

# 1 **Electronic Supplementary Information**

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## 3 **SERS-active Ag@Au core-shell NPs assemblies for DNA** 4 **detection**

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### 11 **Captions:**

#### 12 **Experimental Section**

13 **Fig. S1** Representative TEM images of single Ag NPs.

14 **Fig. S2** (a-f) TEM images of Ag NPs assemblies at 2, 5, 10, 20, 30 and 40 cycles.

15 **Fig. S3** Statistical analysis of Au shell thickness.

16 **Fig. S4** SERS spectrum of Ag NPs assemblies at different cycles.

17 **Fig. S5** UV-vis spectra of Ag@Au core-shell NPs assemblies at different DNA concentration.

18 **Fig. S6** (a, b) TEM images of Ag@Au NPs assemblies in the presence of 1fM DNA<sub>EC</sub>. (c) SERS  
19 intensity of assemblies at different concentration of templates. (1) Control groups (1fM λDNA, 0  
20 cycle); (2) 1fM DNA<sub>EC</sub>, 20 cycles; (3) 200 aM λDNA and 1fM DNA<sub>EC</sub>, 20 cycles; (4) 2 fM λDNA  
21 and 1fM DNA<sub>EC</sub>, 20 cycles.

22 **Table S1.** Detected results of DNA spiked into PCR buffer.

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# 1 **Experimental Section**

## 2 **Materials and Reagents.**

3 Silver nitrate ( $\text{AgNO}_3$ ), poly-N-vinyl-2-pyrrolidone (PVP), sodium borohydride ( $\text{NaBH}_4$ ) and  
4 hydroxylamine hydrochloride ( $\text{NH}_2\text{OH}\cdot\text{HCl}$ ) were purchased from Sinopharm Chemical Reagent  
5 Beijing Co., Ltd., Beijing, China. Chloroauric acid ( $\text{HAuCl}_4$ ), trisodium citrate, L-sodium  
6 ascorbate and thiolated polyethylene glycol ( $\text{PEG}_{1000}\text{-SH}$ , Mw 1000) were purchased from Sigma-  
7 Aldrich. Millipore-Q water used throughout the experiments was purified using the Milli-Q device  
8 (18.2 M $\Omega$ , Millipore, Molsheim, France). All glassware was cleaned with freshly prepared *aqua*  
9 *regia* ( $V_{\text{HNO}_3} : V_{\text{HCl}} = 1 : 3$ ) and rinsed several times with Millipore-Q water. PCR buffer, dNTP  
10 and Taq DNA polymerase were purchased from Shanghai Sangon, China. All DNA fragments  
11 purified by high-performance liquid chromatography were synthesized by Shanghai Sangon  
12 Biological Engineering Technology & Services Co. Ltd, including  $\lambda$ DNA as the template, forward  
13 primers and reverse primers. The amplification length of the primers was 50 bp.

14 Amplified Target Sequences: TGG CTG ACC CTG ATG AGT TCG TGT CCG TAC AAC TGG  
15 CGT AAT CAT GGC CC

16 Forward primers: 5'-SH-( $\text{CH}_2$ )<sub>6</sub>-TGG CTG ACC CTG ATG AGT TCG-3'

17 Reverse primers: 5'-SH-( $\text{CH}_2$ )<sub>6</sub>-GGG CCA TGA TTA CGC CAG TT-3'

## 18 **Preparation of primer-modified Ag NPs.**

19 18.0  $\pm$  2.3 nm Ag NPs were synthesized as follows: 5 mL 1% (by weight) PVP solution as  
20 the stabilizer agent was added to 20 mL Millipore-Q water in a water-ice bath. 0.6 mL 1% (by  
21 weight)  $\text{NaBH}_4$  solution was mixed with the above solution under vigorous stirring. Then, 5 mL  
22 15 mM  $\text{AgNO}_3$  solution and 5 mL 1% PVP solution were slowly injected into the mixture by two  
23 constant-flow pumps at a rate of 30 mL/h. Finally, the reaction solution was kept at 80°C for 2 h to  
24 remove excess  $\text{NaBH}_4$  before being stored at 4°C.

25 The as-fabricated Ag NPs (1 mL) were centrifuged at 5400 g for 10 min, and re-suspended in  
26 200  $\mu\text{L}$  Millipore-Q water. 50  $\mu\text{L}$  concentrated Ag NPs were respectively reacted with 50  $\mu\text{L}$  F<sub>50</sub>  
27 and 50  $\mu\text{L}$  R<sub>50</sub> at a molar ratio of 1:100 for 12 h. The Ag NPs-primer conjugates were centrifuged  
28 at 5400 g for 10 min to remove the unreacted primers, and then re-suspended in 50  $\mu\text{L}$  Millipore-Q

1 water. PEG<sub>1000</sub>-SH was further modified on the Ag NPs-primer conjugates at a molar ratio of 5:1  
2 to improve their stability in PCR buffer.

### 3 **PCR-based Ag NPs assemblies.**

4 5  $\mu$ L 10  $\times$  PCR buffer, 1  $\mu$ L 1 mM dNTP, 0.5  $\mu$ L  $\lambda$ DNA and 0.5 U Taq DNA polymerase  
5 were mixed in 37  $\mu$ L Millipore-Q water. 3  $\mu$ L Ag NPs-F<sub>50</sub> conjugates and 3  $\mu$ L Ag NPs-R<sub>50</sub>  
6 conjugates were added to the above solution. The optimized PCR process was performed as  
7 follows: 94°C (3 min), 94°C (30 s), T<sub>m</sub> 60°C (30 s), 72°C (1 min) and 4°C (10 min) after 2, 5, 10,  
8 20, 30, and 40 cycles. PCR products were centrifuged at 5400 g for 10 min and re-suspended in  
9 Millipore-Q water at 1/5 of the original volume.

### 10 **Construction of Ag@Au core-shell NPs assemblies.**

11 50  $\mu$ L five-fold concentrated Ag NPs assemblies were added to a mixture containing 200  $\mu$ L  
12 0.1 M PBS and 100  $\mu$ L 1% PVP. 50  $\mu$ L 5 mM HAuCl<sub>4</sub> solution and 50  $\mu$ L 10 mM NH<sub>2</sub>OH-HCl  
13 solution were injected into the above solution. The mixture was shaken for 3 h at room  
14 temperature, and then centrifuged and re-suspended in 50  $\mu$ L Millipore-Q water.

### 15 **SERS measurements**

16 4-nitrothiophenol (4-NTP), as a standard Raman reporter molecule, was modified on the  
17 surface of Ag NPs assemblies and Ag@Au core-shell NPs assemblies after 2, 5, 10, 20, 30 and 40  
18 cycles through Ag-SH/Au-SH covalent bonds. The final concentration of 4-NTP was 2  $\mu$ M. The  
19 mixtures reacted for 12 h and were centrifuged at 5400 g for 10 min to remove the unmodified 4-  
20 NTP. SERS spectrum of assemblies bearing 2  $\mu$ M 4-NTP was measured through LabRam-HR800  
21 Micro-Raman spectrometer.

### 22 **SERS signal-based DNA detection.**

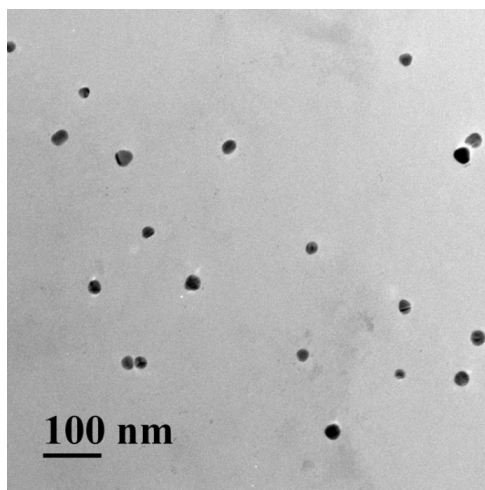
23 Ag NPs assemblies were prepared at 20 cycles under different DNA concentrations ranging  
24 from 1.56 pM to 156 zM, and then a layer of Au shell at 50  $\mu$ L 5 mM HAuCl<sub>4</sub> solution and 50  $\mu$ L  
25 10 mM NH<sub>2</sub>OH-HCl solution were deposited. After centrifugation, SERS intensity of the Ag@Au  
26 core-shell NPs assemblies after modification with 4-NTP was measured. A standard curve was  
27 established by plotting the SERS intensity against the DNA concentration. To evaluate the  
28 accuracy of the Raman sensor in DNA detection, a recovery test was performed by spiking the  
29 PCR buffer with different concentrations of DNA. The SERS signals of interface-PCR products

1 assembled at known DNA concentrations were measured, and the percent recovery was calculated  
2 based on the established standard curve.

### 3 **Instrumentation and Measurement.**

4 The structures of Ag NPs, Ag NP assemblies and Ag@Au core-shell NPs assemblies were  
5 characterized using a JEOL JEM-2100 transmission electron microscope (TEM) operated at 200  
6 kV. The UV-vis spectra of NPs and assemblies were measured by a UNICO 2100 PC UV-vis  
7 spectrophotometer. SERS of the assemblies were obtained by a LabRam-HR800 Micro-Raman  
8 spectrometer with Lab-spec 5.0 software. The slit and pinhole were set at 100 and 400 nm,  
9 respectively, in a confocal configuration with a holographic grating (600 g/mm) and an air-cooled  
10 He-Ne laser for 632.8 nm excitation with a power of ca. 8 mW.

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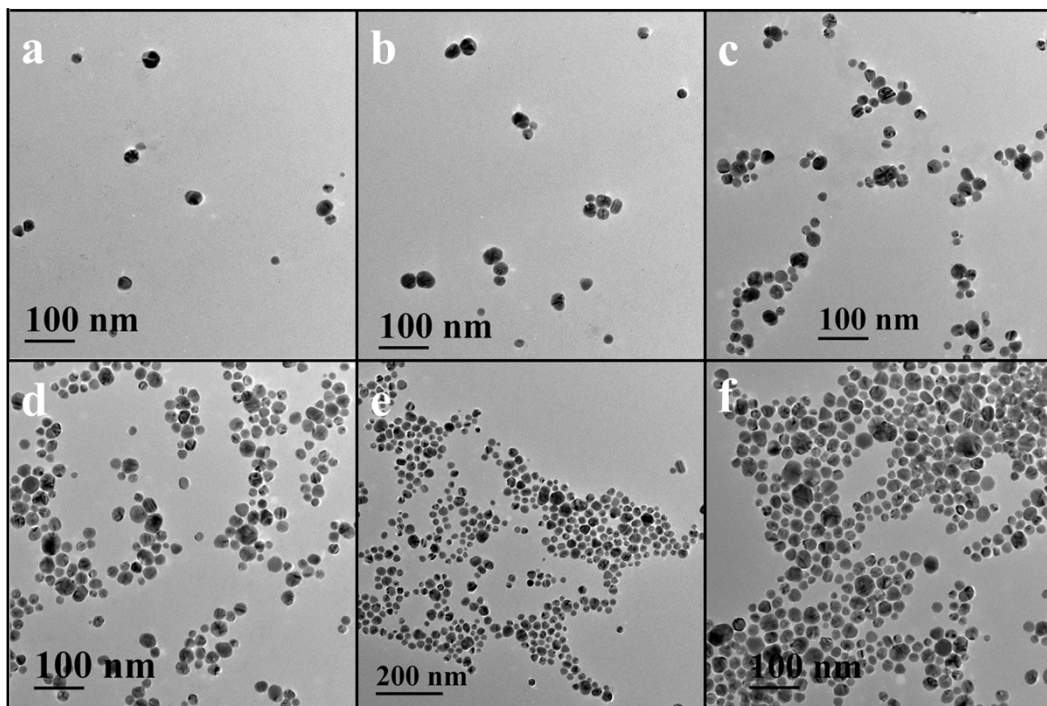


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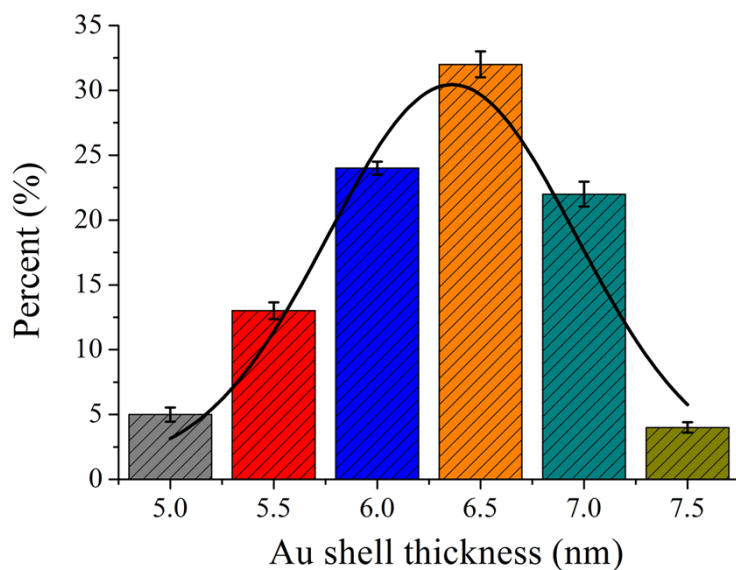
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**Fig. S1** Representative TEM images of single Ag NPs.

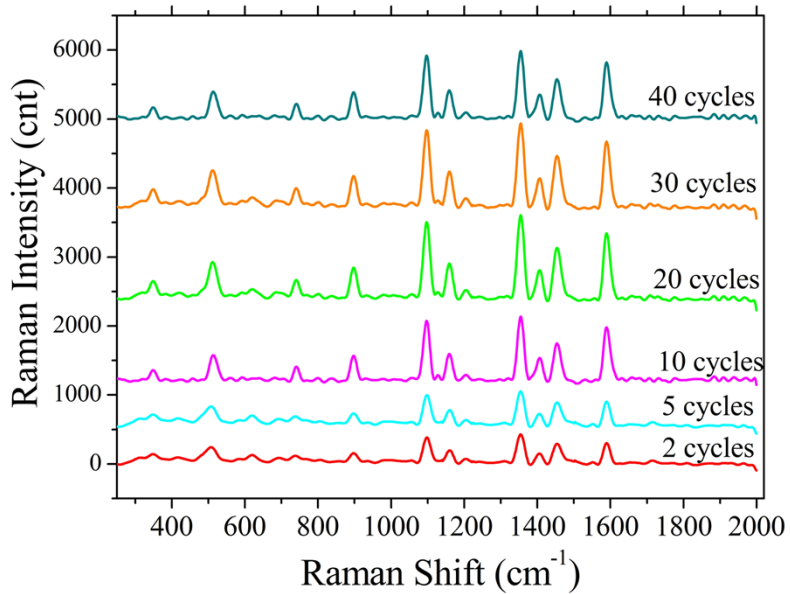


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2 **Fig. S2** (a-f) TEM images of Ag NPs assemblies at 2, 5, 10, 20, 30 and 40 cycles.  
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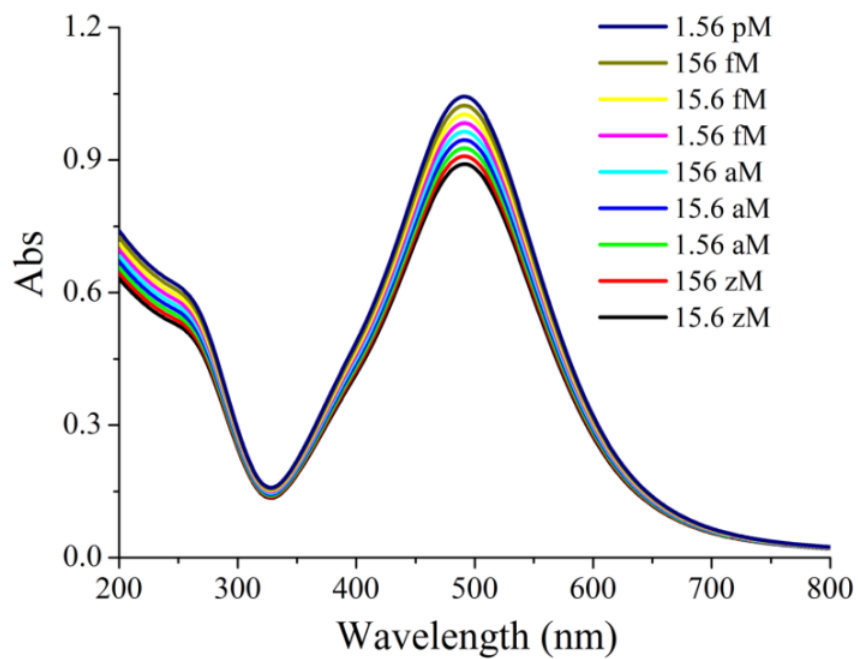


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5 **Fig. S3** Statistical analysis of Au shell thickness.

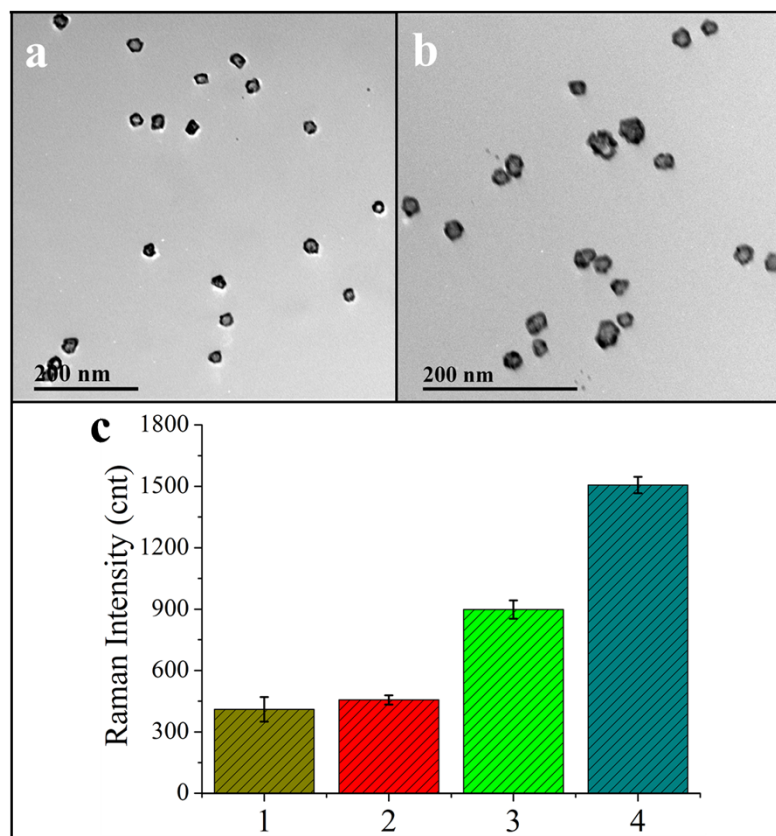
6 The interparticle distance between Ag NPs was 16.5 nm determined by the length of amplified  
7 primers (50 bp, 16.5 nm), and the thickness of Au shell was statistically analyzed to  $6.4 \pm 0.5$  nm,  
8 thus the interparticle gap between Ag@Au core-shell NPs was around  $3.7 \pm 1.0$  nm.  
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**Fig. S4** SERS spectrum of Ag NPs assemblies at different cycles.



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**Fig. S5** UV-vis spectra of Ag@Au core-shell NPs assemblies at different DNA concentration.



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2 **Fig. S6** (a, b) TEM images of Ag@Au NPs assemblies in the presence of 1fM DNA<sub>EC</sub> after 20  
 3 cycles. (c) SERS intensity of Ag@Au NPs assemblies at different concentration of templates. (1)  
 4 Control groups (1fM λDNA, 0 cycle); (2) 1fM DNA<sub>EC</sub>, 20 cycles; (3) 200 aM λDNA and 1fM  
 5 DNA<sub>EC</sub>, 20 cycles; (4) 2 fM λDNA and 1fM DNA<sub>EC</sub>, 20 cycles.

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**Table S1.** Detected results of DNA spiked into PCR buffer.

Spiked concentration (fM)	Detected Concentration Mean ± SD (fM)	Recovery (%) Mean ± SD <sup>a</sup>
100	107.2 ± 5.35	104.51 ± 2.27
10	11.2 ± 1.89	105.24 ± 3.61
1	0.98 ± 0.085	95.68 ± 2.67
0.5	0.48 ± 0.021	97.53 ± 1.29
0.1	0.095 ± 0.0052	96.49 ± 1.86
0.05	0.047 ± 0.0037	93.18 ± 3.78

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<sup>a</sup>SD, standard deviation, was calculated based on three experiments.