1	Engineering an Au Nanostar-based Liquid Phase Interfacial
2	Ratiometric SERS platform with Programmable Entropy-driven
3	DNA Circuits to Detect Protein biomarkers in clinical samples
4	Guanli Fan, ^a Xiaorong Gao, ^a Shuling Xu, ^a Xia Li, ^a Qi Zhang, ^a Caifeng Dai, ^{b*}
5	Qingwang Xue, ^a * Huaisheng Wang ^a
6	^a Department of Chemistry, Liaocheng University, Liaocheng, 252059, Shandong,
7	China
8	^b Center for Reproductive Medicine, Department of Obstetrics and Gynecology, Qilu
9	Hospital of Shandong University, Ji'nan 250012, Shandong, P.R. China
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21	*Corresponding author
22	Tel: $+86.635.8239001$ · Fax: $+86.635.8239001$
23 24	Email: xueqingwang $1983@163$ com: daicaifeng $1982@163$ com
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27	Experimental section.
28	Chemicals and Instrumentations.

Streptavidin magnetic nanosphere (SA-MNS, 350 nm in diameter) were 1 purchased from Bangs Laboratories Inc. (Fishers, IN). Mucin 1(MUC1) ELISA Kit 2 was obtained from North Connaught Biotechnology Co. Ltd. (Shanghai, China). DNA 3 oligonucleotides (Table S1) were synthesized and HPLC-purified by Sangon 4 Biological Engineering Technology & Services Co., Ltd. (Shanghai, China). HAuCl₄ 5 was purchased from Shanghai Civic Chemical Technology Co., Ltd. (Shanghai, 6 China). C₆H₅Na₃O₇•2H₂O was purchased from Tianjin Fengchuan Chemical Reagent 7 Technology Co., Ltd. (Tianjin, China). Ethanol was purchased from Tianjin Fuyu 8 Fine Chemical Co., Ltd. (Tianjin, China). Hexane was purchased from Tianjin 9 Komiou Chemical Reagent Co., Ltd. (Tianjin, China). The other reagents used were 10 analytical grade and can be used directly without further purification. Ultrapure water 11 (Milli-Q, Millipore, resistance $18.2 \text{ M}\Omega$ cm) was used to prepare all solutions. 12

Table 51. Sequences of Ongonacicoliaes Osca in the Study
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Name	Sequence (5'-3')
mucin 1 aptamer	GCAGTTGATCCTTTGGATACCCTGG
P1DNA	GTCCAAAGGATCAACTGCAGCA
DNA1	TGCTGCAGTTGATCCTTTGGACAGGGCCGTAAGTTAGT TGGAGACGTAGGTTTTTTTTTT
DNA2	ROX-CCACATACATCATATTCCCTGTCCAAAGGATCA ACT
DNA3	CCTACGTCTCCAACTAACTTACGG
F-DNA	CCTACGTCTCCAACTAACTTACGGCCCTGTCCAAAGGA TCAACT-MB

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Instrumentation. The spectra of UV-vis absorption was measured on a UH-4150 UV-Vis spectrometer, Transmission electron microscopy (TEM) was performed using a JEM-2100 (JEOL, Japan). The morphology features of materials and oil-water interface were observed by ascanning electron microscope (SEM, Hitachi, Japan). Surface-enhanced Raman scattering spectrometer were conducted using a Renishaw InVia Reflex confocal microscope equipped with a 50× objective and a high-

resolution grating with 1800 grooves per centimeter. SERS spectra were acquired of
 633 nm as the excitation wavelength with an exposure time of 1 s.

3 Self-Assembled Au Nanostars (Au NSs) on Liquid-Liquid Interface

The multangular Au nanostars (Au NSs) were prepared through a seed-mediated growth method. ^{1,2} Briefly, 300 μ L of aqueous 10 μ M HAuCl₄ were first injected into 30 mL boiling deionized water under vigorous stirring, next, 100 mL of 40 mM sodium citrate was added. The solution was finally cooled slowly to room temperature under stirring with 700 rpm until the color of the gold colloidal sol turns burgundy to get the Au seed solution.

10 The Au NSs were synthesized by seed-mediated growth. First, ~10 nm Au seeds 11 were synthesized through a modified turkevich method. Then, 25 μ L of aqueous 100 12 mM HAuCl₄ was put into 10 mL of deionized water under vigorous stirring. 13 Subsequently, 50 μ L of gold seeds, 22 μ L of 1% sodiumcitrate, and 1000 μ L of 30 14 mM hydroquinone were added one by one. Finally, the solution was kept under 15 stirring at room temperature for 30 minutes to obtain AuNSs.

The self-assembled multangular Au NSs at the hexane-water interface was obtained. Briefly, 1.0 mL Au NSs and 1.3 mL hexane were added into a centrifuge tube. Then, ethyl alcohol, which was responsible for the inducer of the self-assembly on the immiscible interface, was injected constantly below the interface. Finally, inerratic Au NSs on the liquid-liquid interface were obtained with continuous shaking.

21 Preparation of multi-chain composite structure DNA probe

5 µL of 1 µM DNA1, 5 µL of 1 µM DNA2, and 5 µL of 1 µM DNA3 were first 22 added to 20 μ L of 10 mM PBS buffer (pH = 7.4), and reacted for 30 min at room 23 temperature to form an DNA3-DNA1-DNA2 dsDNA, a three-chain composite 24 structure DNA probe. Subsequently, 20 µL (1 mg mL⁻¹) of streptavidin magnetic 25 nanosphere (MNS) were washed three times to remove surfactants with 200 µL of 26 PBS-T buffer (pH 7.4), and were added to the above-mentioned three-chain 27 composite structure DNA probe solution and reacted for 60 min. Then, the resultant 28 MNS-DNA3-DNA1-DNA2 composite magnetic probe were rinsed with PBS-T and 29

PBS, respectively, three times. Finally, the magnetic probe was resuspended in 35 μL
 of PBS buffer, and stored at 4 °C.

3 Procedure of mucin 1 analysis by the ratiometric SERS strategy based on 4 Entropy-driven DNA Circuits-Cooperated Liquid–Liquid Self-Assembled Au 5 Nanostars Interface

First, 5 µL of 15 µM P1DNA and 5 µL of 10 µM aptamer were added to 10 µL 6 of 10 mM PBS buffer, reacted for 30 min at room temperature to form P1-aptamer 7 double-stranded DNA (dsDNA). Then, 5 µL of different concentrations mucin 1 8 protein were added to the above solution and incubated for 30 min at room 9 temperature, to finish the competition reaction and release free P1DNA. Subsequently, 10 5 µL composite magnetic probe and 5 µL of 1.0 µM MB-labeled fuel-DNA(F-DNA) 11 were added to the above solution and incubated at 37 °C for 3 h, to finish the entropy-12 driven DNA circuits amplification reaction and release free ROX-labeled DNA2. 13 Finally, the resultant supernate was separated and added into the self-assembled mult-14 angular Au NSs at the hexane-water interface, and the Raman signals were absorbed 15 along with Au NSs on the immiscible interface to finish the SERS measurement using 16 a 633 nm laser excitation by a Renishaw InVia Raman microscope. The Raman signal 17 ratio of I_{ROX}/I_{MB} is proportional to the mucin 1 concentration. 18

19 Preliminary Analysis of Real Sample

Healthy human serum was filtered with 100 kDa ultrafiltration membranes at 10000 rpm 10 min to remove the ions and macromolecules. The ultrafiltrates were spiked with Mucin 1 (1.0 fg/mL, 10 fg/mL, 100 fg/mL, 1 pg/mL, and 10 pg/mL final concentration). The following procedures were the same as those describe above in buffer solution.

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26

27 3. Results and discussion

28 Assessment of Entropy-Driven DNA Circuit System



Fig. S1 Native PAGE characterization of different samples in the entropy-driven
DNA circuit system. Lane M, 300 bp marker; Lane 1, 2.5 μM DNA1; Lane 2, 5.0
μM DNA2; Lane 3, 2.5 μM DNA3; Lane 4, 2.5 μM P1DNA(mimic target); Lane 5,
2.5 μM F-DNA; Lane 6, 2.5 μM DNA1 + 2.5 μM DNA2 + 2.5 μM DNA3; Lane 7,
2.5 μM DNA1 + 2.5 μM DNA2 + 2.5 μM DNA3 + 1.0 μM P1DNA; Lane 8, 2.5 μM
DNA1 + 2.5 μM DNA2 + 2.5 μM DNA3 + 5.0 μM F-DNA; Lane 9, 2.5 μM DNA1 +
8 2.5 μM DNA2 + 2.5 μM DNA3 + 1.0 μM P1 DNA + 5.0 μM F-DNA.

9 In the Ratiometric SERS platform, the entropy-driven DNA circuits plays a key role for signal transmit and amplification. Native polyacrylamide gel electrophoresis 10 (PAGE) were performed to investigate the process of entropy-driven DNA circuit. As 11 shown in Fig. S1, the purified DNA1, DNA2, DNA3, P1DNA (mimic target), F-DNA 12 show the bands in lanes 1-5, respectively. After the reaction of the same concentration 13 of DNA1, DNA2, and DNA3, a bright band with slow migration appeared (lane 6) 14 than the incubating single strand DNA (lanes 1-3), indicating the formation of a high 15 molecular weight product of three-chain structured DNA substrate. In the presence of 16 mimic target P1-DNA, lane 7 show additional bands compared with lane 6, indicating 17 that part of the three-chain structured DNA substrate DNA1-DNA2-DNA3 was 18 converted to byproduct DNA1-DNA3-P1DNA and DNA2 according to the 19 ratiocination of base count. The three-chain structured DNA substrate was stable 20 when Fuel-DNA was introduced (lane 8), and FDNA and DNA2 cannot be separated 21 due to their nuance of DNA bases. Meanwhile, we observed that the intensity of same 22 concentration DNA 3-DNA 1-DNA 2 dsDNA are not same in Lane 6 and Lane 8. The 23 5

1 cause of this phenomenon may be attributed to the loss of sample injection quantity when the sample is added to the sample tank in gel electrophoresis experiment. 2 Although there is a difference bright difference in Lane 6 and Lane 8, the bright 3 difference in Lane 6 and Lane 8 does not affect the gel electrophoresis experimental 4 result that the three-chain structured DNA substrate was stable when Fuel-DNA was 5 introduced. Moreover, compared with lane 7, P1-DNA and DNA3 were released 6 when the F-DNA was added, and the intermediate DNA1-DNA3-P1DNA was 7 8 converted to byproduct DNA1-FDNA. It can be seen that the bands of the DNA1-F-DNA and DNA1-P1DNA-DNA3 cannot be separated due to their similar amount of 9 DNA bases (lane 9). Also, P1DNA cannot be observed due to the trigger of next 10 entropy-driven signal amplification process. The result verified that the entropy-11 driven DNA circuit based on three-chain-structured DNA substrate was successfully 12 performed. 13

14 Characterization of AuNSs and liquid-liquid Self-Assembled Au Nanostars15 interface



16 17

(A)



3 Fig. S2 (A) SEM images of AuNPs. (B) UV-vis absorption spectrum of AuNPs.

4 Detection Conditions Optimization

1 2

In this study, the concentration of aptamer-P1 DNA dsDNA probe caused great 5 effect on the product P1-DNA mimic target as initiator for DNA circuits amplification. 6 Thus, the optimum concentration of aptamer-P1DNA dsDNA detection probe was 7 investigated under 10 pg mL $^{-1}$ target MUC1. Fig. S3A revealed the I_{ROX}/I_{MB} signals 8 corresponding to different concentration of aptamer-P1DNA detection probe. The 9 I_{ROX}/I_{MB} signal increase dgradually between 0.5 and 10 μ M and reached a relatively 10 stable value at 10 µM. Therefore, 10 µM was selected as the optimum reaction 11 concentration of aptamer-P1DNA dsDNA probe to accelerate the DNA circuits and 12 improve the sensitivity of the proposed biosensor. 13

In the ratiometric SERS strategy, the I_{ROX}/I_{MB} Raman signal responses were 14 dependent upon the amount of the freed ROX-modified DNA2, and the MB-modified 15 F-DNA bound to magnetic bead. The greater the number of freed ROX-modified 16 DNA2 present, the greater the amount of MB-modified F-DNA bound to magnetic 17 bead. So, a DNA circuits reaction time was expected to yield enhanced I_{ROX}/I_{MB} 18 Raman signal. Fig. S3B depicts the effect of entropy-driven DNA circuit reaction 19 time on the I_{ROX}/I_{MB} Raman signal. One observed that the I_{ROX}/I_{MB} increased rapidly 20 with the DNA circuit reaction time up to 2 h and became saturated over 2 h due to the 21

exhaustion of signal probe. Thus, 2 h was selected as the optimum time for the
 entropy-driven DNA circuit reaction.

3 Beyond that, the concentration of MB-modified fuel-DNA affects the DNA circuit reaction and further had great effect on the I_{ROX}/I_{MB} Raman signal. Under low 4 concentration conditions, the DNA circuit reaction could not achieve adequate 5 performance, resulting in a decrease in the release of ROX-modified DNA2 from 6 7 magnetic bead. On the contrary, high concentration would increase the amount of MB-modified fuel-DNA unbound to magnetic bead, resulting in a high background 8 signal of IMB in separate solution. To investigate the influence of fuel-DNA 9 concentration, a concentration range from 0.1 to 2.5 μ M was used for entropy-driven 10 DNA circuit reaction. Fig. S3C showed that a peak value of I_{ROX}/I_{MB} appeared at 1.0 11 μ M. Therefore, 1.0 μ M was chosen as the optimum concentration of Fuel-DNA. 12

Moreover, the parameter of Au NSs volume affecting the SERS platform was also investigated in **Fig. S3D**. When no target exists, with the increasing volume of Au NSs, I_{ROX} remains in a low value due to the trace absorption in the liquid–liquid interface and the I_{MB} enhances because of the different enhancement factor of the substrate. Therefore, the I_{ROX} / I_{MB} decreases until the volume of Au NSs is 1.0 mL, indicating the optimal state of the liquid–liquid interface.



8





Fig S3. Optimization of (A) aptamer-P1-DNA concentration, (B) entropy-driven
DNA circuit reaction time, (C) F-DNA concentration, (D) the volume of Au NSs. The
concentration of MUC1 was 10 pg/mL.

7 Table S2. Comparison of MUC1 Detection Based on Different Methods

Method	System	Linear range	LOD Refer	rence
FL	RCA-based Immunoassay	0.001-20 ng/mL	0.23 pg/mL	3
ECL	Tetrahedral DNA nanostructure	1.135 fg/ml-0.1135 ng/mL	0.37 fg/mL	4
FL	DNA Tweezer and Fluorescence	0.01-100 pg/mL	2.6 fg/mL	5
FL	CHA and QDs	1 fg/mL-1 pg/mL	0.15 fg/mL	6
ECL	3-D DNA nanomachine	10 ⁻³ -10 ³ pg/mL	0.62 fg/ml	7
ECL	T7 Exo-RCA and DNA nanoflower	s 10 ⁻³ -10 ⁴ pg/mL	0.23 fg/ml	8
ECL	Tetraphenylethylene microcrystals	1 fg/mL ⁻¹ -1 ng/mL	0.29 fg/mL	9
SERS	Au-Au-UCNP-trimers	0.01-10 fM	0.25	fg/mL
10				
EC	Nanochannel-sensor	1-10 ⁴ fg/mL	0.0364fg/mL	11
SERS	Electrohydrodynamic-Immunoassay	/ 100 pg/mL-10 fg/mL	10 fg/mL	12
ECL	Doped metal-organic nanoplate EC	L 10 ng/mL-10 fg/mL	0.14 fg/mL	13
SERS	DNA circuits and ratiometric	1 fg/mL-10 pg/mL	0.15 fg/m	nL this
work				

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6 Fig. S4 Specificity of the ratiometric SERS sensing platform (A) Raman spectra of
7 the SERS platform with differentanalyst (a) 10 pg/mL of MUC1, (b) blank, (c) 10
8 ng/mL of AFP, (d) 10 ng/mL of CEA,(e) a mixture of the samples mentioned above.
9 (B) The corresponding Raman I_{ROX} /I_{MB} of the differentanalyst. The error bar
10 represents the standard deviation of three measurements.





Fig S5. (A) 20 different spots on the same substrate generating a 2D spectral mapping
of 5.0 × 10⁻⁷ M 4-MBA. (B) Histogram of SERS intensities at 1081 cm⁻¹ of the 20
spectra. (C) the corresponding Raman intensity of the 20 spots.





Fig. S6 Change in the Raman spectra (A), and the ratio value (I_{ROX} /I_{MB})value (B) of
reaction solution with different concentrations of mucin 1 in human serum. Error bars
were estimated from three replicate measurements.

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7 MUC1 Concentration Detection Using a Commercial ELISA Kit

8 The Mucin 1(MUC1) ELISA Kit assay was carried out according to the 9 instruction. Firstly, a standard curve was performed using standard MUC1 samples at 10 a concentration range from 0.6 to 10 ng/mL. Afterwards, MUC1 concentration of 11 different samples was evaluated by comparison with the standard curve.



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13 Fig S7. Linear relationship between optical density at 450 nm and standard MUC1

14 concentration using a Mucin 1(MUC1) ELISA Kit.

Table S3. Recovery Results for MUC1 Determination in Human Serum Samples					
Spiked (pg/mL) ELISA(pg/mL) Recovery (%) Our strategy(pg/mL) Recovery (%)					
(%)					
1.00	Not detected	\	0.96±0.04	96	
5.00	Not detected	\	5.1±0.02	102	
10.00	Not detected	\	10.3±0.5	103	

Fable S4	Comparison	of real blood	sample	detection.
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	ELISA		Our strateg	gy
Sample	MUC1(ng/mL)	RSD	MUC1(ng/mL)	RSD
1	9.056	0.035	9.125	0.042
2	8.527	0.04	8.483	0.038
3	8.713	0.032	8.658	0.045
4	9.567	0.05	9.612	0.028

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