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## **Electronic Supplementary Information**

### **Exonuclease-Assisted Cascaded Recycling Amplification for Label-Free Detection of DNA**

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1 **Experimental Section**

2 **Materials.** Oligonucleotides were custom-synthesized by Sangon Biotech Co., Ltd. (Shanghai,  
 3 China) (sequences see Table S1).

4 **Table S1. Oligonucleotide Sequences Used in This Study**

Name	Sequences (5' to 3') <sup>a</sup>
MB <sub>1</sub>	$\underbrace{\text{CGAGAGGGG}}_b \underbrace{\text{GG}}_d \underbrace{\text{TAGGG}}_{f_1} \underbrace{\text{CGGGTTGGG}}_{f_2} \underbrace{\text{CCCTCTCGG}}_{e} \underbrace{\text{CTCTCGG}}_{d^*} \underbrace{\text{CTCGG}}_{b^*} \underbrace{\text{CTCGGCTGATGAT}}_{a^*}$
MB <sub>2</sub>	$\underbrace{\text{GGGTAGGG}}_f \underbrace{\text{CATCATCTAAA}}_{a_1} \underbrace{\text{AGCCCTACCC}}_g \underbrace{\text{CTCTCG}}_{f^*} \underbrace{\text{CTCTCG}}_{d^*} \underbrace{\text{CTCTCG}}_{b^*}$
MB <sub>3</sub>	$\underbrace{\text{GGCATCAT}}_{f_2} \underbrace{\text{CAGCCGAGAG}}_a \underbrace{\text{GCTTGATGATGAT}}_{b^*} \underbrace{\text{GCCCTACCC}}_c \underbrace{\text{GCCCTACCC}}_{a_1^*} \underbrace{\text{GCCCTACCC}}_{f_2^*} \underbrace{\text{GCCCTACCC}}_{f_1^*} \underbrace{\text{GCCCTACCC}}_{d^*}$
perfectly matched DNA target	$\underbrace{\text{ATCATCAGCCGAGAG}}_a \underbrace{\text{GCTTGAT}}_b \underbrace{\text{GCTTGAT}}_c$
single-base mismatched DNA target	<i>ATCATCATCCGAGAGCTTGAT</i>
three-base mismatched DNA target	<i>ATCATCATCCTATAGCTTGAT</i>
completely mismatched DNA target	<i>AGAGGTAGTAGGTTGCATAGT</i>

<sup>a</sup>Underlines indicate complementary sequences of stem-loop DNA molecular beacons. Italic letters indicate mismatched bases. Domain x\* is the complement of domain x.

5

6 The stock solution of DNA (0.1 mM) were prepared in the TE buffer (10 mM Tris-HCl, 1 mM  
 7 EDTA, 12.5 mM MgCl<sub>2</sub>, pH 8.0) and diluted to desired concentration using the same TE buffer.

8 Exo-III was purchased from Fermentas (Canada). Hemin, tris(hydroxymethyl)aminomethane  
 9 hydrochloride (Tris), 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) disodium salt

1 (ABTS<sup>2-</sup>), 4-(2-hydroxyethyl)piperazine-1 ethanesulfonic acid sodium salt (HEPES) were ordered  
2 from Aladdin Chemistry Co. Ltd (China), and used as supplied. A hemin stock solution (5 mM)  
3 was prepared by dissolving 0.0326 g of hemin in 10 mL of DMSO and stored in dark at -20 °C.  
4 The human serum sample was supplied by Qingdao Center Hospital. All chemicals were used as  
5 received without further purification. Water was used in all of the experiments.

6 **Exo-CRA Reaction for DNA Assay.** Previously, the DNA solutions of MB<sub>1</sub> ( $1.0 \times 10^{-5}$  M), MB<sub>2</sub>  
7 ( $1.0 \times 10^{-5}$  M) and MB<sub>3</sub> ( $1.0 \times 10^{-5}$  M) were heated at 90 °C for 10 min, followed by gradually  
8 cooling down to room temperature. The Exo-CRA reaction was performed by mixing  $2.0 \times 10^{-6}$  M  
9 MB<sub>1</sub>,  $2.0 \times 10^{-6}$  M MB<sub>2</sub>,  $2.0 \times 10^{-6}$  M MB<sub>3</sub>, 4.5 μL of 10 × reaction buffer, 50 units of exonuclease  
10 III and varying concentrations of DNA target to a final volume of 45 μL, followed by incubating  
11 at 25 °C for 30 min.

12 **Colorimetric Measurement.** The experiment was performed by mixing the above products, 800  
13 μL of hemin ( $2.5 \times 10^{-6}$  M), and 400 μL of ABTS<sup>2-</sup> (10 mM) in a buffer solution consisting of 25  
14 mM HEPES, 20 mM KCl, 200 mM NaCl, Triton X-100 (0.05%, w/v), and DMSO (1%, v/v), pH  
15 7.4. The reaction started upon the quick addition of 755 μL of H<sub>2</sub>O<sub>2</sub> (5.3 mM). The absorption  
16 spectra were recorded with a Cary50 UV-vis spectrophotometer (Varian, USA).

17 **Nondenaturing Polyacrylamide Gel Electrophoresis.** The assembly and disassembly of the  
18 fabricated DNA nanoball structure were characterized by 12.5% native polyacrylamide gel  
19 electrophoresis. The samples were by 6×loading buffer. 1×Tris-acetate-EDTA (TAE) was used as  
20 the separation buffer. Electrophoresis were carried out at 120 V for 1 h at room temperature. The  
21 gels were stained with ethidium bromide (EB, 0.5 μg/mL) for 30 min. The visualization and  
22 photography were performed using a digital camera under UV illumination.

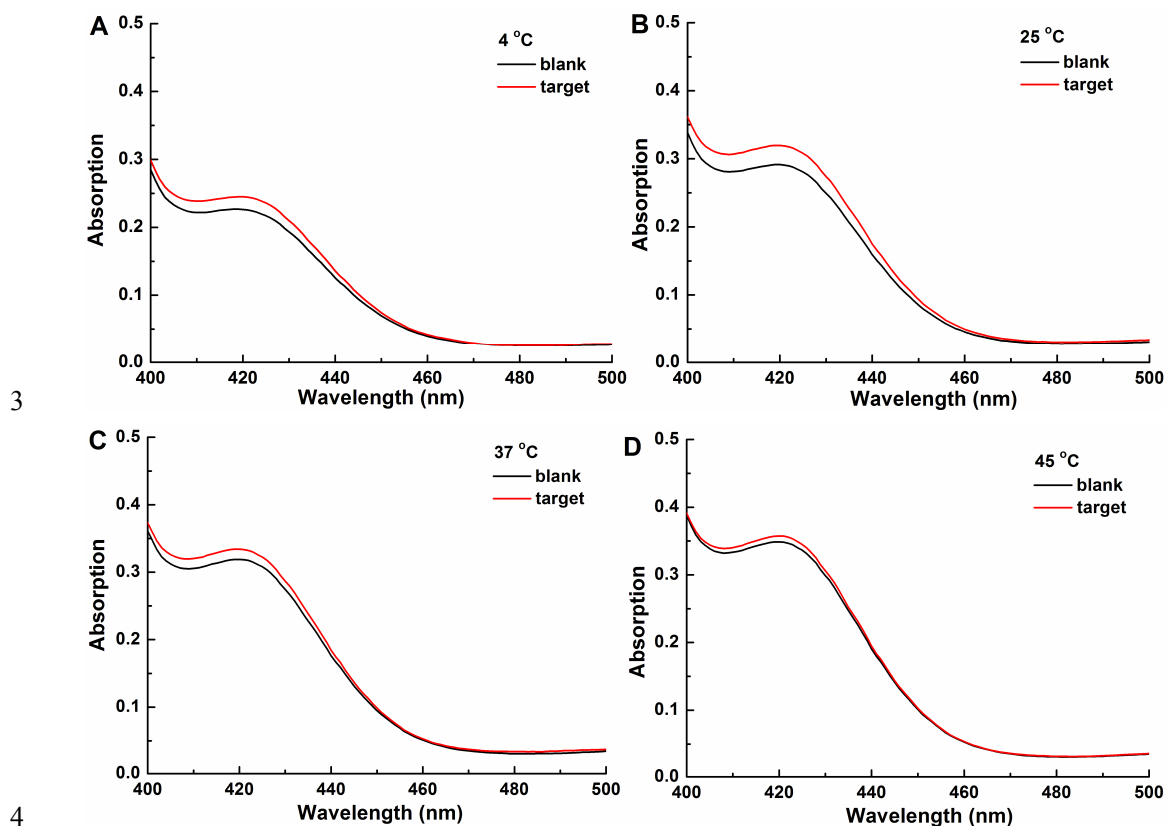
1 **Fluorescence Imaging.** Three samples were prepared as follows. Sample 1: the mixture of  
2 annealed MB<sub>1</sub> ( $1.0 \times 10^{-6}$  M), MB<sub>2</sub> ( $1.0 \times 10^{-6}$  M) and MB<sub>3</sub> ( $1.0 \times 10^{-6}$  M). Sample 2: the mixture  
3 of annealed MB<sub>1</sub> ( $1.0 \times 10^{-6}$  M), MB<sub>2</sub> ( $1.0 \times 10^{-6}$  M), MB<sub>3</sub> ( $1.0 \times 10^{-6}$  M) and target DNA ( $1.0 \times$   
4  $10^{-7}$  M). Sample 3: the mixture of annealed MB<sub>1</sub> ( $1.0 \times 10^{-6}$  M), MB<sub>2</sub> ( $1.0 \times 10^{-6}$  M), MB<sub>3</sub> ( $1.0 \times$   
5  $10^{-6}$  M), target DNA ( $1.0 \times 10^{-7}$  M) and Exo-III (50 units). All the samples were incubated at 25 °C  
6 for 30 min, followed by reacting with 5  $\mu$ L of  $10 \times$  SYBR Green I dye (Invitrogen) to final  
7 volume of 50  $\mu$ L. The fluorescence imaging was carried out on a Leica DMI600B CS inverted  
8 microscope. The samples were excited with Leica FL6000 fluorescence light source through I3  
9 filter (450~490 nm), and observed with Leica HCX PLAN APO 100x/1.46 objective. The images  
10 were recorded with an Andor iXon X3 EMCCD camera.

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## 12 **Optimization of the Exo-CRA Machine.**

13 **Effect of Reaction Temperature.** The activity of Exo-III is highly sensitive to temperature that is  
14 also closely related to the conformation of the constructed MBs. Thus, as an essential factor of this  
15 assay, the reaction temperature was first investigated by detecting  $5.0 \times 10^{-12}$  M target DNA at 4,  
16 25, 37, 45 °C, respectively. The blank sample at each temperature was treated in the same way for  
17 Exo-CRA without target DNA. As shown in Fig. S1, the UV-vis absorption for not only target  
18 DNA but also blank was increased with an increase of reaction temperature. It is reasonable that as  
19 the temperature increased, the activity of Exo-III increased, which facilitate the Exo-CRA reaction.  
20 However, on the other hand, the conformation of the MBs could be destroyed as the increase of  
21 temperature, which increases the background signal. Additionally, the exonuclease also degrades  
22 some of the closed molecular beacon under relatively high temperature.<sup>S1</sup> Fig. S1B shows the

1 maximum interval of the UV-vis absorption between target and the blank. Therefore, 25 °C was  
2 considered to be the optimum reaction temperature used in the Exo-CRA reaction.

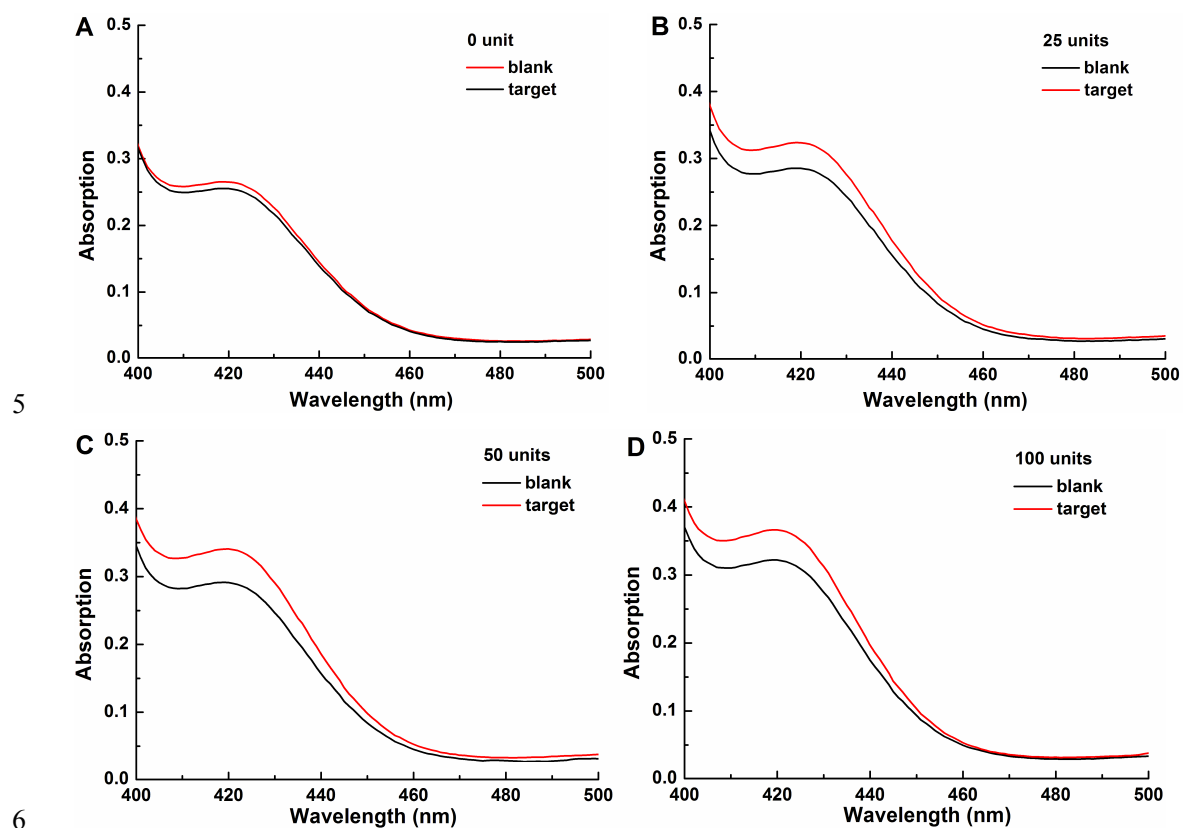


5 **Fig. S1** The influence of reaction temperature. The UV-vis curves were obtained by  $5.0 \times 10^{-12}$  M  
6 target DNA (red) and the blank (black) with Exo-CRA machine produced DNazymes. The  
7 Exo-CRA reaction and UV-vis measurement were carried out according to the procedures  
8 mentioned in the Experimental Section except the temperature used for Exo-CRA as (A) 4 °C, (B)  
9 25 °C, (C) 37 °C, and (D) 45 °C.

10

11 **Effect of the Amount of Exo-III.** To investigate the influence of the amount of Exo-III used in  
12 Exo-CRA machine on DNA detection, the UV-vis curves produced by  $5.0 \times 10^{-12}$  M target DNA  
13 was measured by using 0, 25 units, 50 units, and 100 units Exo-III, respectively. The blank sample  
14 was treated in the same way for Exo-CRA without target DNA. Fig. S2 depicts the influence of

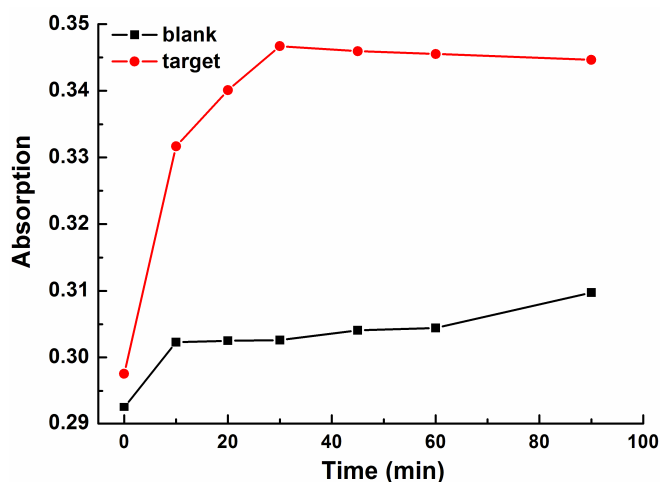
1 the amount of Exo-III used in the proposed Exp-CRA machine on the UV-vis intensities of target  
2 DNA and the blank. The maximum interval of the UV-vis absorption between target and the blank  
3 was obtained at 50 units Exo-III (Fig. S2C). Therefore, 50 units of Exo-III was selected for the  
4 Exo-CRA machine.



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8 **Fig. S2** The influence of the amount of Exo-III. The UV-vis curves were obtained by  $5.0 \times 10^{-12}$  M  
9 target DNA (red) and the blank (black) with Exo-CRA machine produced DNAzymes. The  
10 Exo-CRA reaction and UV-vis measurement were carried out according to the procedures  
11 mentioned in the Experimental Section except the amount of Exo-III used for Exo-CRA as (A) 0,  
12 (B) 25 units, (C) 50 units, and (D) 100 units.

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1 **Effect of Reaction Time.** Subsequently, we investigated the influence of the reaction time for the  
2 performance of the Exo-CRA machine upon analyzing target DNA at a concentration  
3 corresponding to  $5.0 \times 10^{-12}$  M. As shown in Fig. S3, the UV-vis absorption intensities were  
4 greatly increased with increasing the time at the early stage, and reached the maximum after ~30  
5 min, while no obvious UV-vis absorption change was observed for the blank. Therefore, the  
6 reaction time of 30 min was adopted for the proposed Exo-CRA machine used in DNA assay.



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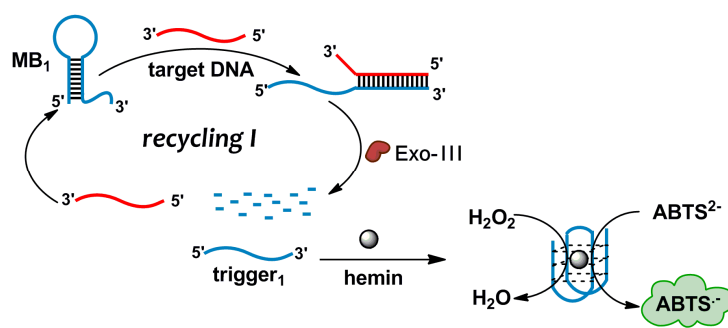
8 **Fig. S3** The influence of the reaction time. The UV-vis absorption was obtained by  $5.0 \times 10^{-12}$  M  
9 target DNA (red) and the blank (black) with Exo-CRA machine produced DNazymes. The  
10 Exo-CRA reaction and UV-vis measurement were carried out according to the procedures  
11 mentioned in the Experimental Section except the reaction time used for Exo-CRA as 0, 10, 20, 30,  
12 45, 60, and 90 min, respectively.

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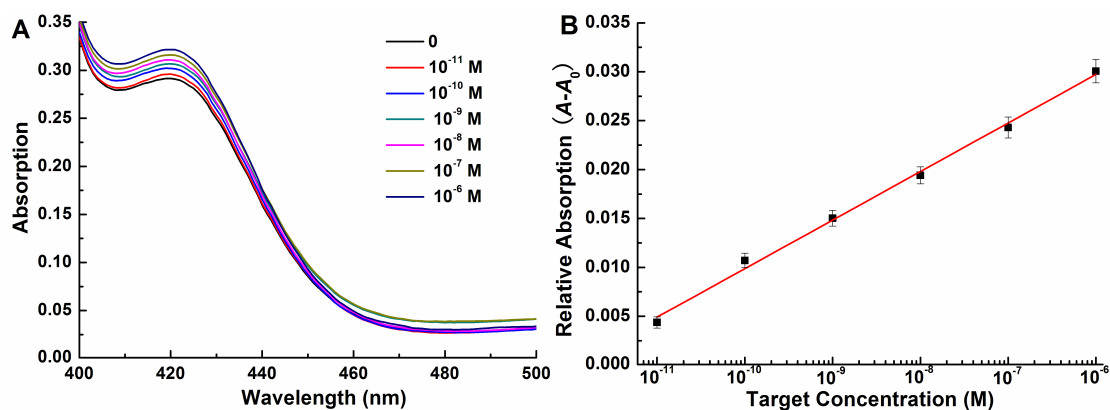
#### 14 **Control Experiments.**

15 The first control experiment of exonuclease-assisted target recycling that only employed MB<sub>1</sub> was  
16 carried out as Scheme S1. Upon the addition of target DNA, the stem-loop structure of MB<sub>1</sub> is  
17 opened and forms a blunt 3' terminus, which facilitates the 3'- to -5' exonucleolytic activity of

1 Exo-III, liberating trigger<sub>1</sub> and ultimately releasing the target. The released target can then  
2 hybridize with a new MB<sub>1</sub> and catalyze a new cycle of MB<sub>1</sub> transformation, achieving the  
3 recycling I and amplification of the signal. From the results of Fig. S4, the UV-vis absorption that  
4 is obtained by the produced DNAzymes increases with increasing concentrations of target DNA  
5 ranging from 10.0 pM to 1.0 μM with a linear correlation equation as  $\Delta A = 0.0050 \lg C + 0.0595$   
6 ( $\Delta A$  is the relative UV-vis absorption intensity;  $C$  is the concentration of target DNA;  $n=6$ ,  $R =$   
7 0.9982) and a limit of detection (LOD) of 10.0 pM.



8  
9 **Scheme S1** Illustration of ssDNA target triggered exonuclease-assisted amplification that only  
10 employs one kind of MB, MB<sub>1</sub>. The signal can be easily readout by binding the generated trigger<sub>1</sub>  
11 with hemin to yield DNAzymes to catalyze the oxidation of ABTS<sup>2-</sup> by H<sub>2</sub>O<sub>2</sub> to form a green  
12 colored product, ABTS<sup>•-</sup>.

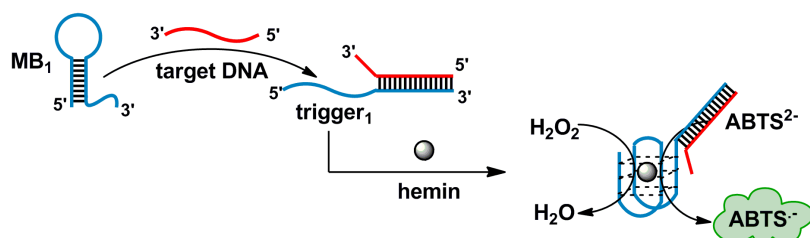


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14 **Fig. S4** (A) UV-vis absorption spectra for analyzing the peroxidation product (ABTS<sup>•-</sup>) of the  
15 ABTS<sup>2-</sup>-H<sub>2</sub>O<sub>2</sub> system catalyzed by the HRP-mimicking DNAzyme that is yielded in Scheme S1



1 strategy corresponding to different concentrations of target DNA from 0 to  $1.0 \times 10^{-6}$  M. (B) The  
2 corresponding calibration curve of relative UV-vis absorbance (at 419 nm) versus the  
3 concentration of target DNA. Relative UV-vis absorbance ( $A - A_0$ ) is calculated by  $A - A_0$ , where  
4  $A_0$  and  $A$  are the UV-vis absorbance without and with target DNA, respectively. The concentration  
5 of each kind MB is  $2.0 \times 10^{-6}$  M. Error bars are standard deviation of three repetitive  
6 measurements.

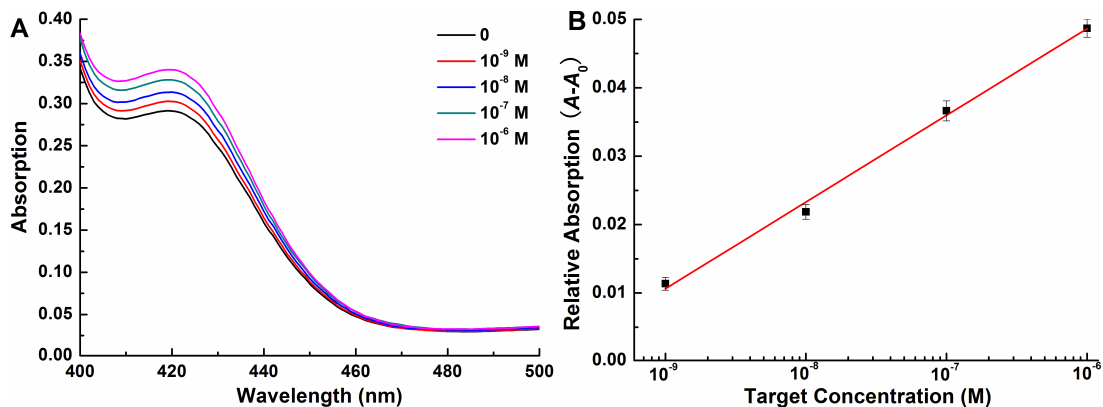
7  
8 The other control experiment that only employs MB<sub>1</sub> without exonuclease amplification was  
9 illustrated in Scheme S2. Upon the addition of target DNA, the stem-loop structure of MB<sub>1</sub> is  
10 opened and forms a blunt 3' terminus. Because no Exo-III exists in this system, no recycling  
11 occurs. The signal is obtained by binding the newly exposed sticky end of MB<sub>1</sub> (trigger<sub>1</sub>) with  
12 hemin to generate a DNAzyme. This 1:1 hybridization ratio seriously limits the sensitivity. From  
13 the results of Fig. S5, the UV-vis absorption that is obtained by the produced DNAzymes only  
14 increases with increasing concentrations of target DNA ranging from 1.0 nM to 1.0 μM with a  
15 linear correlation equation as  $\Delta A = 0.0127 \lg C + 0.1247$  ( $\Delta A$  is the relative UV-vis absorption  
16 intensity;  $C$  is the concentration of target DNA;  $n = 4$ ,  $R = 0.9981$ ) and a limit of detection (LOD)  
17 of 1.0 nM.



18 **Scheme S2** Illustration of ssDNA target detection that only employs MB<sub>1</sub> without exonuclease  
19 amplification. The signal can be easily readout by binding the generated trigger<sub>1</sub> with hemin to  
20

1 yield DNAzymes to catalyze the oxidation of  $\text{ABTS}^{2-}$  by  $\text{H}_2\text{O}_2$  to form a green colored product,  
2  $\text{ABTS}^{\cdot-}$ .

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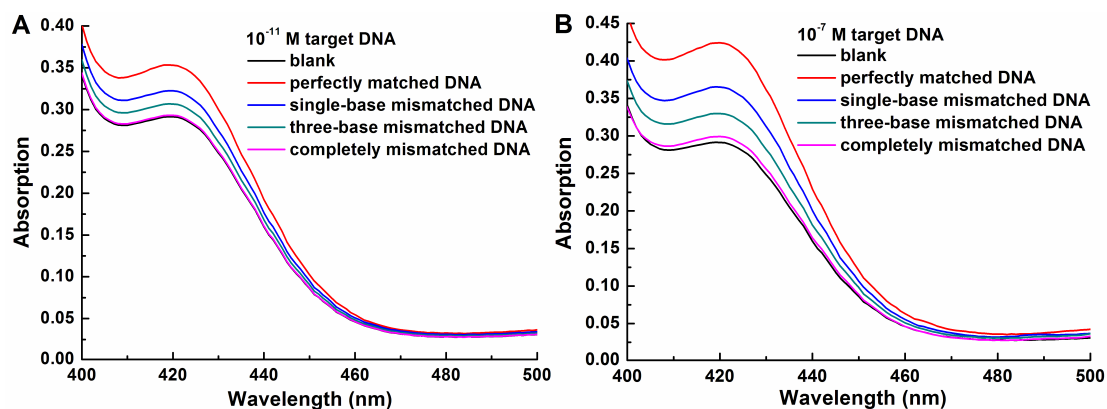
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5 **Fig. S5** (A) UV-vis absorption spectra for analyzing the peroxidation product ( $\text{ABTS}^{\cdot-}$ ) of the  
6  $\text{ABTS}^{2-}$ - $\text{H}_2\text{O}_2$  system catalyzed by the HRP-mimicking DNAzyme that is yielded in Scheme S2  
7 strategy corresponding to different concentrations of target DNA from 0 to  $1.0 \times 10^{-6}$  M. (B) The  
8 corresponding calibration curve of relative UV-vis absorbance (at 419 nm) versus the  
9 concentration of target DNA. Relative UV-vis absorbance ( $A - A_0$ ) is calculated by  $A - A_0$ , where  
10  $A_0$  and  $A$  are the UV-vis absorbance without and with target DNA, respectively. The concentration  
11 of each kind MB is  $2.0 \times 10^{-6}$  M. Error bars are standard deviation of three repetitive  
12 measurements.

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1 **Selectivity of the Assay.**

2 To evaluate the specificity of the assay, the proposed Exo-CRA strategy was challenged to  
3 perfectly matched, single-base-mismatched, three-base-mismatched, and completely mismatched  
4 target DNA sequences, respectively. From the results of Fig. S6, no matter the targets are at low  
5 concentration ( $1.0 \times 10^{-11}$  M) or at high concentration ( $1.0 \times 10^{-7}$  M), the UV-vis signal produced  
6 by the completely complementary DNA could be well separated from those produced by other  
7 mismatched targets. The completely mismatched sequence showed no response that was equal to  
8 the blank. Thus, the presented DNA assay with Exo-CRA could readily discriminate between  
9 mismatched targets, even single nucleotide polymorphisms. The high specificity could be  
10 attributed to the specific hybridization of DNA and digestion property of Exo-III on the duplex  
11 from the blunt 3'-OH terminus.



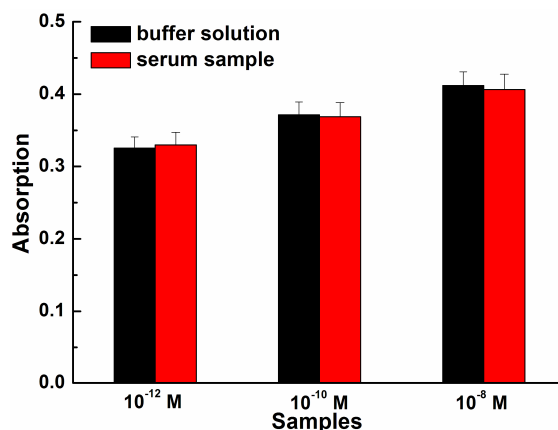
12  
13 **Fig. S6** UV-vis absorption spectra for analyzing the peroxidation product ( $\text{ABTS}^{\bullet-}$ ) of the  
14  $\text{ABTS}^{2-}$ - $\text{H}_2\text{O}_2$  system catalyzed by the HRP-mimicking DNAzyme that is yielded in the proposed  
15 Exo-CRA machine corresponding to perfectly matched and mismatched DNA targets at  $1.0 \times 10^{-11}$   
16 M (A) and  $1.0 \times 10^{-7}$  M (B) target concentrations.

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1 **Real Sample Assay.**

2 To investigate the applicability of the proposed Exo-CRA machine in a real human serum sample,  
3 we performed spike and recovery experiments. The serum sample was respectively spiked with  
4  $1.0 \times 10^{-12}$ ,  $1.0 \times 10^{-10}$ , and  $1.0 \times 10^{-8}$  M target DNA to test the performances of the assay in  
5 complex matrixes. From Fig. S7, the UV-vis absorbance obtained from serum sample decreases  
6 slightly compared to that in buffer solution. By using calibration method to determine the  
7 concentration of target DNA in serum sample, the recovery was calculated to be  $99 \pm 5\%$ ,  
8 indicating the potentiality of the proposed assay for DNA detection in real biological samples.



9

10 Fig. S7 UV-vis absorption spectra for analyzing the peroxidation product ( $\text{ABTS}^{\cdot-}$ ) of the  
11  $\text{ABTS}^2-\text{H}_2\text{O}_2$  system catalyzed by the HRP-mimicking DNAzyme that is yielded in the proposed  
12 Exo-CRA machine corresponding to different concentrations of target DNA ( $1.0 \times 10^{-12}$ ,  $1.0 \times$   
13  $10^{-10}$ , and  $1.0 \times 10^{-8}$  M) in a buffer solution and a serum sample, respectively. Error bars are  
14 standard deviation of three repetitive measurements.

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16 **References.**

17 S1 X. Zuo, F. Xia, Y. Xiao and K. W. Plaxco, *J. Am. Chem. Soc.*, 2010, **132**, 1816-1818.