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## **Supporting Information**

## **Base-Resolution Analysis of 5-Hydroxymethylcytidine by Selective Oxidation and Reverse Transcription Arrest**

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DNA/RNA	Sequence	Figure
RNA1(X)	5' -AXA-3'	Fig. 2, S1-2
	$(\mathbf{X} = ^{hm5}C \text{ or } C)$	
RNA2(X)	5' -CACUXGCUUCCUCCAGAUGA-3'	Fig. 3, 4, S1, S3-6
	$(\mathbf{X} = ^{\mathrm{hm5}}\mathrm{C})$	
Primer DNA1	5' -Fluorescein-TCATCTGGAGGA-3'	Fig. 3, S6
Primer DNA2	5' -Fluorescein-TCATCTGGAGGAAGC-3'	Fig. S3
Primer DNA3	5' -Fluorescein-TCATCTGGAGGAAG-3'	Fig. S4, S6
Cleaved RNA	5' -GCUUCCUCCAGAUGA-3'	Fig. S5
		<b>D</b> ' <b>4</b>
Linker DNA	5' -rAppCTGTAGGCACCATCAAT/3ddC/-3'	F1g. 4
RT primer	5' -/Phos/AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Fig. 4, 5
	TGTAGATCTCGGTGGTCGC/SpC18/CACTCA/SpC18/TT	
	CAGACGTGTGCTCTTCCGATCTATTGATGGTGCCTAC	
	AG-3'	
PCR primers	5' -AATGATACGGCGACCACCGAGATCTACAC-3'	Fig. 4, 5
	5' -CAAGCAGAAGACGGCATACGAGAT/NNNNNN/GTGA	
	CTGGAGTTCAGACGTGTGCTCTTCCG-3'	
RNA3(X)	5' -GGGAGGUGAGAGUGAGAGUAUGUAUAGAAUUGA	Fig. S7
	UAUXGAAAUGAGUAGGUGAUGGAAGUGGUAGGUAA	
	GGGAA-3'	
	$(X = {}^{hm5}C, {}^{m5}C, or C)$	
RNA4	5' -GGGGUAGGAUGUGUGAUGAGAAA <sup>hm5</sup> CUUAUAAG	Fig. 5
	GAGUAAUGUGGGAUGUGUAGAGGAUUAGAUUAUGA	
	GGUAGAUUGUGAUAUGAAGUGGAGAGUGAUGAGUG	
	GUAAGGGAAUGAGUGGAAAUGA-3'	
RNA5	5' -GGGGUAUGAUGUAUGAGGAGAAACUUAUGAGGA	Fig. 5
	GUGAUGUGGGAUGUUGAGAAGAUUGAUUAAUGAGG	
	AGUAUUGUGAUAGUAAGGUAGAGGUGGUAGUAGGU	
	AAGGAGUAGAUGGGAAUGAA-3'	

Table S1. DNA/RNA sequences used in this paper.



**Fig. S1** HPLC traces and MALDI-TOF MS data of synthesized <sup>hm5</sup>C-containing oligonucleotides. Purified RNA1(<sup>hm5</sup>C) and RNA2(<sup>hm5</sup>C) was analyzed by HPLC (A and C) and MALDI-TOF-MS (B and D), respectively.



**Fig. S2** MALDI-TOF MS charts of HPLC-purified products derived from RNA1(<sup>hm5</sup>C) after 1-h incubation with peroxotungstate. The chromatogram of each peak was shown in Fig. 1(A).



**Fig. S3** RNA2(<sup>hm5</sup>C) was monitored by MALDI-TOF-MS after the incubation at 50 °C with peroxotungstate. Oxidized RNA2(<sup>hm5</sup>C) showed mass of <sup>th</sup>T-containing RNA2 (<sup>th</sup>T).



**Fig. S4** (A) RNA2 ( $X = {}^{hm5}C$  or  ${}^{th}T$ ) before or after peroxotungstate-oxidation was hybridized with primer DNA2 and reverse-transcribed in the presence of dATP, dGTP, dCTP, or dTTP. (B) Denaturing PAGE analysis of reverse-transcribed products. Incorporation of dNTPs into fluorescein-labeled primer DNA2 hybridized with template RNA2( ${}^{hm5}C$ ) or RNA2( ${}^{th}T$ ) was analyzed.



**Fig. S5** (A) The 14-nt fluorescein-labeled primer DNA3 was hybridized to 20-nt template RNA2( $X = h^{m5}C$  or  $h^{th}T$ ) and elongated using several reverse transcriptases. (B) Denaturing PAGE analysis of the reverse-transcribed product using several reverse transcriptases: AMV reverse transcriptase, M-MuLV transcriptase, WarmStart reverse-transcriptase, and SuperScript III transcriptase. 14, 15, 16, 20-nt oligonucleotides were used as a marker for truncated product.



Fig. S6 (A) After the oxidation, 15-nt RNA product may exist if oxidized RNA2 is cleaved at <sup>th</sup>T site.
(B) Denaturing PAGE analysis showed no cleavage in RNA2 after the oxidation with peroxotungstate in 5 hours. 15-nt RNA was used as a marker for cleavage product at the <sup>th</sup>T site.



**Fig. S7** Optimization of reverse-transcription condition to maximize truncation efficiency. 20-nt RNA2(<sup>th</sup>T) was hybridized with 12-nt primer DNA1 or 14-nt primer DNA3 and reverse-transcribed using SuperScript III RTase under several conditions. (A) Incubation temperature, (B) dNTP concentration, (C) DTT concentration, and (D) RTase amount were optimized.



**Fig. S8** (A) Denaturing PAGE analysis of immunoprecipitated C, <sup>m5</sup>C, or <sup>hm5</sup>C-containing RNA3 using polyclonal anti-<sup>5hm</sup>C antibody (rabbit) with 150 mM sodium chloride in the buffer. (B) The gray value of the gel bands of precipitated RNA3 was analyzed.



**Fig. S9** Denaturing PAGE analysis of <sup>hm5</sup>C-containing RNA3 before and after the oxidation with peroxotungstate in 5 hours.



**Fig. S10** Peak value and read coverage tracks of RNA4. (A) Peak values around <sup>hm5</sup>C position (27<sup>th</sup> position) in RNA4 showing the highest peak value at the <sup>hm5</sup>C position. (B) Read coverage tracks and alignment tracks of RNA4 (top) before and (bottom) after the peroxotungstate-mediated oxidation visualized using Integrative Genomics Viewer (IGV). After the oxidation, the coverage was decreased at the <sup>hm5</sup>C position (the center C position), suggesting truncation occurred at the site.



Fig. S12 <sup>13</sup>C NMR spectrum of nucleoside 2 in CDCl<sub>3</sub>.



Fig. S13 COSY NMR spectrum of nucleoside 2 in CDCl<sub>3</sub>.



Fig. S14 ESI-MS spectrum of nucleoside 2.



Fig. S15 <sup>1</sup>H NMR spectrum of nucleoside 3 in DMSO-d<sub>6</sub>.



Fig. S16 <sup>1</sup>H NMR spectrum of nucleoside 3 in DMSO-d6 with a drop of  $D_2O$ .



Fig. S17 COSY NMR spectrum of nucleoside 3 in DMSO-d<sub>6</sub>.



Fig. S18<sup>13</sup>C NMR spectrum of nucleoside 3 in DMSO-d<sub>6</sub>.



Fig. S19 ESI-MS spectrum of nucleoside 3.



Fig. S20 <sup>1</sup>H NMR spectrum of nucleoside 4 in CDCl<sub>3</sub>.



Fig. S21 <sup>13</sup>C NMR spectrum of nucleoside 4 in CDCl<sub>3</sub>.



Fig. S22 COSY NMR of nucleoside 4 in CDCl<sub>3</sub>.



Fig. S23 ESI-MS spectrum of nucleoside 4.



Fig. S24 <sup>1</sup>H NMR spectrum of nucleoside 5 in CDCl<sub>3</sub>.



Fig. S26 COSY NMR of nucleoside 5 in DMSO-d<sub>6</sub>.



Fig. S27 ESI-MS spectrum of nucleoside 5.



Fig. S28 <sup>1</sup>H NMR spectrum of nucleoside 6 in CDCl<sub>3</sub>.



Fig. S29<sup>13</sup>C NMR spectrum of nucleoside 6 in CDCl<sub>3</sub>.



Fig. S30 ESI-MS spectrum of nucleoside 6.



Fig. S31 <sup>1</sup>H NMR spectrum of phosphoramidite 7 in CDCl<sub>3</sub>.



Fig. S32 <sup>31</sup>P NMR spectrum of nucleoside 7 in CDCl<sub>3</sub>.



Fig. S33 ESI-MS spectrum of nucleoside 7.