

Supporting Information

for

**Location analysis of 8-oxo-7,8-dihydroguanine in DNA by polymerase-mediated
differential coding**

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Table S1. The sequences of the oligodeoxynucleotides used in this study.

ODNs	Sequence (from 5'to 3')
FAM-primer-1	5'-FAM-CGCATAACCCTAACC-3'
DNA-G	5'-GCGTATTGGGATTGGGATTGACACG-3'
DNA-T	5'-GCGTATTGGGATTGGTATTGACACG-3'
DNA-A	5'-GCGTATTGGGATTGGAATTGACACG-3'
DNA-C	5'-GCGTATTGGGATTGGCATTGACACG-3'
DNA-OG	5'-GCGTATTGGGATTGG(OG)ATTGACACG-3'
Cy3-primer	5'-Cy3-TAACCCCTAACCCCTAACC-3'
Cy5-primer	5'-Cy5-CCTAACCCCTAACCCCTAAC-3'
FAM-primer-2	5'-FAM-CCCTAACCCCTAACCCCTAA-3'
T-DNA-1	5'-GTTA GGG TAGGGTTAGGGTTAGGG-3'
T-DNA-2	5'-GTTA(OG) GGT TAGGGTTAGGGTTAGGG-3'
T-DNA-3	5'-GTTA G(OG) GTTAGGGTTAGGGTTAGGG-3'
T-DNA-4	5'-GTTA GG(OG) TTAGGGTTAGGGTTAGGG-3'
L-DNA-G	5'- GCCCAAGTGCTGAGGCTGATAATAATCGGGGCGGCGATCAGACAGCCCCGGTGTGGGAAAT CGTCCGCCCCGGTCTCCCTAAGTCCCCGAAGTCGCCTCCCACTTTTGGT G ACTGCTTGTAT TTACATGCAGinvertedT-3'
L-DNA-OG1	5'- GCCCAAGTGCTGAGGCTGATAATAATCGGGGCGGCGATCAGACAGCCCCGGTGTGGGAAAT CGTCCGCCCCGGTCTCCCTAAGTCCCCGAAGTCGCCTCCCACTTTTGGT(OG)ACTGCTTGTAT ATTACATGCAGinvertedT-3'
L-DNA-OG2	5'- GCCCAAGTGCTGAGGCTGATAATAATCGGGGCGGCGATCAGACAGCCCCGGTGTGGGAAAT CGTCCGCCCCGGTCTCCCTAAGTCCCCGAAGTC(OG)CCTCCCACTTTTGGT(OG)ACTGCTTGT TTATTACATGCAGinvertedT-3'
L-DNA-OG3	5'- GCCCAAGTGCTGAGGCTGATAATAATCGGGGCGGCGATCAGACAGCCCCGGTGTGGGAAAT CGTCCGCCCCGGTCTCCCTAAGTCCCC(OG)AAGTC(OG)CCTCCCACTTTTGGT(OG)ACTGC TTGTTATTACATGCAGinvertedT-3'
L-primer	5'-TGAGCAGATGTGTGACGGCTACACTGCATGTAAATAACAAGC-3'
PCR reverse primer	5'-GCCCAAGTGCTGAGGCTGATAA-3'
PCR forward primer	5'-TGAGCAGATGTGTGACGGCTAC-3'
NN-OG-NN	5'-CCAGATGACGACTGGCACTAATGNN(OG)NNTGCTGCGTGGATCGACATCGAGinvertedC-3'
NN-L-Primer	5'-TGAGCAGATGTGTGACGGCTACGCTCGATGTCGATCCACG-3'
NN-F-Primer	5'-CCAGATGACGACTGGCAC-3'
NN-R-Primer	5'-TGAGCAGATGTGTGACGGCTAC-3'

Table S2. PCR primers used for the single-base resolution analysis of OG in HeLa genomic DNA by sequencing.

Gene / Amplified region	Sequence (from 5' to 3')
<i>VEGFA</i> / chr6: 43772151- 43772344	<i>VEGFA</i> -L (Primer-L): TGAGCAGATGTGTGACCACCGCCACGACTTCTGACAGTGA <i>VEGFA</i> -F: TCTCCAGACCCTACCTCTGC <i>VEGFA</i> -R: TGAGCAGATGTGTGACCACC
<i>TP53</i> / chr17: 7686438 -7686641	<i>TP53</i> -L (Primer-L): GAGCAGATGTGTGACGGCTAGCAGCTCACTATTCAACCGA <i>TP53</i> -F: TGGGGCACACCATTCAAAGA <i>TP53</i> -R: GAGCAGATGTGTGACGGCTA
<i>KRAS</i> / chr12: 25248470 - 25248719	<i>KRAS</i> -L (Primer-L): GGTTAGAGCAGATGTGACGCCCTCCCAGCCCATGATCTTC <i>KRAS</i> -F: GAGGGGTCGTTAAGGCCAAA <i>KRAS</i> -R: GGTTAGAGCAGATGTGACGC

Table S3. Steady-state kinetics for primer extension with dATP or dCTP opposite G- or OG-containing DNA template using different DNA polymerases.

DNA polymerase	dNTP	DNA template	$V_{\max}$ (% min ⁻¹)	K_M (μM)	$V_{\max}/K_M$ (min ⁻¹ μM ⁻¹)
<i>Bsu</i>	dATP	DNA-G	14.5 ± 2.3	178.6 ± 4.9	0.8 × 10 ⁻³
	dATP	DNA-OG	25.1 ± 2.4	9.2 ± 0.6	27.3 × 10 ⁻³
	dCTP	DNA-G	42.2 ± 0.6	1.8 ± 0.1	234.4 × 10 ⁻³
	dCTP	DNA-OG	27.8 ± 2.3	107.5 ± 6.3	2.6 × 10 ⁻³
<i>Tth</i>	dATP	DNA-G	5.4 ± 0.5	228.3 ± 15.4	0.2 × 10 ⁻³
	dATP	DNA-OG	6.2 ± 0.6	275.8 ± 18.2	0.2 × 10 ⁻³
	dCTP	DNA-G	50.4 ± 2.6	2.5 ± 0.3	201.6 × 10 ⁻³
	dCTP	DNA-OG	29.7 ± 1.4	174.3 ± 23.5	1.7 × 10 ⁻³

$V_{\max}$, the maximum rate of the enzyme reaction.

K_M , the Michaelis constant.

Figure S1. Steady-state kinetics for primer extension with dATP opposite G- or OG-containing DNA template using different DNA polymerases.

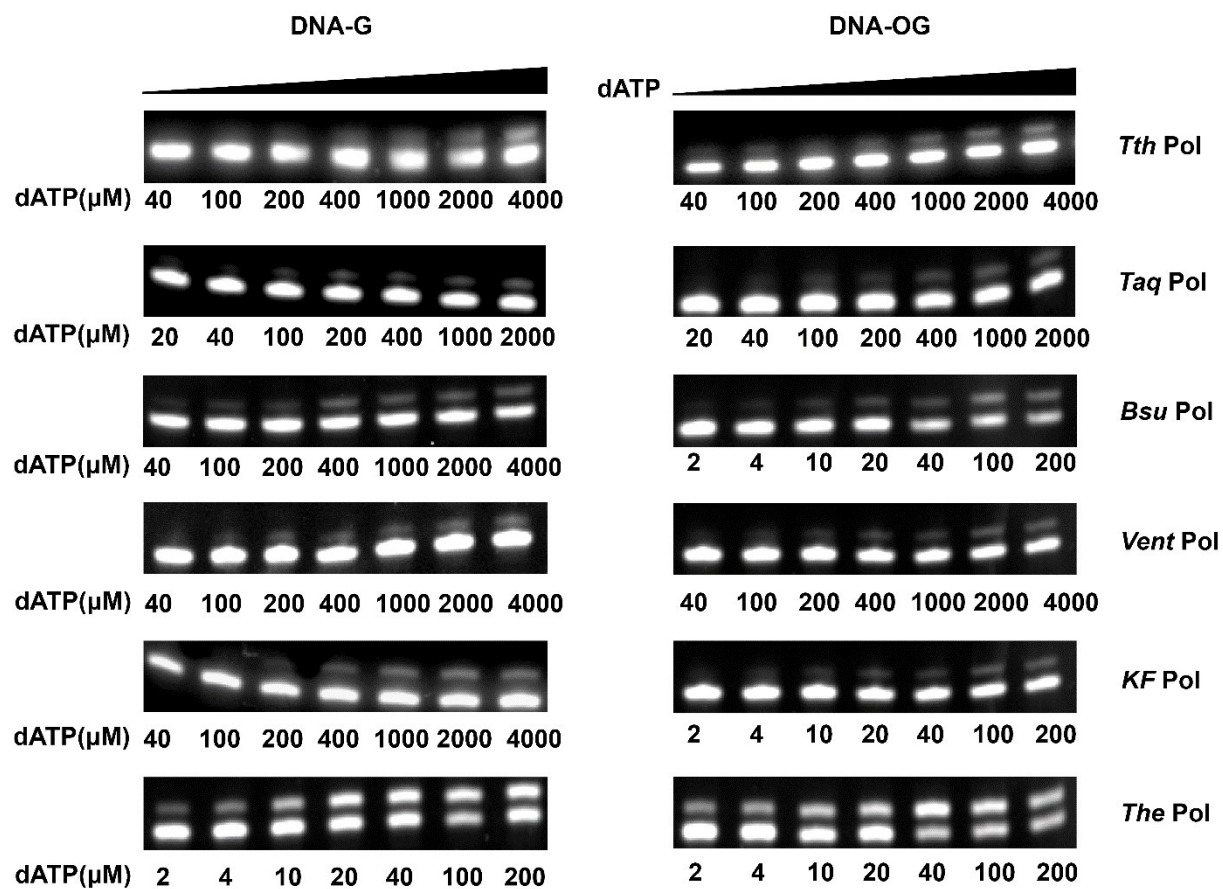


Figure S2. Steady-state kinetics for primer extension with dATP or dCTP opposite G- or OG-containing DNA template using different DNA polymerases.

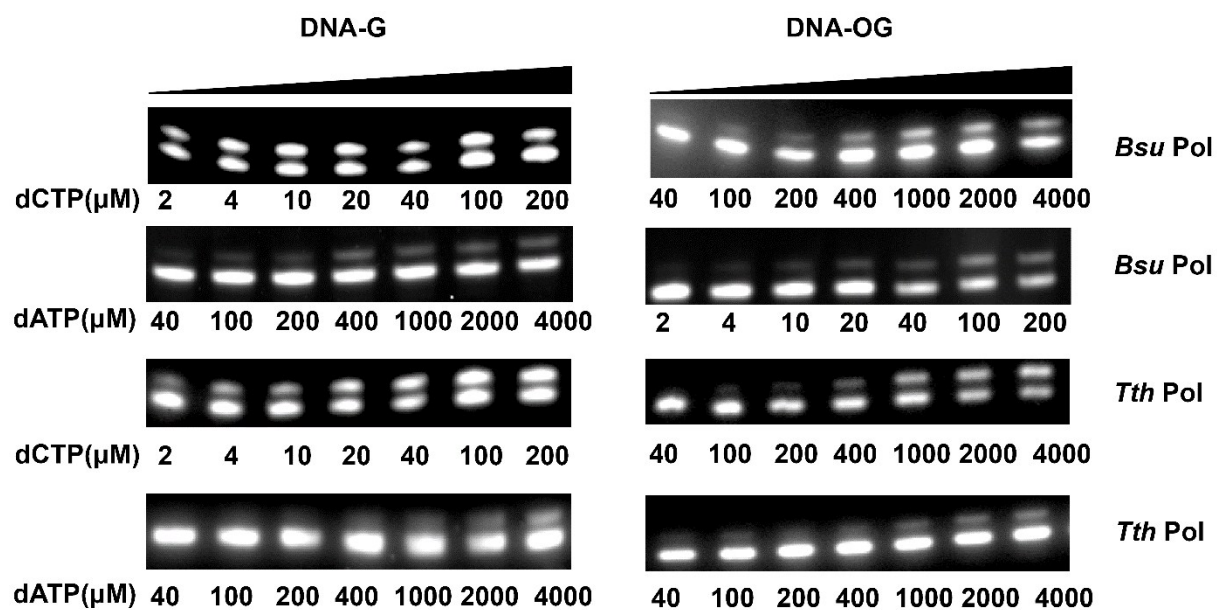


Figure S3. Four DNA templates (DNA-A, DNA-T, DNA-G and DNA-C, detailed sequence information can be found in Table S1 in Supporting Information) with a single site that has different nucleobases (A, T, G or C) were used to perform the primer extension assay by *Bsu* polymerase using dATP as the substrate. The reaction products were analyzed by 20% denaturing PAGE.

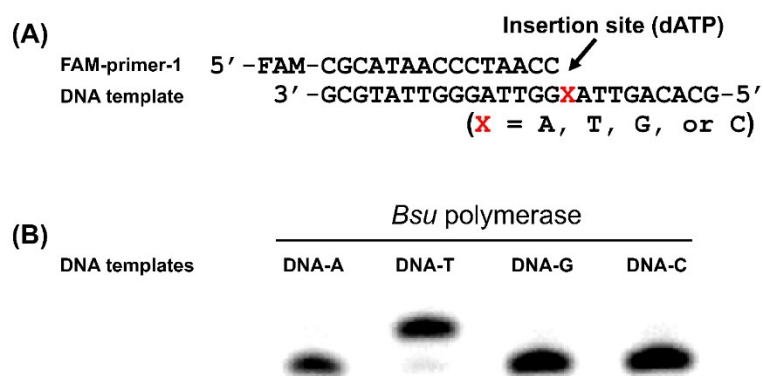


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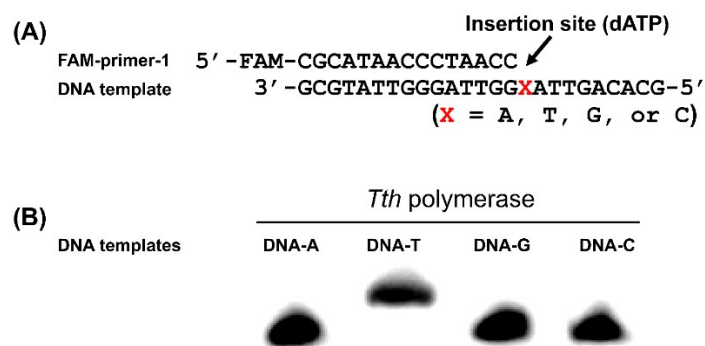


Figure S5. Single nucleotide primer extension reaction by *Tth* polymerase using the mixture of DNA-G and DNA-T with the percentage of DNA-T ranging from 0% to 10%.

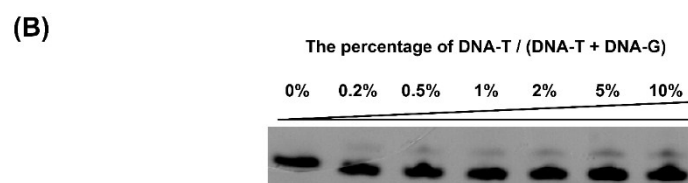
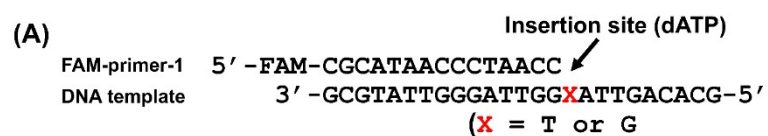


Figure S6. The single nucleotide primer extension reaction by *Tth* polymerase using 5 µg HeLa DNA and different fluorophores-labeled primers (5 pmol for each) that target different guanosine sites in telomeric DNA.

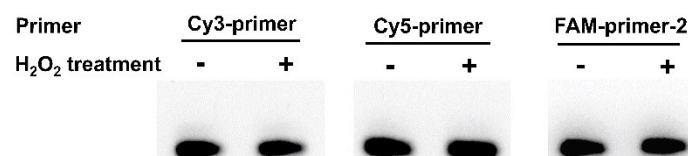


Figure S7. Single-base resolution analysis of multiple OG sites in DNA by sequencing. The primer extension products by *Bsu* Pol with DNA templates of L-DNA-G, L-DNA-OG1 (one OG site), L-DNA-OG2 (two OG sites), or L-DNA-OG3 (three OG sites). The detailed sequence information of DNA templates can be found in Table S1 in Supporting Information.

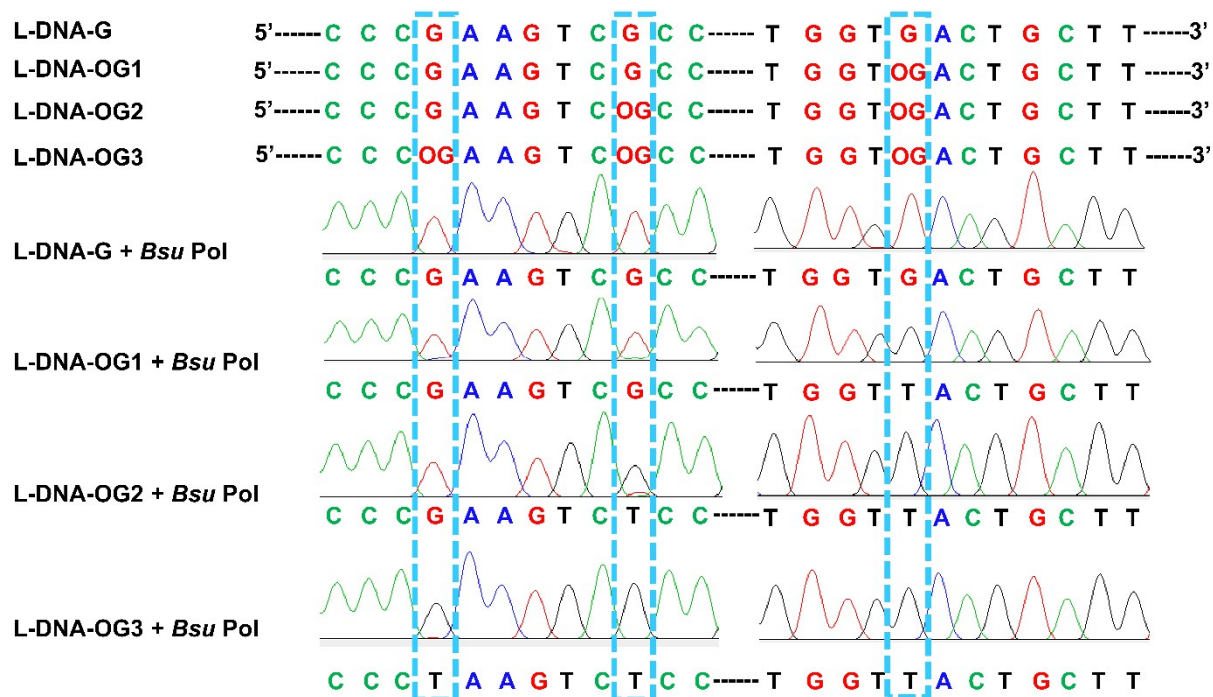


Figure S8. Single-base resolution analysis of multiple OG sites in DNA by sequencing. The primer extension products by *Tth* Pol with DNA templates of L-DNA-G, L-DNA-OG1 (one OG site), L-DNA-OG2 (two OG sites), or L-DNA-OG3 (three OG sites). The detailed sequence information of DNA templates can be found in Table S1 in Supporting Information.

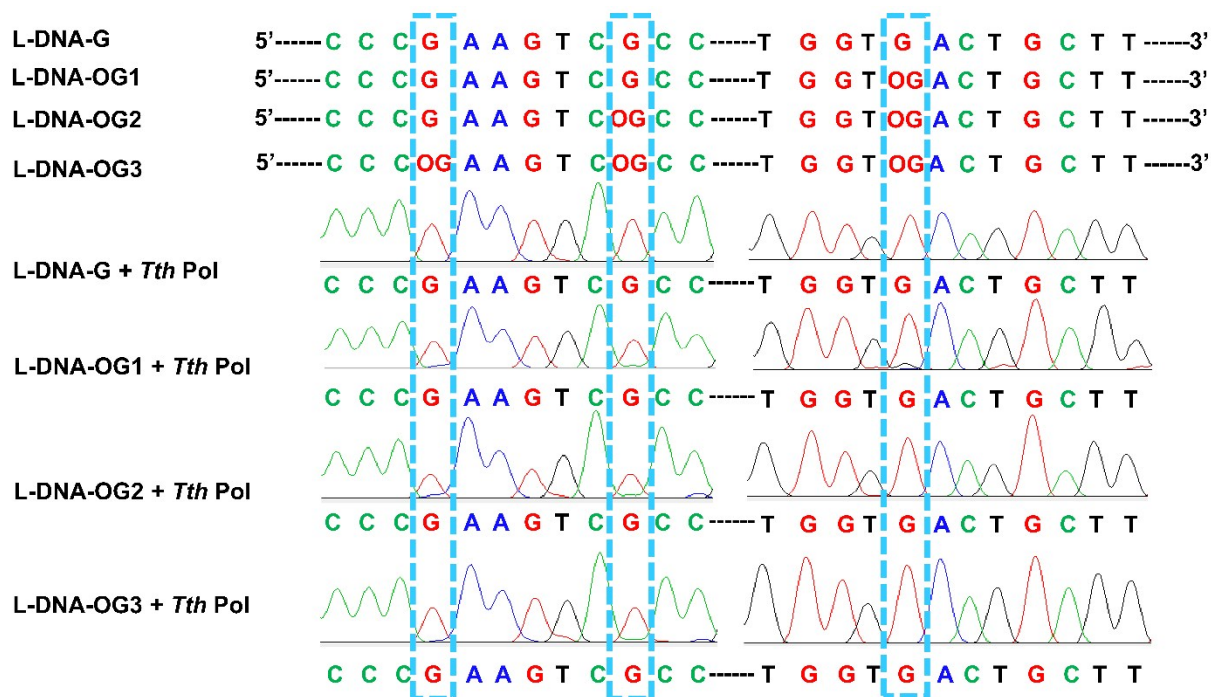


Figure S9. Quantitative evaluation of the level of OG in DNA using various ratios of L-DNA-OG1/L-DNA-G (0%, 0.1%, 1%, 10%, 20%) as the DNA template by high-throughput sequencing.

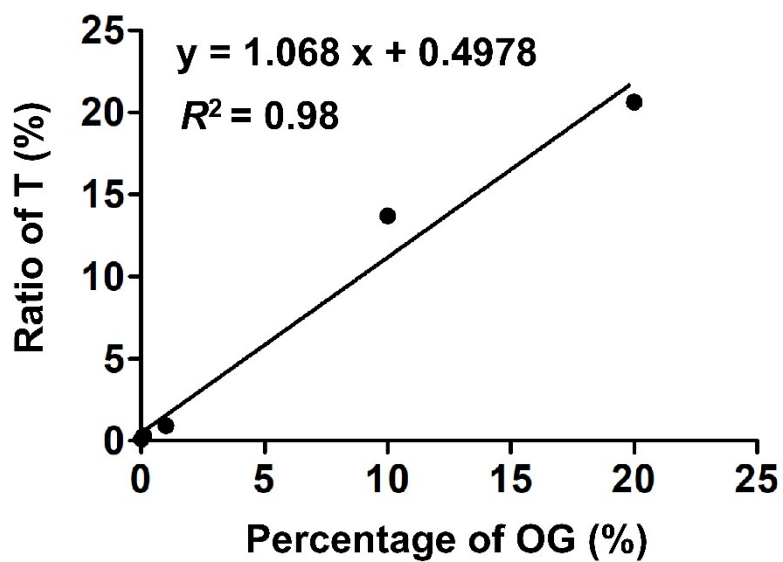


Figure S10. Schematic illustration of the procedure for the library construction.

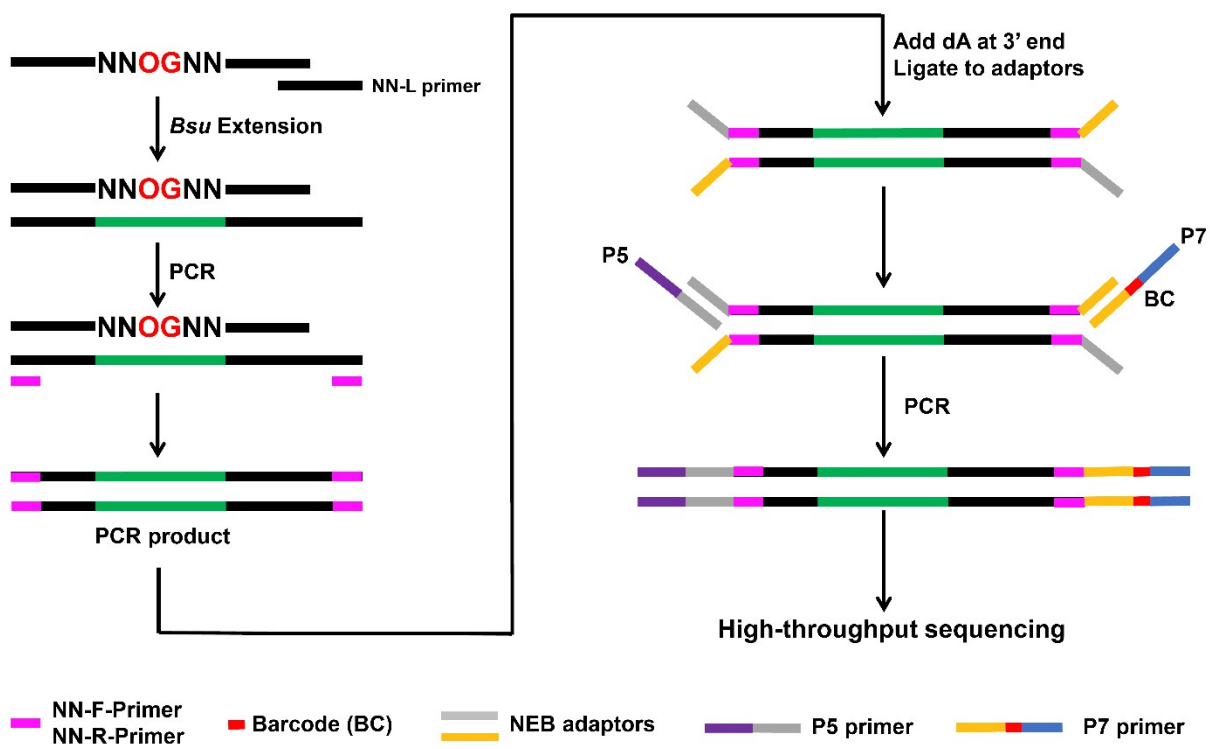


Figure S11. Schematic illustration of the analysis of OG in genomic DNA of HeLa cells. HeLa genomic DNA was denatured and annealed with the corresponding extension primers (Primer-L, Table S2 in Supporting Information). *Bsu* Pol or *Tth* pol was added for the primer extension. The extension product was purified as template for PCR amplification and then subjected to Sanger sequencing.

