## **Supplementary Information**

# Element Coding Based Accurate Evaluation of CRISPR/Cas9 Initial Cleavage

Jianyu Hu, <sup>a</sup> Rui Liu, <sup>b</sup> Jing Zhou<sup>a</sup> and Yi Lv<sup>a, b</sup>\*

<sup>a</sup> Analytical & Testing Center, Sichuan University, Chengdu 610064, China.

<sup>b</sup> Key Laboratory of Green Chemistry & Technology, Ministry of Education, College of Chemistry,

Sichuan University, Chengdu 610064, China

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#### Table S1. Oligonucleotides sequence

Primer	Sequence	Modification
ntDNA	ATATATTAGCTCATCGGGAGAACACACACT <b>TTTT</b> A TGGAGTCGAGCTCG	
ntDNA-1	ATATATTAGCTCATCGGGAGAACACACAC <b>TTTT/iC</b> HCHdT/ATGGAGTCGAGCTCG	Int CHCH-dT
ntDNA-2	ATATATTAGCTCATCGGGAGAACACACAC <b>TTTT/iCH</b> CHdT/TATGGAGTCGAGCTCG	Int CHCH-dT
ntDNA-3	ATATATTAGCTCATCGGGAGAACACACAC <b>TTT/iCHC</b> HdT/TTATGGAGTCGAGCTCG	Int CHCH-dT
ntDNA-4	ATATATTAGCTCATCGGGAGAACACACAC <b>TT/iCHCH</b> dT/TTTATGGAGTCGAGCTCG	Int CHCH-dT
ntDNA-5	ATATATTAGCTCATCGGGAGAACACACACT/iCHCHd T/TTTTATGGAGTCGAGCTCG	Int CHCH-dT
ntDNA-6	ATATATTAGCTCATCGGGAGAACACACAC/ <b>iCHCHdT</b> / <b>TTTTT</b> ATGGAGTCGAGCTCG	Int CHCH-dT
biotin-tDNA-SH	CTCGACTCCAT <b>AAAAAAA</b> GTGTGTGTGTTCTCCCGAT GAGCTAATATAT	3`SH C6 5`Biotin
sgRNA	GGAGAACACACACUUUUUUAGAGCUAGA AAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAA CUUGAAAAAGUGGCACCGAGUCGGUGCUU	
Primer 1		
(T7 promoter contained)	TAATACGACTCACTATAGG <u>GGAGAACACACACTTTT</u> <u>TTA</u> GTTTTAGAGCTAGAAATAGC	
Primer 2 (Reverse)	AAGCACCGACTCGGTGCCTCTTTTTCAAGTTGATAA CGGACTAGCCTTATTTTAACTTGCTATTTCTAGCTC TAAAAC	
M-1	GGAGAACACACUUUUUUCG	
M-2	GGAGAACACACUUUUUCAG	
M-3	GGAGAACACACUUUUCUAG	
M-4	GGAGAACACACUUUCUUAG	
M-5	GGAGAACACACUUCUUUAG	
M-6	GGAGAACACACUCUUUUAG	
M-7	GGAGAACACACCUUUUUAG	
M-8	GGAGAACACACAAUUUUUUAG	
M-9	GGAGAACACACCCUUUUUUAG	
M-10	GGAGAACACAAACUUUUUUAG	

M-11	GGAGAACACCCACUUUUUUAG
M-12	GGAGAACAACACUUUUUUAG
M-13	GGAGAACCCACACUUUUUUAG
M-14	GGAGAAAACACACUUUUUUAG
M-15	GGAGACCACACUUUUUUAG
M-16	GGAGCACACACUUUUUUAG
M-17	GGACAACACACUUUUUUAG
M-18	GGCGAACACACUUUUUUAG
M-19	GCAGAACACACUUUUUUAG
19'-1	GCAGAACACACUUUUUUAG
19'-2	GCCGAACACACUUUUUUAG
19'-3	GCCCAACACACUUUUUUAG
19'-4	GCCCCACACACUUUUUUAG
18'-1	GGCGAACACACUUUUUUAG
18'-2	GGCCAACACACUUUUUUAG
18'-3	GGCCCACACACUUUUUUAG
18'-4	GGCCCCCACACUUUUUUAG
17'-1	GGACAACACACUUUUUUAG
17'-2	GGACCACACACUUUUUUAG
17'-3	GGACCCCACACUUUUUUAG
17'-4	GGACCCAACACUUUUUUAG

### Table S2. Operating conditions of ICPMS

Parameters	Values	
La (m/z)	138.906	
Ce (m/z)	139.905	
Pr (m/z)	140.907	
Eu (m/z)	152.929	
Tb (m/z)	158.925	
Ho (m/z)	164.93	
Tm (m/z)	168.934	
ICP RF Power (W)	1300	
Plasma Gas Flow (L/min)	18	
Auxiliary Gas Flow (L/min)	1.20	
Nebulizer Gas Flow (L/min)	0.94	
Deflector Voltage (V)	11.75	
Pulse Stage Voltage (V)	1050	
Analog Stage Voltage (V)	1825	
Sample Uptake Rate (mL/min)	0.25	
Resolution	2060	
Dwell Time (µs)	50	
Detecting Time (s)	10	

Element	Isotope	Mass	Abundance	Interferences
La	La 138	137.907	0.090	138Ba, 138Ce
	La 139	138.906	99.910	
Ce	Ce 136	135.907	0.185	136Ba, 136Xe
	Ce 138	137.906	0.251	137Ba, 138La
	Ce 140	139.905	88.450	
	Ce 142	141.909	11.114	142Nd
Pr	Pr 141	140.907	100.000	
Eu	Eu 151	150.92	47.810	135BaO
	Eu 153	152.929	<b>52.1</b> 90	137BaO
Tb	Tb 159	158.925	100.000	143NdO
Но	Ho 165	164.93	100.000	149SmO
Tm	Tm169	168.934	100.000	153EuO

Figure S1. Isotope abundance and interferences of selected elements

Figure S2. Chemical structure of [La]-ntDNA.



Gray part: thymine mononucleotide

Orange part: alkyne modification

Purple part: N<sub>3</sub>-DOTA-[La]



Figure S4. The ESI-MS results of six N<sub>3</sub>-DOTA-[Ln].



**Figure S5.** The MADI-TOF-MS characterization of original ssDNA (blue), DOTA modified ssDNA (green) and final lanthanide labeled ssDNA (yellow), respectively.



Figure S6. The EDS result of EC-CRISPR probes captured by SA-MBs.



1. EDS spectrum of naked SA-MBs.

2. EDS spectrum of EC-CRISPR probes captured by SA-MBs.



Control groups in Cas9/sgRNA concentration study: (a) Neither Cas9 nor sgRNA was introduced. (b) Only Cas9 protein was introduced. (c) Cas9 protein and non-specific sgRNA. Control groups in reaction temperature study: (d) Neither Cas9 nor sgRNA was introduced. (e) Only Cas9 protein was introduced. (f) Cas9 protein and non-specific sgRNA. All experimental conditions keep the same as Figure 3.

Figure S8. PAGE image of CRISPR/Cas9 cleavage products in varies Cas9/sgRNA concentrations.



Reaction conditions: Cas9/sgRNA pre-incubated for 30 min (0.3, 3, 30, 300 nM, 3 µM and 30 µM), followed by introducing 30 nM mixed biotin-dsDNA substrate. Then incubated for 2h at 37 °C. 3'-terminal biotin labeled tDNA was removed by SA-MBs after heat to TM.

Figure S9. PAGE image of CRISPR/Cas9 cleavage products in varies temperature.



Reaction conditions: 300 nM Cas9/sgRNA pre-incubated for 30 min, followed by introducing 30 nM mixed biotin-dsDNA substrate. Then incubated for 2h at 15, 25, 30, 33, 37, 40 and 45 °C. 3'-terminal biotin labeled tDNA was removed by SA-MBs after heat to TM.

Figure S10. PAGE image of CRISPR/Cas9 cleavage products with multiple mismatches.



Reaction conditions: 300 nM mismatch sgRNA containing mismatch base was pre-incubated with Cas9 for 30 min, followed by introducing 30 nM mixed bioting-dsDNA substrate. Then incubated for 2h at 37 °C. 3'-terminal biotin labeled tDNA was removed by SA-MBs after heat to TM.

Figure S11. [Ln] raw concentrations of different single mismatch site.







Figure S13. [Ln] raw concentrations of initial cleavage kinetic research.





Figure S15. IVT procedure of sgRNA



- a. IVT procedures, including primers PCR amplification and T7 transcription.
- b. Gel electrophoresis characterization of (1) two primers, (2) product of PCR amplification and (s) sgRNA product.







Figure S18. Raw ICPMS intensity of [Ln] in reaction temperature research





Figure S20. Raw ICPMS intensity of [Ln] in multiple mismatches research



