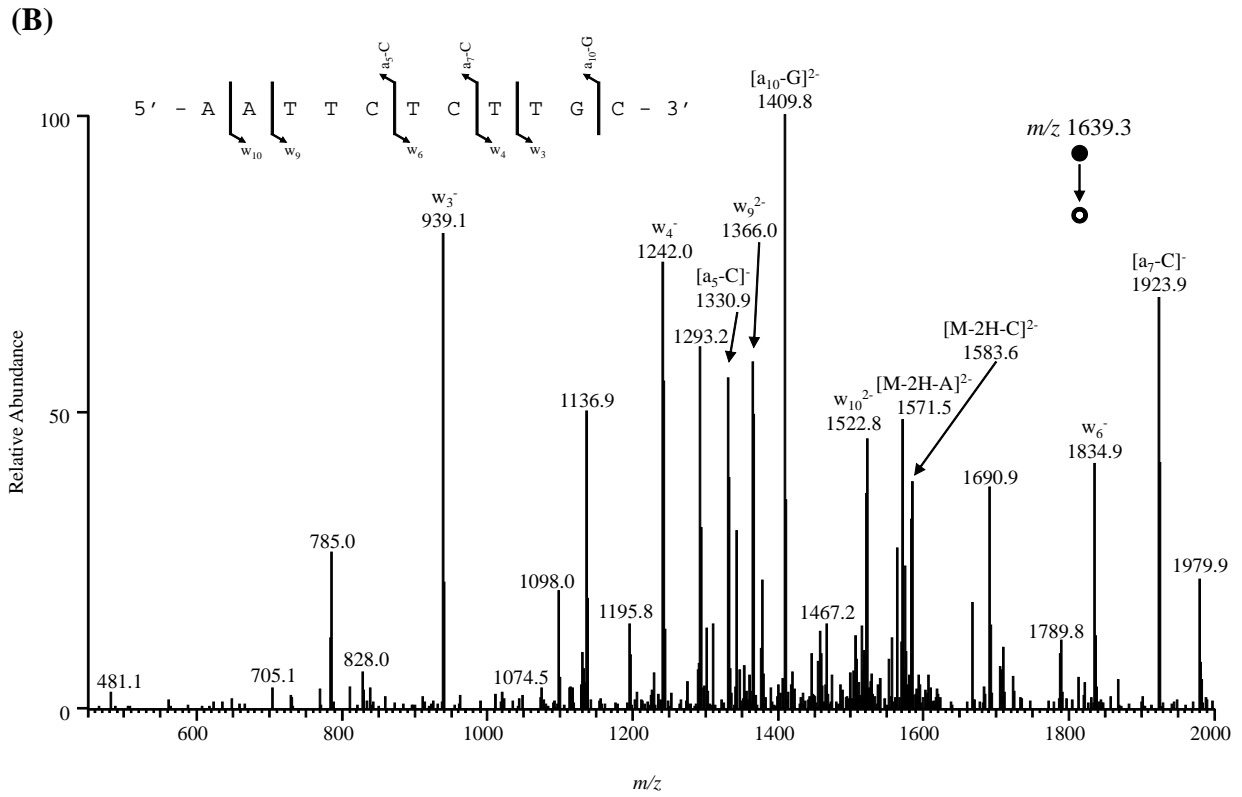
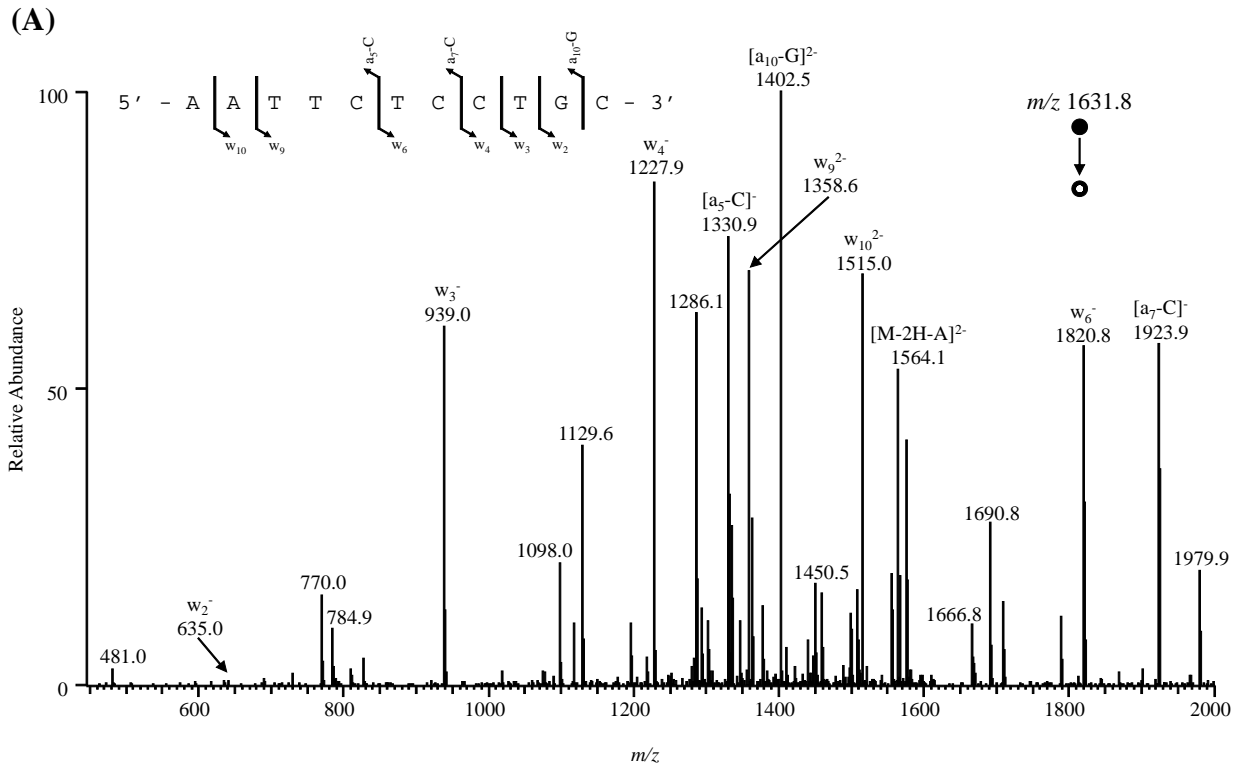


Figure S8.

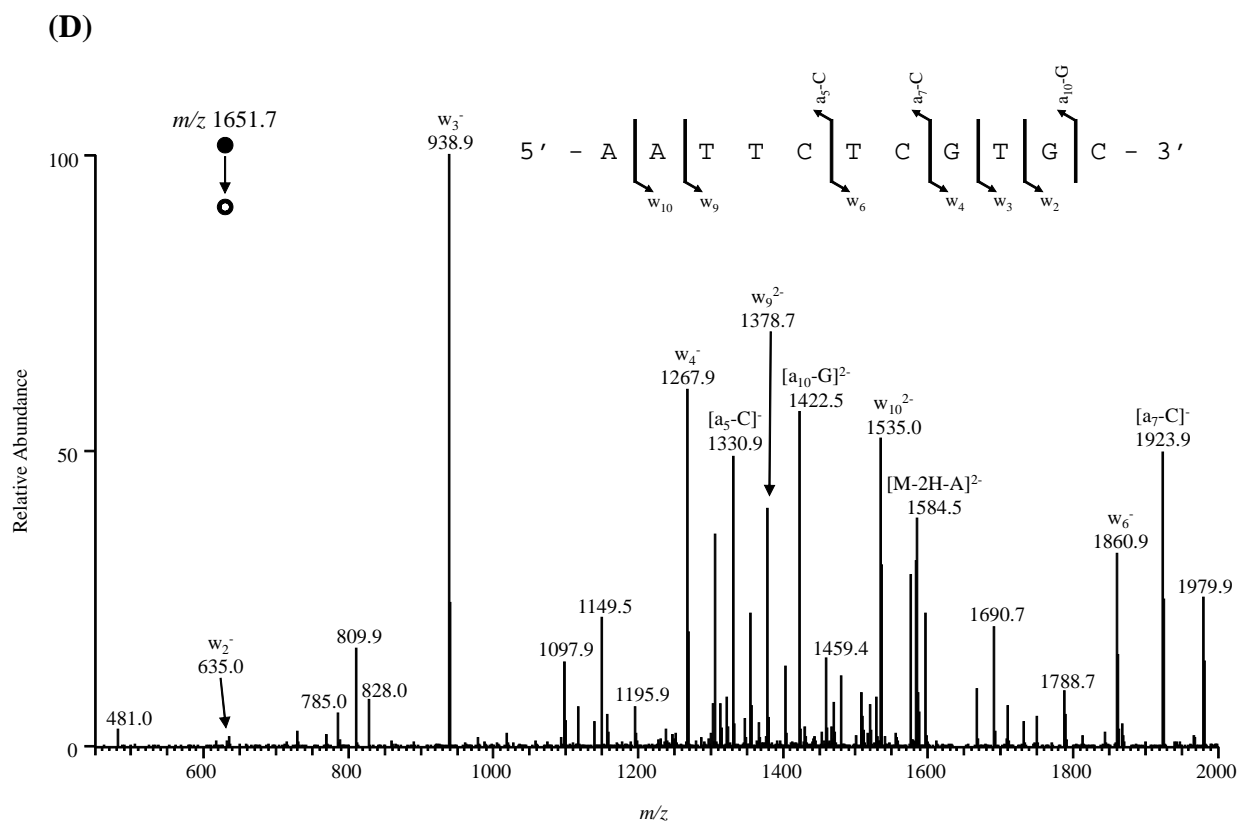
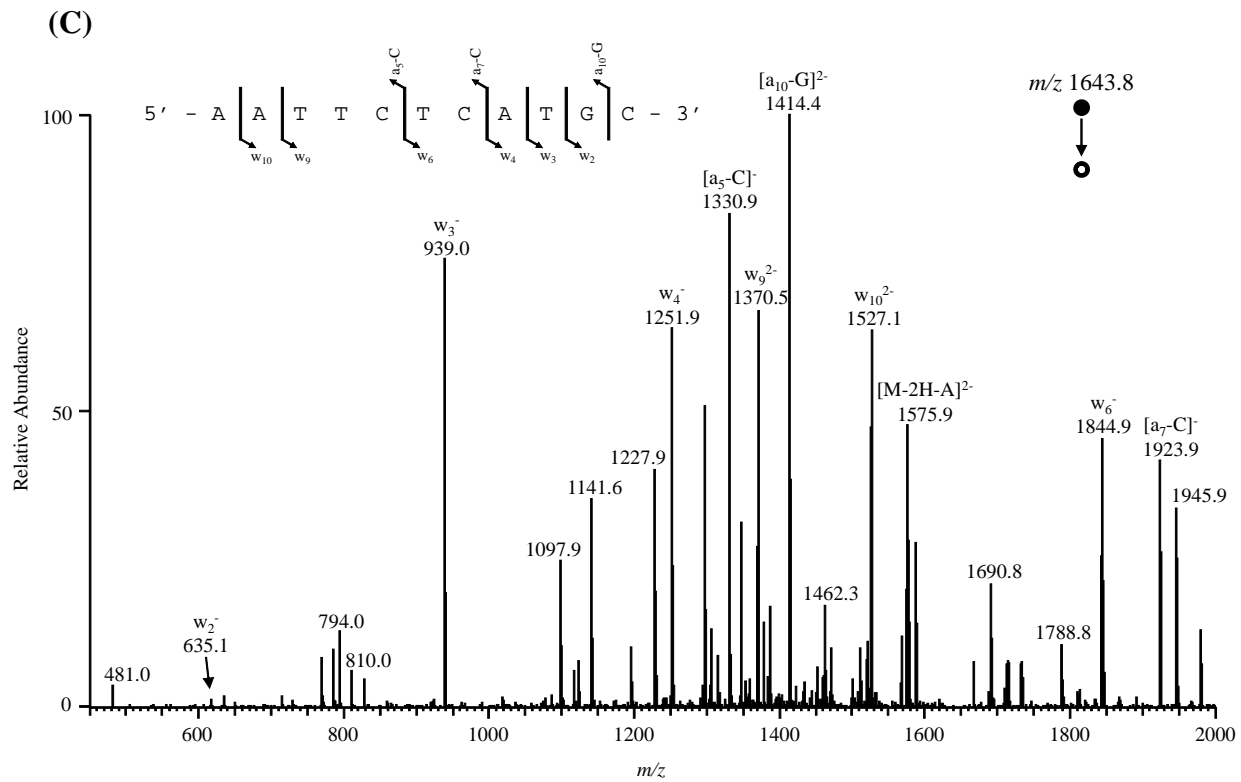
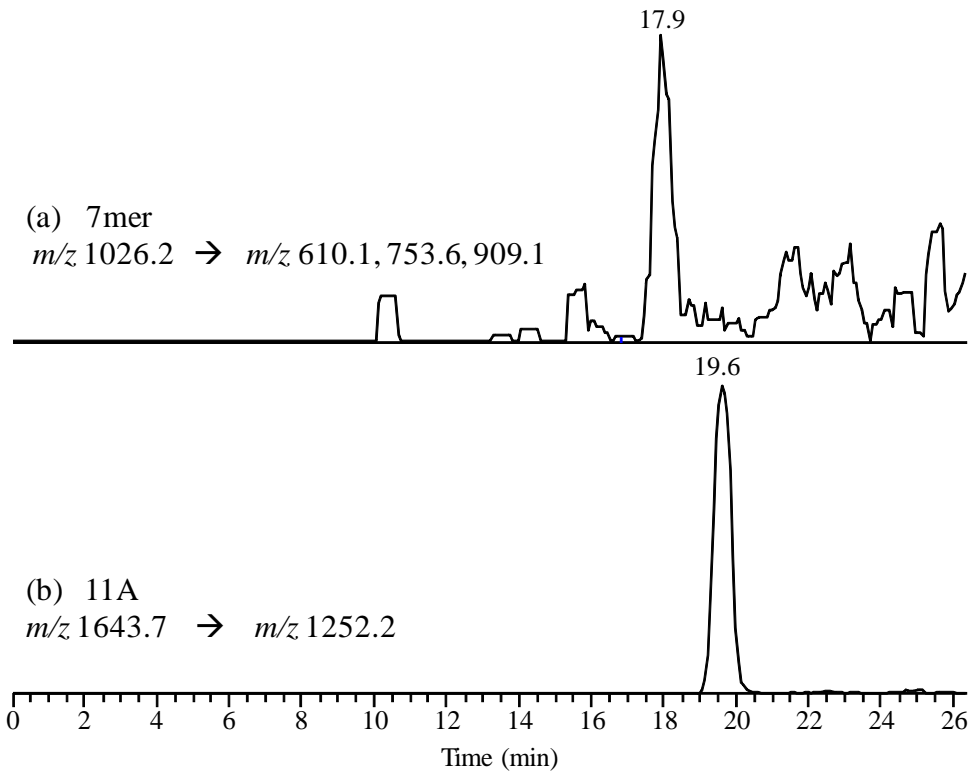


Figure S8.

(A)



5' - GC **AXG** AGA ATT -3'
3' - C TCT TAA -5'
3' - CG TAC TCT TAA -5'

7mer
11A

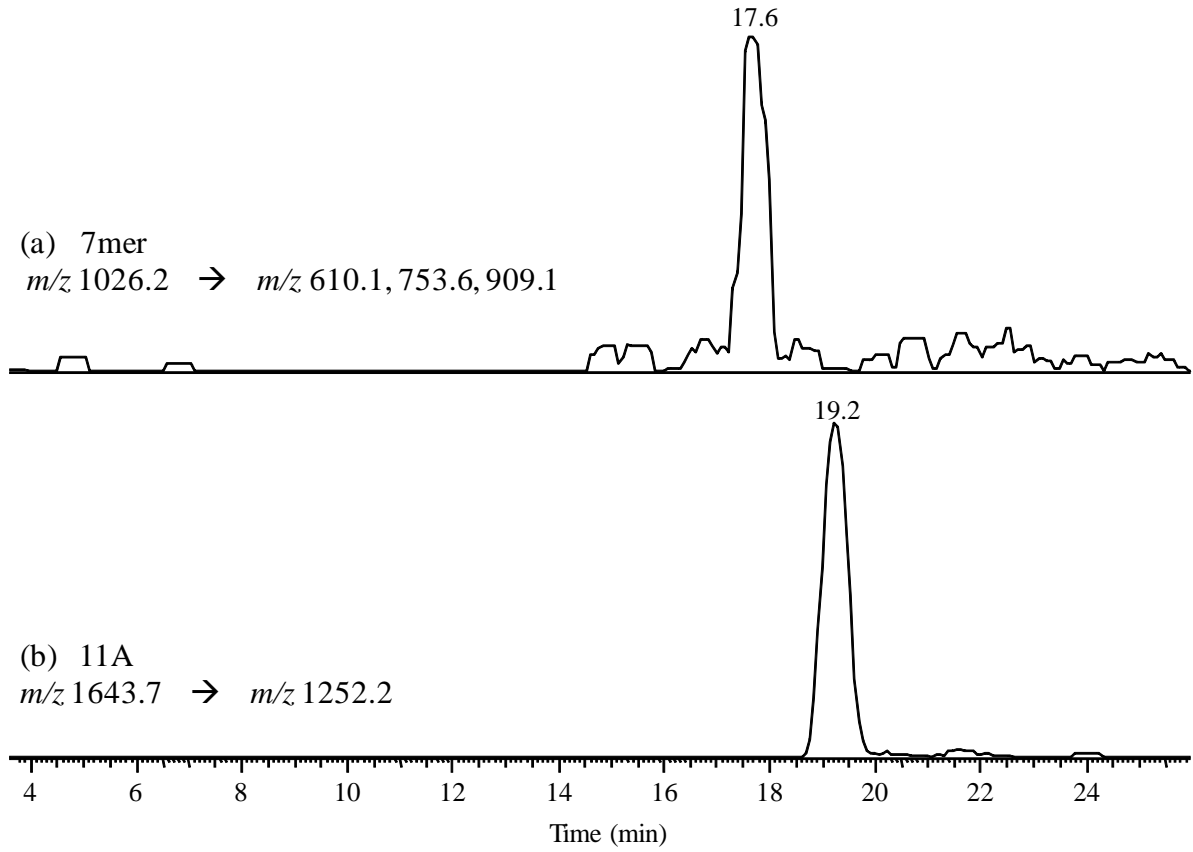
2%
98%

}
}

**dT Replication
From Klenow
fragment exo-**

Figure S9.

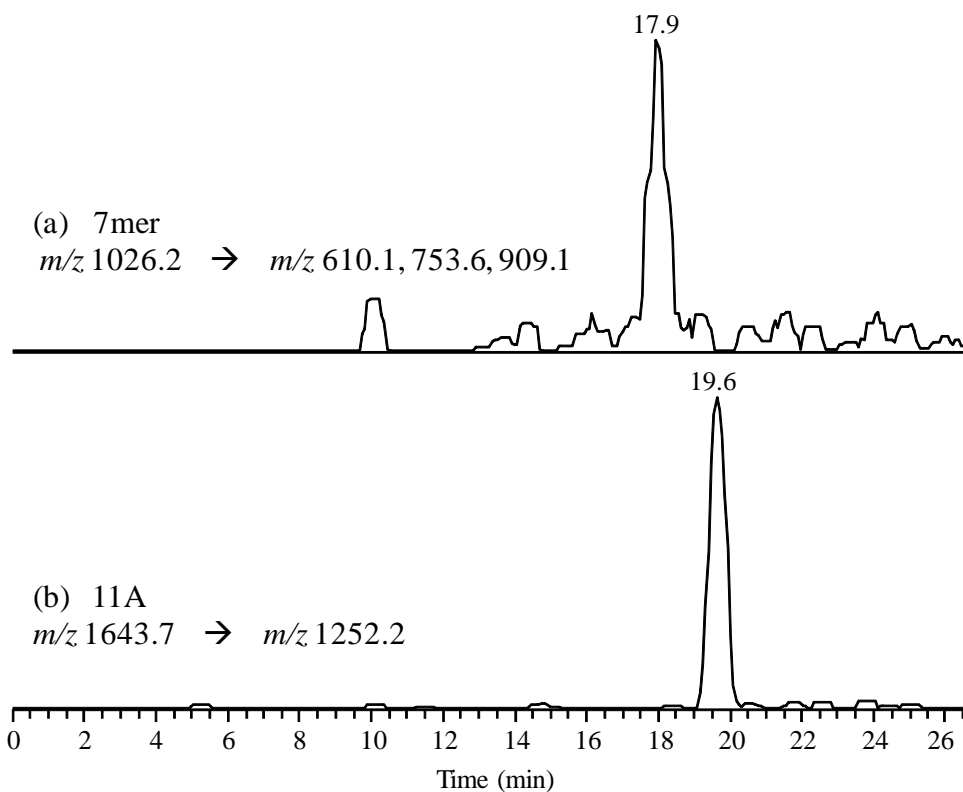
(B)



5' - GC AXG AGA ATT -3'			
3' - C TCT TAA -5'	7mer	4%	} dT Replication From pol η
3' - CG TAC TCT TAA -5'	11A	96%	

Figure S9.

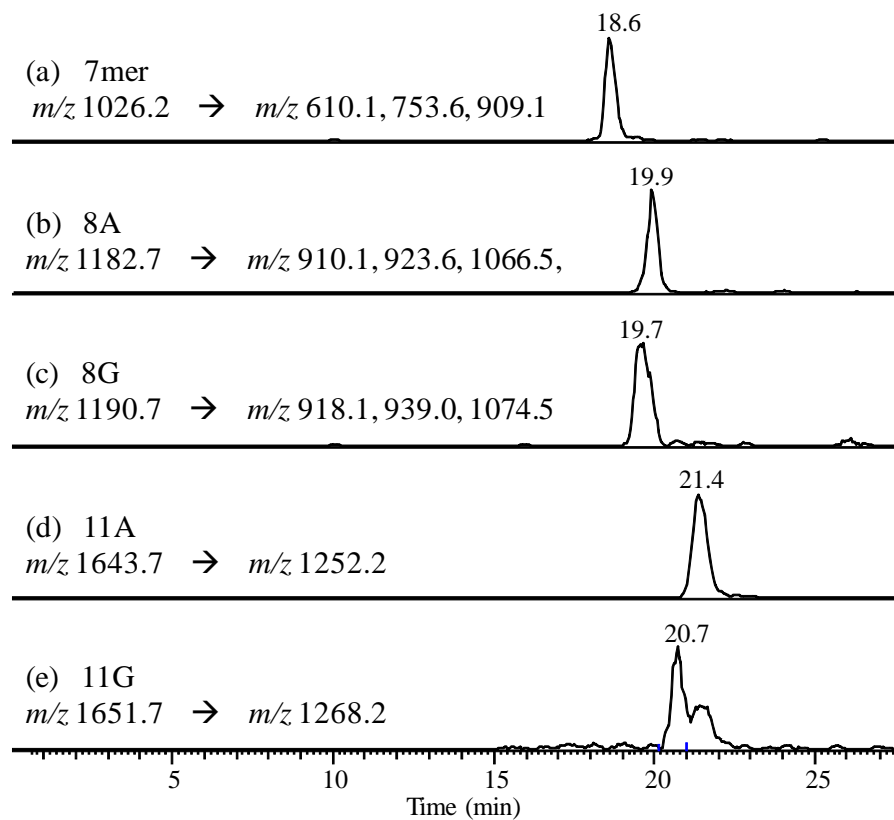
(C)



5' - GC AXG AGA ATT -3'			
3' - C TCT TAA -5'	7mer	1%	} dT Replication From pol κ
3' - CG TAC TCT TAA -5'	11A	99%	

Figure S9.

(A)



5' - GC AXG AGA ATT -3'
3' - C TCT TAA -5'
3' - AC TCT TAA -5'
3' - GC TCT TAA -5'
3' - CG TAC TCT TAA -5'
3' - CG TGC TCT TAA -5'

7mer	2%
8A	9%
8G	4%
11A	77%
11G	7%

***O*²-MdT
Replication From
Klenow fragment
exo⁻**

Figure S10.

(B)

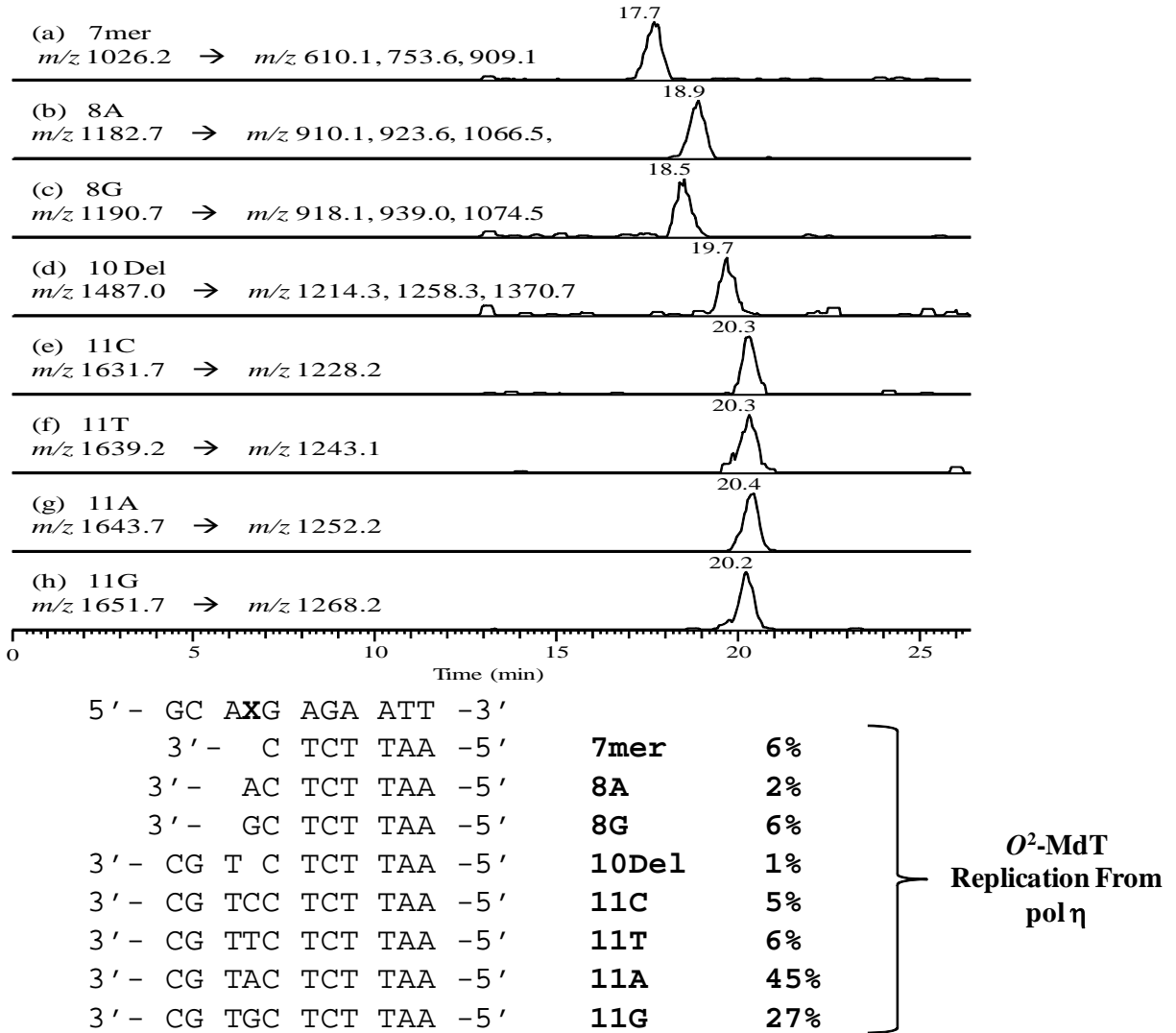
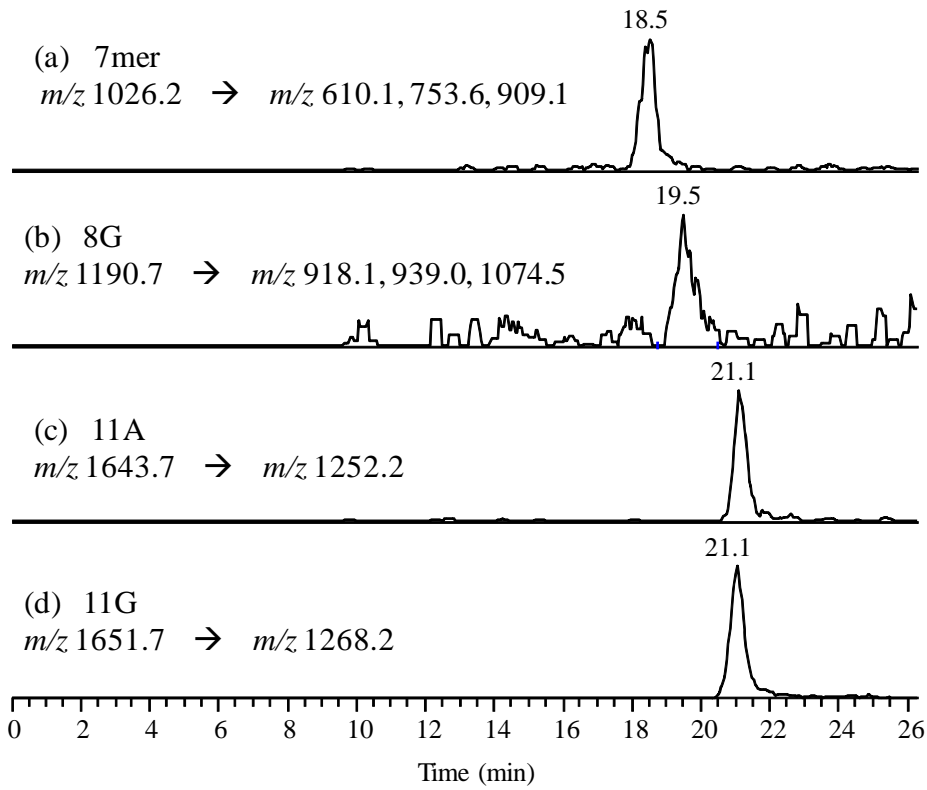


Figure S10.

(A)



5' - GC AXG AGA ATT -3'			
3' - C TCT TAA -5'	7mer	7%	} <i>O</i>⁴-MdT Replication From Klenow fragment exo'
3' - GC TCT TAA -5'	8G	5%	
3' - CG TAC TCT TAA -5'	11A	7%	
3' - CG TGC TCT TAA -5'	11G	80%	

Figure S11.

(B)

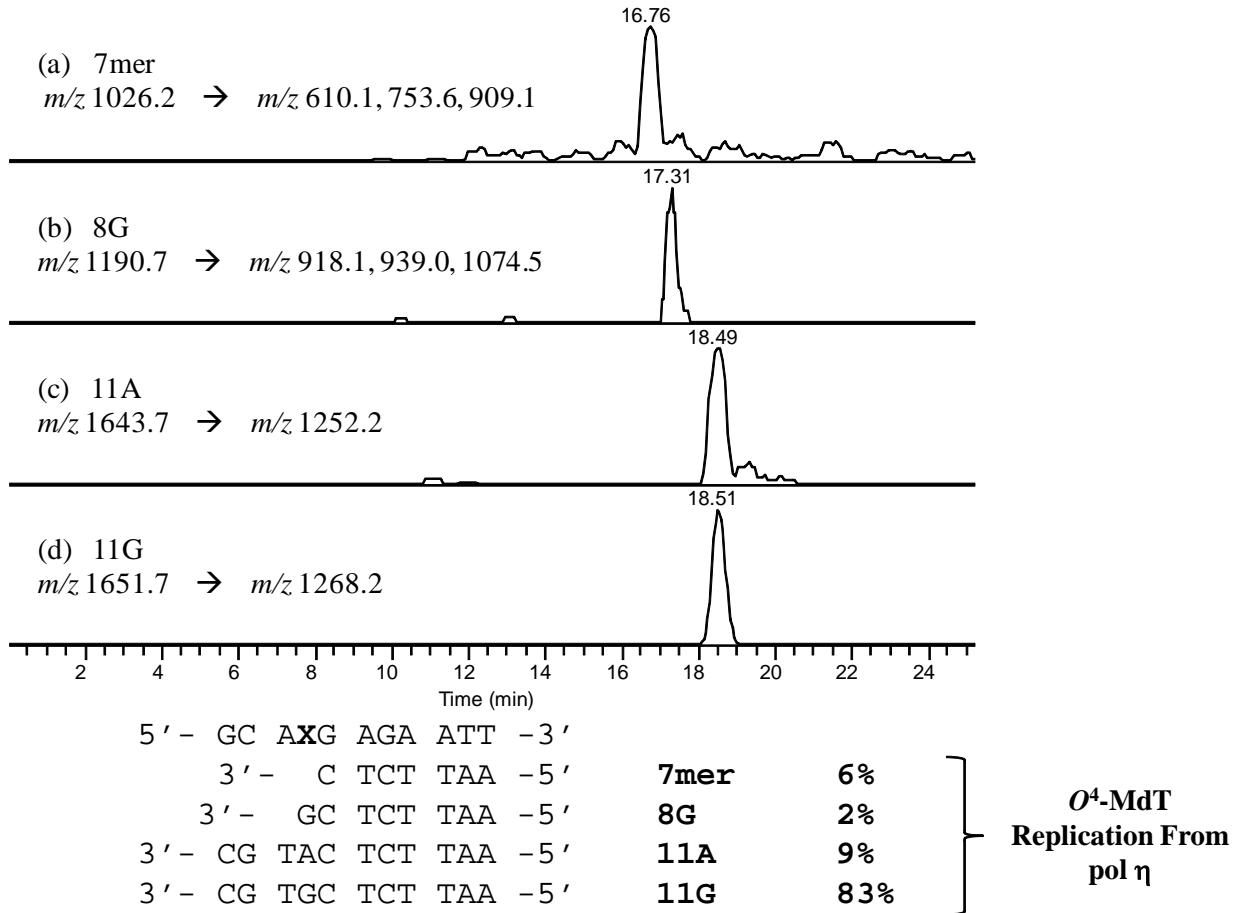
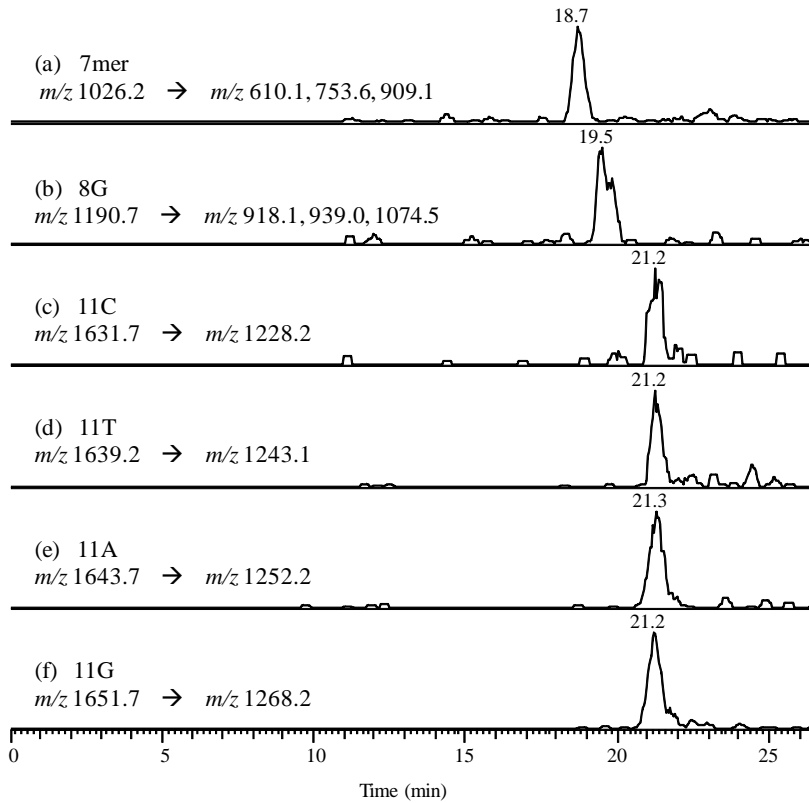


Figure S11.

(C)



5' - GC AXG AGA ATT -3'		
3' - C TCT TAA -5'	7mer	11%
3' - GC TCT TAA -5'	8G	18%
3' - CG TCC TCT TAA -5'	11C	2%
3' - CG TTC TCT TAA -5'	11T	3%
3' - CG TAC TCT TAA -5'	11A	8%
3' - CG TGC TCT TAA -5'	11G	58%

} ***O*⁴-MdT
Replication From
polκ**

Figure S11.

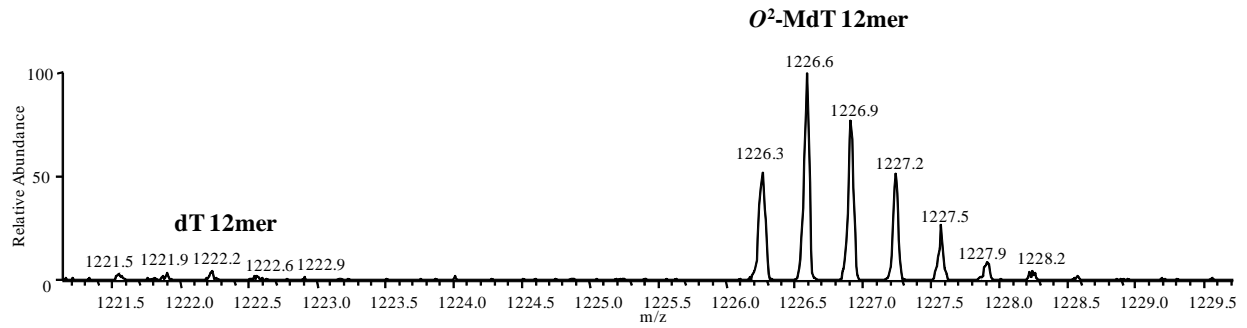
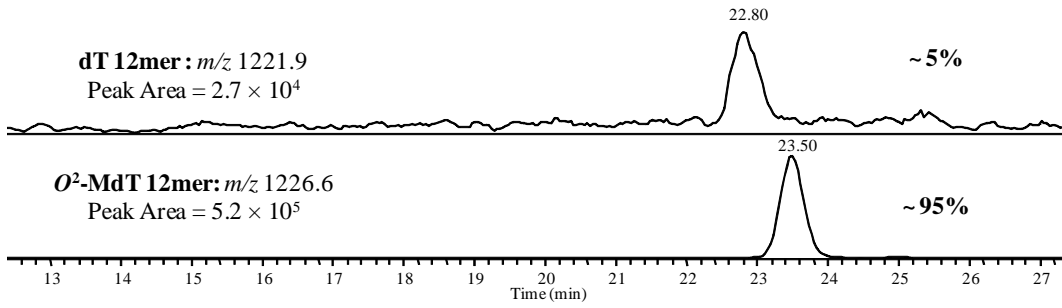


Figure S12.

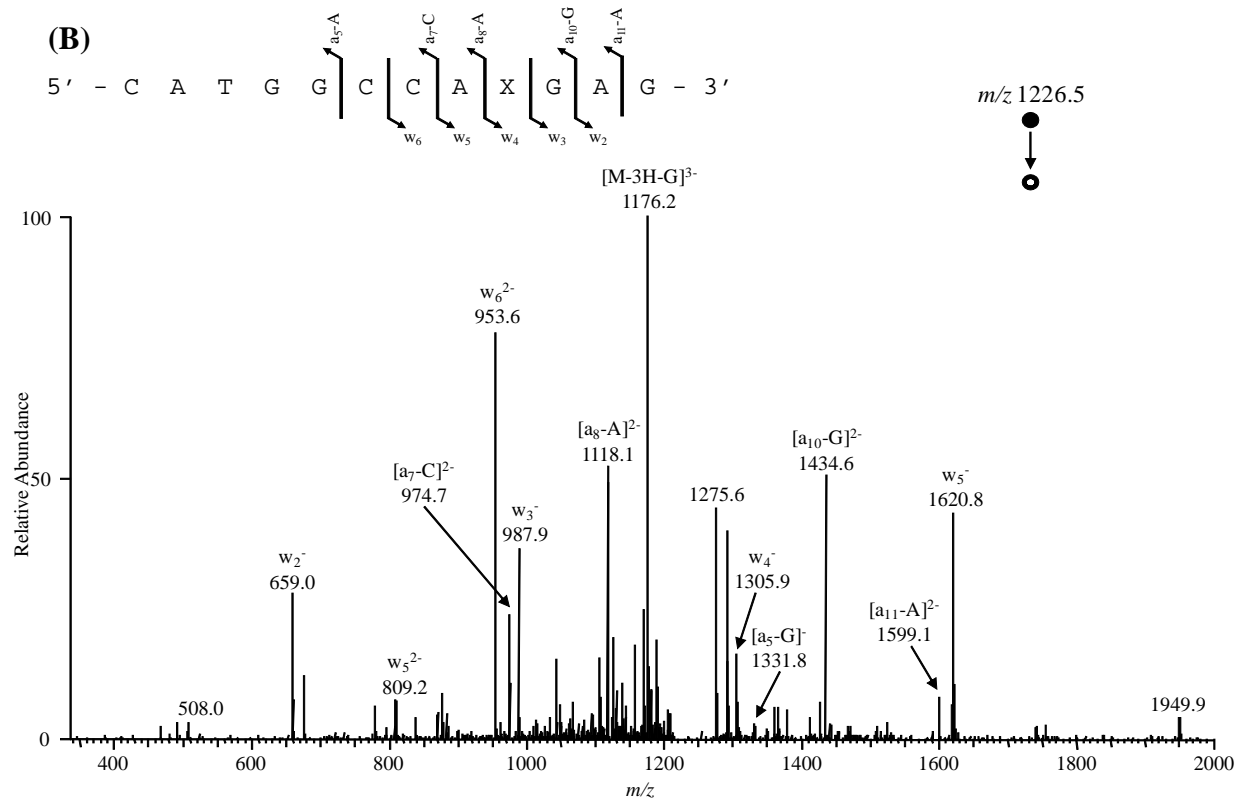
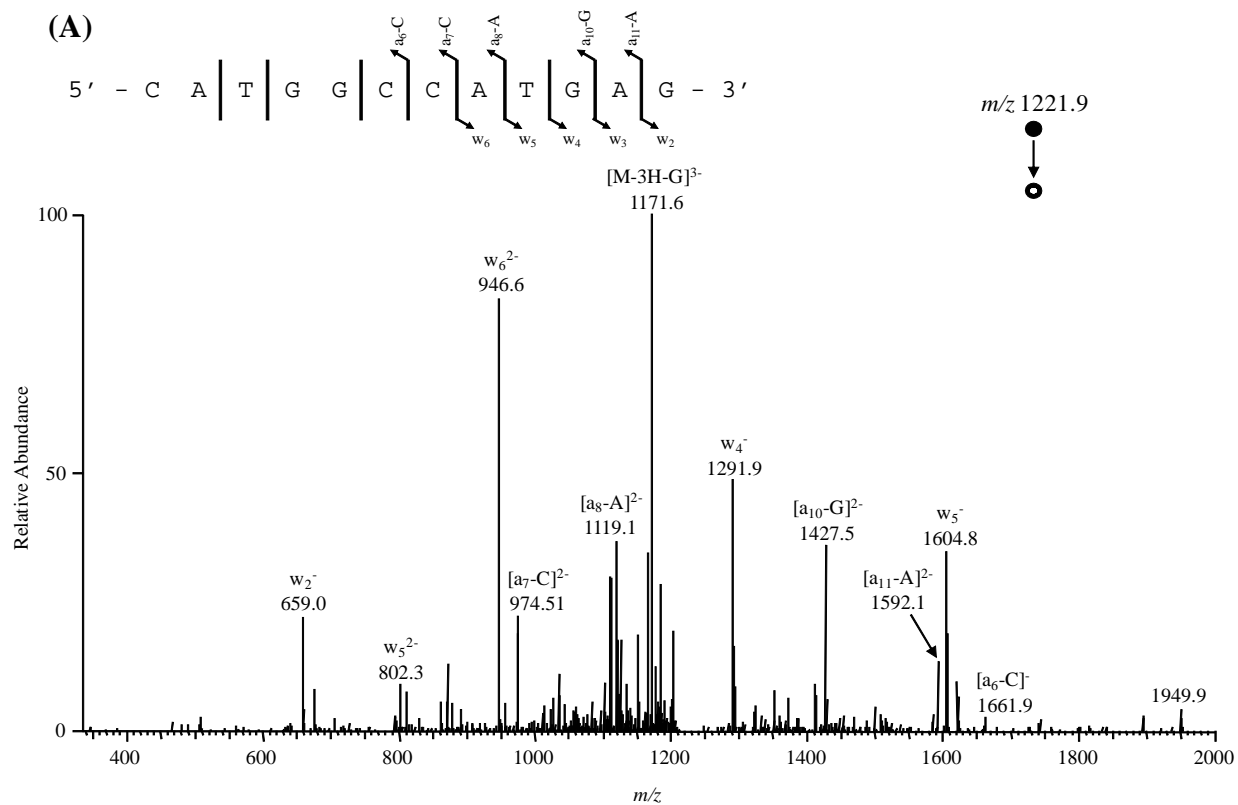
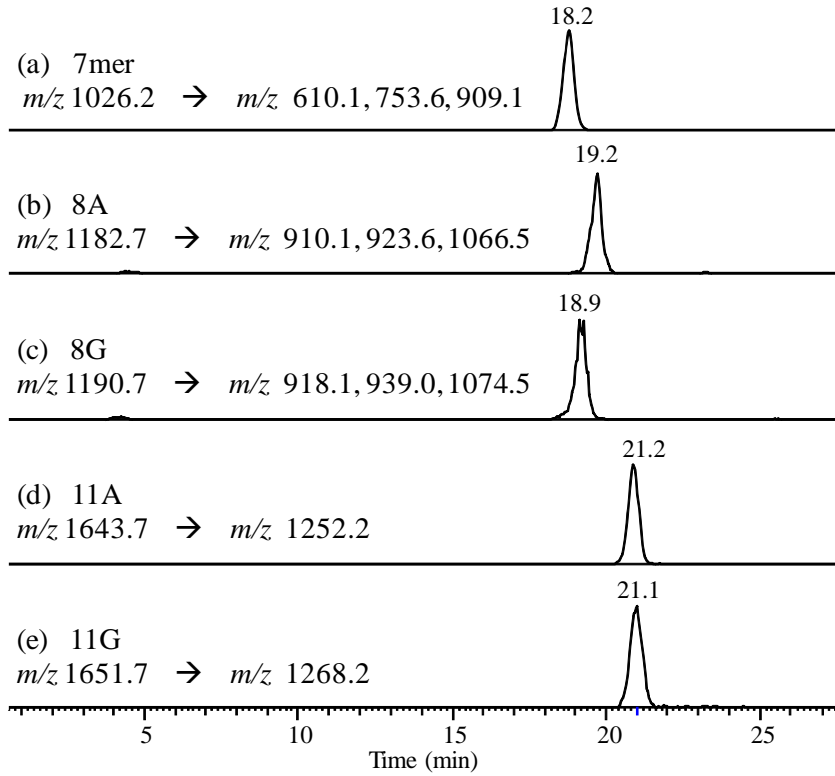


Figure S13

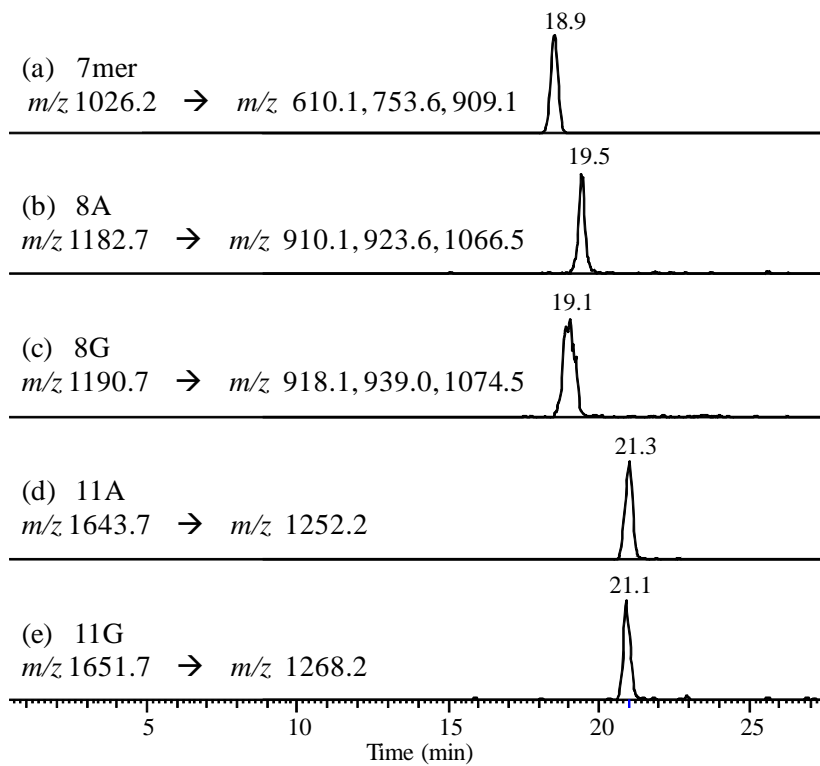
(A)



5' - GC AXG AGA ATT -3'			
3' - C TCT TAA -5'	7mer	5%	} <i>O</i>⁴-MdT Replication From pol η (low dNTPs)
3' - AC TCT TAA -5'	8A	3%	
3' - GC TCT TAA -5'	8G	8%	
3' - CG TAC TCT TAA -5'	11A	10%	
3' - CG TGC TCT TAA -5'	11G	73%	

Figure S14.

(B)

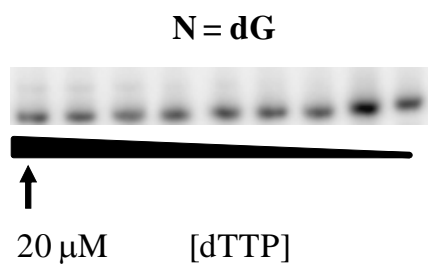
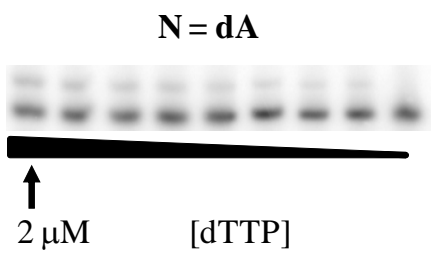


5' - GC AXG AGA ATT -3'			
3' - C TCT TAA -5'	7mer	26%	} <i>O</i>⁴-MdT Replication From pol η (6 hr)
3' - AC TCT TAA -5'	8A	3%	
3' - GC TCT TAA -5'	8G	7%	
3' - CG TAC TCT TAA -5'	11A	3%	
3' - CG TGC TCT TAA -5'	11G	62%	

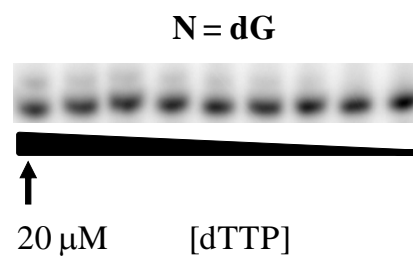
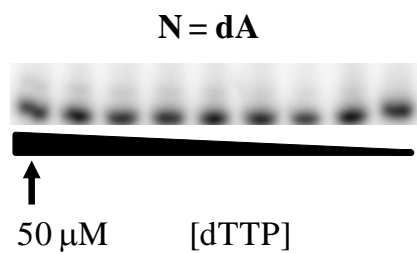
Figure S14.

Primer: 5'- pGCTAGGATCATAGAATTCTC [N] \downarrow dTTP
 Template: 3'- GATCCTAGTATCTTAAGAG [X] ACGGTACC-5'

(A) X = [dT]



(B) X = [*O*²-MdT]



(C) X = [*O*⁴-MdT]

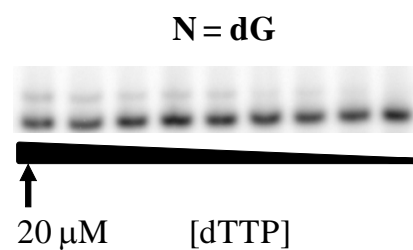
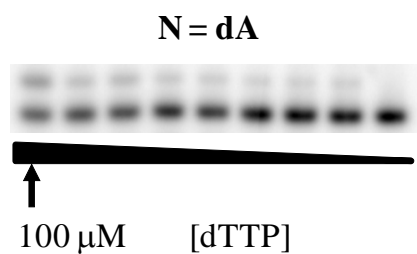


Figure S15

Name	Sequence	<i>O</i> ⁴ -MdT (low dNTPs)	<i>O</i> ⁴ -MdT (6 hr)
Yeast Polymerase η			
7mer	d(AATTCTC)	6	26
8mer	d(AATTCTCA)	3	3
8mer	d(AATTCTCG)	8	7
11A	d(AATTCTCATGC)	10	3
11G	d(AATTCTCGTGC)	73	62

Table S1.

dNTP	k_{cat} (min⁻¹)	K_m (μM)	k_{cat}/K_m (mM⁻¹ min⁻¹)	f_{ext}
Extension with dTTP				
dT:dATP	9.5 ± 0.4	0.56 ± 0.02	17	1
dT:dGTP	5.3 ± 0.1	2.2 ± 0.3	2.5	0.15
<i>O</i> ² -MdT:dATP	9.5 ± 0.4	7.8 ± 0.8	1.2	1
<i>O</i> ² -MdT:dGTP	13 ± 1	7.5 ± 0.5	1.7	1.4
<i>O</i> ⁴ -MdT:dATP	10 ± 1	26 ± 2	0.38	1
<i>O</i> ⁴ -MdT:dGTP	27 ± 2	11 ± 1	2	5.2

*The K_m and k_{cat} were average values based on three independent measurements

Table S2.