| 1        | <b>Electronic Supplementary Information</b>   |
|----------|---|
| 2        | Establishment of a universal and sensitive plasmonic biosensor  |
| 3        | platform based on the hybridization chain reaction (HCR)  |
| 4        | amplification induced by a triple-helix molecular switch  |
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| Name                      | Sequence (5' to 3')                                     |  |  |  |  |  |
|---------------------------|---|--|--|--|--|--|
| UT                        | AGAGAGAGAGAGAGGGAAAGAGAGAGAGACACACAC                    |  |  |  |  |  |
|                           | AC  |  |  |  |  |  |
| M1                        | CTCTCTCTTTCCCTCTCTCTCTCTCGGCAGAGAGA                     |  |  |  |  |  |
|                           | GAGAGGGAAAG TTTTTTTTTTTTTTTTT                           |  |  |  |  |  |
| M2                        | AGAGAGAGAGAGGGAAAGAGAGAGAGCTTTCCCTC                     |  |  |  |  |  |
|                           | TCTCTCTCTGCCG TTTTTTTTTTTTTTTT                          |  |  |  |  |  |
| P1 for miRNA detection    | CTCCCTTT <i>TCAACATCAGTCTGATAAGCTA</i> TTTCCCT          |  |  |  |  |  |
|                           | С   |  |  |  |  |  |
| P2 for ATP detection      | CTCCCTTTACCTGGGGGGGGGGGGGGGGGGGGGGGGGGG                 |  |  |  |  |  |
|                           | TTTCCCTC  |  |  |  |  |  |
| P3 for thrombin detection | TCCCTTT GGTTGGTGTGGTTGG TTTCCCT                         |  |  |  |  |  |
|                           |   |  |  |  |  |  |
| miRNA-21(DNA sequence)    | TAGCTTAUCAGACTGATGTTGA                                  |  |  |  |  |  |
| MIDNIA 141 (DNIA)         |   |  |  |  |  |  |
| MIRNA-141 (DNA sequence)  | IAACACIGICIGGIAAAGAIGG                                  |  |  |  |  |  |
| MiRNA-155 (DNA sequence)  | TTA ATG CTA ATC GTG ATA GGG GT                          |  |  |  |  |  |
|                           |   |  |  |  |  |  |
| SH-DNA for DNA-AuNPs      | 's SH-(CH <sub>2</sub> ) <sub>6</sub> -AAAAAAAAAAAAAAAA |  |  |  |  |  |
| probes                    |   |  |  |  |  |  |

## **Table S1.** DNA sequences used in this study



30 Fig. S1 UV-visible absorption spectrum (A) and dynamic Light Scattering (B) of



## $\begin{array}{c} 32 \\ 33 \\ 34 \\ 35 \\ 300 \ bp \\ 200 \ bp \\ 150 \ bp \\ 50 \ b$

32 Characterization of P1 and UT THMS complex assembly and disassembly

Fig. S2 3.5% agarose gel electrophoresis demonstrates P1 and UT THMS complex
assembly and disassembly: lane 1: 25~500 bp ladder markers; lane 2:1.0 μM P1; lane
3: 1.0 μM UT; lanes 4: 1.0 μM P1+1.0 μM UT; lanes 5, 1.0 μM P1+1.0 μM UT+0.5
μM miRNA-21;



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Fig. S3 3.5% agarose gel electrophoresis demonstrates HCR products in miRNA-21 system. Lane 1: the DNA marker; Lane 2: M1(1 $\mu$ M); Lane 3: M2(1 $\mu$ M); Lane 4: M1(1 $\mu$ M) + M2(1 $\mu$ M); Lane 5: M1(1 $\mu$ M) + M2(1 $\mu$ M) + UT (0.2  $\mu$ M); Lane 6: M1(1 $\mu$ M) + M2(1 $\mu$ M) + miRNA-21(0.2  $\mu$ M); Lane 7: M1(1 $\mu$ M) + M2(1 $\mu$ M) + P1-UT THMS(0.2  $\mu$ M); Lane 8: M1(1 $\mu$ M) + M2(1 $\mu$ M) +P1-UT THMS(0.2  $\mu$ M) + miRNA-21(0.2  $\mu$ M).

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Fig. S4 3.5% agarose gel electrophoresis demonstrates P2 and UT THMS complex
assembly and disassembly: lane 1: 25~500 bp ladder markers; lane 2:1.0 μM P2; lane
3: 1.0 μM UT; lanes 4: 1.0 μM P2+1.0 μM UT; lanes 5, 1.0 μM P2+1.0 μM UT+0.5
μM ATP;



Fig. S5 3.5% agarose gel electrophoresis demonstrates HCR products in miRNA-21 system. Lane 1: the DNA marker; Lane 2: M1(1 $\mu$ M); Lane 3: M2(1 $\mu$ M); Lane 4: M1(1 $\mu$ M) + M2(1 $\mu$ M); Lane 5: M1(1 $\mu$ M) + M2(1 $\mu$ M) + UT (0.2  $\mu$ M); Lane 6: M1(1 $\mu$ M) + M2(1 $\mu$ M) + ATP(1  $\mu$ M); Lane 7: M1(1 $\mu$ M) + M2(1 $\mu$ M) + P2-UT THMS(0.2  $\mu$ M); Lane 8: M1(1 $\mu$ M) + M2(1 $\mu$ M) +P2-UT THMS(0.2  $\mu$ M) + ATP(1  $\mu$ M).

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Fig. S6 3.5% agarose gel electrophoresis demonstrates P3 and UT THMS complex assembly and disassembly: lane 1: 25~500 bp ladder markers; lane 2:1.0  $\mu$ M P3; lane 3: 1.0  $\mu$ M UT; lanes 4: 1.0  $\mu$ M P3+1.0  $\mu$ M UT; lanes 5, 1.0  $\mu$ M P3+1.0  $\mu$ M UT+0.5  $\mu$ M Tmb.



119Fig. S7 3.5% agarose gel electrophoresis demonstrates HCR products in Tmb. Lane 1: the DNA120marker; Lane 2: M1(1µM); Lane 3: M2(1µM); Lane 4: M1(1µM) + M2(1µM); Lane 5: M1(1µM)121+ M2(1µM) + UT (0.2 µM); Lane 6: M1(1µM) + M2(1µM) + miRNA-21(0.2 µM); Lane 7:122M1(1µM) + M2(1µM) + P3-UT THMS(0.2 µM); Lane 8: M1(1µM) + M2(1µM) + P3-UT123THMS(0.2 µM) + Tmb(0.2 µM).



140 Fig. S8 Effects of (A) the HCR temperature, lane 1: the DNA marker; Lane 2: M1(1µM); Lane 3: 141 M2(1 $\mu$ M); Lane 4: M1(1 $\mu$ M) + M2(1 $\mu$ M); Lane 5: M1(1 $\mu$ M) + M2(1 $\mu$ M) + UT (0.2  $\mu$ M) 4 °C for 2 h; Lane 6:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M)$  25 °C for 2 h; Lane 7:  $M1(1\mu M) +$ 142 143 M2(1 $\mu$ M) + UT (0.2  $\mu$ M) 37 °C for 2 h; (B) the HCR time, lane 1: the DNA marker; Lane 2:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 0 min at 37$ °C; Lane 3:  $M1(1\mu M) + M2(1\mu M) +$ 144  $\mu$ M) for 30 min at 37 °C; Lane 4: M1(1 $\mu$ M) + M2(1 $\mu$ M) + UT (0.2  $\mu$ M) for 1h at 37 °C; Lane 5: 145 146  $M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + UT (0.2 \mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + M2(1\mu M) + M2(1\mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + M2(1\mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + M2(1\mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + M2(1\mu M) + M2(1\mu M) 1.5 min at 37 °C; Lane 6: M1(1\mu M) + M2(1\mu M) + M2(1\mu$ 147  $\mu$ M) 2h at 37 °C; Lane 7: M1(1 $\mu$ M) + M2(1 $\mu$ M) + UT (0.2  $\mu$ M) 4h at 37 °C; Lane 8: M1(1 $\mu$ M) + 148 M2(1µM) + UT (0.2 µM) 8h at 37 °C; (C) and (D)Effects of DNA-AuNPs probes and HCR 149 products aggregation time and temperature. The error bars represent the standard deviations of 150 three replicates.

152 Calculation of limit of detection (LOD)

153 Limit of detection was calculated using the following formula (Anal. Chem., 2012, 84,

- 154 2837–2842, Biosens. Bioelectron., 2015, **63**, 311–316.):
- 155 LOD=  $3\sigma/s$ ;

156 where  $\sigma$  is the standard deviation of the response and s is the slope of the calibration

157 curve of the analyte.

158 For example, the calculation of the LOD for miRNA was shown here:

159 The linear equation was expressed as  $y=0.01571+3.4452\times10^{-4}$  x, which was obtained

160 from Fig.4C in the manuscript, so we can know the  $s=3.4452\times10^{-4}$ . The standard

- 161 deviation of the response was  $\sigma=0.002298$ , which was obtained from the standard
- 162 deviation of signal of the blank sample. Then, the LOD was calculated as follows:
- 163 LOD= $3\sigma/s=3\times0.002298/3.4452\times10^{-4}\approx 20$  pM.
- 164 Similarly, we can use the same method to calculate the LOD of ATP and thrombin.

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| 172 | TableS2   | Comparison | of t | he | proposed | method | with | other | methods | for | miRNA |
|-----|-----------|------------|------|----|----------|--------|------|-------|---------|-----|-------|
| 173 | detection |            |      |    |          |        |      |       |         |     |       |

| Detection Method                          | Linear range | Limit of detection | Reference  |  |  |  |
|---|--------------|--------------------|--|--|--|--|
| Fluorescent                               | 1-50 nM      | 330 pM             | Anal. Methods, 2016,<br><b>8</b> , 8492-8497                     |  |  |  |
| Electrochemical                           | 0.2–755 nM   | 100 pM             | Bioelectrochemistry, 2017, <b>116</b> , 17-23.                   |  |  |  |
| Plasmonic biosensor                       | 10 nM-20 μM. | 300 pM             | ACS Appl. Mater.<br>Interfaces, 2015, <b>7</b> ,<br>2459-2466.   |  |  |  |
| Fluorescence resonance<br>energy transfer | 0.1–200 nM   | 100 pM             | ACS Appl. Mater.<br>Interfaces, 2015, <b>7</b> ,<br>16152–16156. |  |  |  |
| Surface plasmon resonance                 | 0.02–10 pM   | 45 pM              | <i>Microchim. Acta,</i><br>2017, <b>184,</b><br>2637-2644.       |  |  |  |
| Plasmonic biosensor-HCR                   | 20-200 pM    | 20 pM              | Our work   |  |  |  |

**Table S3** Comparison of the proposed method with other methods for ATP detection

| Detection Method                          | Linear range      | Limit of detection                                 | Reference   |  |  |  |
|---|-------------------|--|---|--|--|--|
| Fluorescence Polarization<br>Strategy     | 0.067-26.7 μM     | 34.4 nM  | <i>Anal. Chem.</i> 2018, <b>90</b> , 13708–13713. |  |  |  |
| Electrochemical                           | 1 nM-100 μM       | $\begin{array}{c} 21.33 \pm 4.1 \\ nM \end{array}$ | Anal. Chem. 2018,<br><b>90</b> , 4968–4971        |  |  |  |
| Fluorescence resonance<br>energy transfer | 0.03–2 mM         | 0.03 mM  | Anal. Chem. 2017,<br><b>89</b> , 10941–10947      |  |  |  |
| Surface plasmon resonance                 | 12.4 pM-2.0<br>nM | 12.4 pM  | Anal. Chem. 2012,<br><b>84</b> , 2837–2842        |  |  |  |
| Plasmonic biosensor-HCR                   | 20–500 nM         | 15.6 nM  | Our work  |  |  |  |

| -   | Detection Method        | Linear range  | Limit of detection | Reference   |  |  |  |
|-----|-------------------------|---------------|--------------------|---|--|--|--|
| _   | Fluorescent             | 62.5–187.5 pM | 31.3 pM pM         | <i>Anal. Chem.</i> 2010, <b>82,</b> 2341–2346.              |  |  |  |
| _   | Electrochemical         | 10 pM-50 nM   | 5.6 pM             | <i>Anal. Chem.</i> 2016, <b>88,</b> 8218–8223.              |  |  |  |
|     | Colorimetric biosensor  | 0.1–15 nM     | 0.1 nM             | ACS Appl. Mater.<br>Interfaces 2016, <b>8</b> ,<br>102–108. |  |  |  |
| _   | Paper analytical device | 0-2 μM        | 16 nM              | <i>Anal. Chem.</i> 2014, <b>86,</b> 6166–6170.              |  |  |  |
| _   | Plasmonic biosensor-HCR | 20-800 pM     | 18.4 pM            | Our work  |  |  |  |
| 178 |                         |               |                    |   |  |  |  |
| 179 |                         |               |                    |   |  |  |  |
| 180 |                         |               |                    |   |  |  |  |
| 181 |                         |               |                    |   |  |  |  |
| 182 |                         |               |                    |   |  |  |  |
| 183 |                         |               |                    |   |  |  |  |
| 184 |                         |               |                    |   |  |  |  |
| 185 |                         |               |                    |   |  |  |  |
| 186 |                         |               |                    |   |  |  |  |

| 176 | TableS4   | Comparison | of | the | proposed | method | with | other | methods | for | thrombin |
|-----|-----------|------------|----|-----|----------|--------|------|-------|---------|-----|----------|
| 177 | detection |            |    |     |          |        |      |       |         |     |          |