

## **Supporting Information**

## Sensitive Detection of Antibiotics using Aptamer Conformation Cooperated Enzymeassisted SERS Technology

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**Figure S1.** Minimum free energy (MFE) structures of different oligos and oligo hybridization with annotation of free energy calculated by NUPACK.



**Figure S2**. Theoretical calculations of the energy changes for the competitive hybridizations between DNA oligos. (a-b) Gibbs free energy changes and the calculated efficiencies for hybridization in silica:  $A \cap T$  or  $P \cap T$ . (c-d) Gibbs free energy changes and the calculated efficiencies for hybridization in silica:  $P \cap C$  or  $R \cap C$ .  $\cap$  symbols hybridization of the oligos. (The temperature at 25 °C )



**Figure S3.** SERS spectra of Cy5 (1  $\mu$ M) collected from 40 random spots of additional three separate Au NPs@Si substrates. Baseline correction was made for individual spectrum primarily using the software built-in function of automatic adjustment. The occasional issue of baseline over-processing may require manual adjustment for correction.



**Figure S4** Gel electrophoresis validation of the ACCESS assay including both the first step of aptamer-CAP recognition-induced releasing and the second step of enzymatic cleavage in a single-tube experiment. 1: P+T; 2: R; 3: A+T+P+Exo III; 4: A+T+CAP+P+Exo III. GelRed nucleic acid stain used in the experiment. The red rectangle drawn as a visual guide for comparison of the band position.



**Figure S5.** Optimization of the incubation time and Exo III enzyme concentration in the cleavage reaction. (a-b) SERS spectra and intensity quantification at 1366 cm<sup>-1</sup> peak in the titration experiments of the enzyme incubation time. (c-d) SERS spectra and intensity quantification at 1366 cm<sup>-1</sup> peak in the titration experiments of the enzyme concentration. Error bar: standard deviation (n = 3). Baseline correction was made for individual spectrum primarily using the software built-in function of automatic adjustment.



**Figure S6.** SERS spectra of CAP (150 pM) collected from 30 random spots of three identical Au NPs@Si substrates. Baseline correction was made for individual spectrum primarily using the software built-in function of automatic adjustment. The occasional issue of baseline over-processing may require manual adjustment for correction.



**Figure S7.** Raman intensities of the characteristic SERS peaks at 1138, 1219, 1267, 1366, 1465 and 1606 cm<sup>-1</sup> with logarithmic CAP concentrations in water.



**Figure S8.** Raman intensities of the characteristic SERS peaks at 1138, 1219, 1267, 1366, 1465 and 1606 cm<sup>-1</sup> with logarithmic CAP concentrations in milk.



**Figure S9.** The chemical structures of different antibiotics, including thiamphenicol (TAP); tetracycline (TE); OT:oxytetracycline (OT); S:streptomycin (S).

DNA	Sequences $(5^{\prime} \rightarrow 3^{\prime})$
Probe	CCCCTCGCCGGGGTAGGGCGGGTTGGGCCCCGGCGAGTCGGTGGTA
Capture	CCGGCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Target	TACCACCGACTCGCCGACCGTG
Residue	CCCCTCGCCGGGGTAGGGCGGGTTGGGCCC
Aptamer	ACTTCAGTGAGTTGTCCCACGGTCGGCGAGTCGGTGGTAG

## Table 1. The sequences of DNA oligos

## Table 2. Performance comparison of different assays for CAP detection

Assay principle	LOD	Linear Range	Reference
SERS	310 nM	310 nM-15.5 pM	46
Aptamer + Realtime q-PCR	3.1 nM	3.1 nM-62 nM	10
Surface plasmon resonance	164 nM	N/A	47
Chemiluminescent Immunoassay	0.25 nM	3.1 pM-31 pM	48
Electrochemical sensor	2.9 nM	10 nM-1000nM	19
Photoresponsive colormetric immunoassay	0.03 nM	0.03 nM-12.5 nM	15
Our work	15 fM	15 fM - 150 pM	