Supporting Information

Surface acoustic wave biosensor synergizing DNA-mediated in-situ silver nanoparticle growth for highly specific and signal-amplified nucleic acid assay

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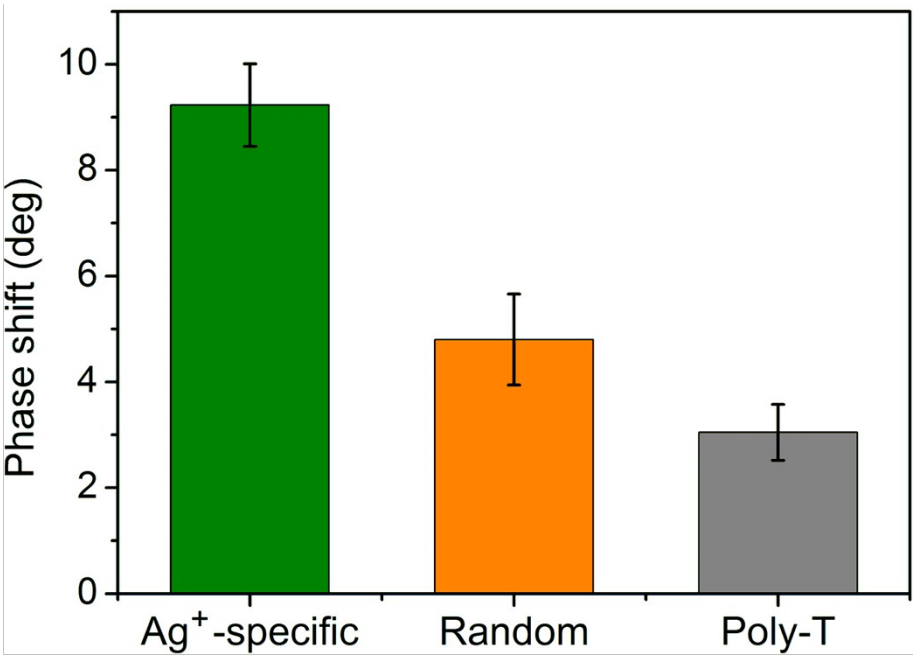

Figure S1. The Love-SAW phase shift of using of different sequences (Ag^+-specific probe, random sequence and poly-T in Table 1) in the presence of 0.5 nM target DNA with synergic signal amplification.

Gel electrophoresis

2% agarose gel was prepared using 1×TBE buffer. 5 μL target (50 μM) was mixed with 5 μL dATP (100 mM), 2 μL TdT (14 U/μL) and 4 μL TdT buffer (5×) together. The mixture was diluted to 20 μL via water and reacted for 2 h at 37℃ prior to inactivation of TdT at 70℃ for 10 min. The loading samples were prepared by mixing 10 μL of the extended product with 2 μL 6×loading buffer. DNA gel electrophoresis was carried out in 1×TBE buffer (89 mM Tris, 89 mM boric acid, 2.5 mM EDTA, pH 8.1) on a horizontal electrophoresis system (DYY-6C, Beijing Liuyi Instrument Factory, China) at 110 mA for 35 min. The size of the extended product was estimated using a 0.1-1 Kb DNA ladder from Takara Biotechnology Co. Ltd. (Dalian, China). As shown in Figure S3, lane 1 had no band, but in lane 2, there were significant band between 300 bp and 900 bp. The results of agarose gel electrophoresis offer direct evidence to show TdT enzymes have a strong chain extension capability.

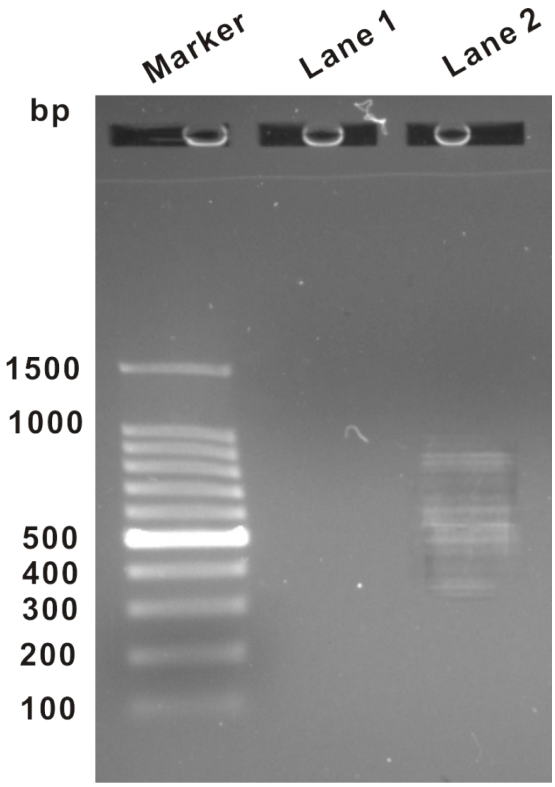

Figure S2. Agarose gel analysis of the extended product of the target sequence at roughly 500 bp (lane 2), and the target without extension (lane 1) that signifies the flowing-out of the short target sequence. In the marker, the bands between 500 bp and 1000 bp are 600, 700, 800 and 900 bp, respectively.

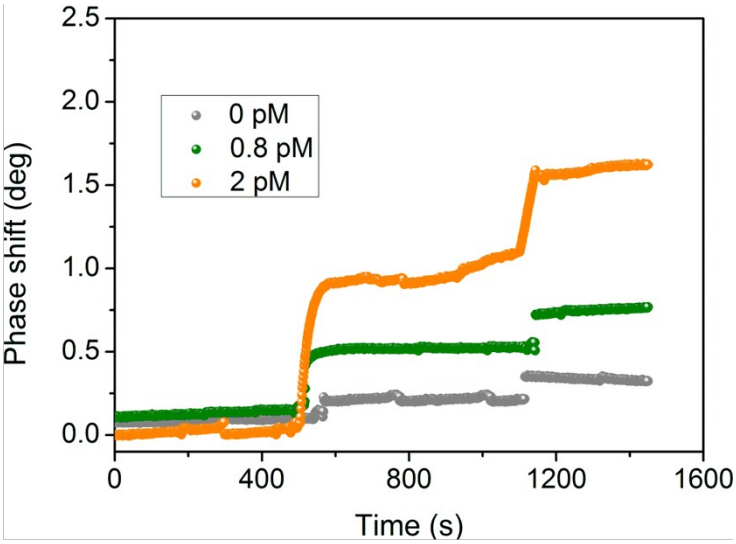

Figure S3. The phase shift of the Love-SAW sensor in response to different concentrations of target DNA with synergic signal amplification. The detection limit of 0.8 pM is detectable.

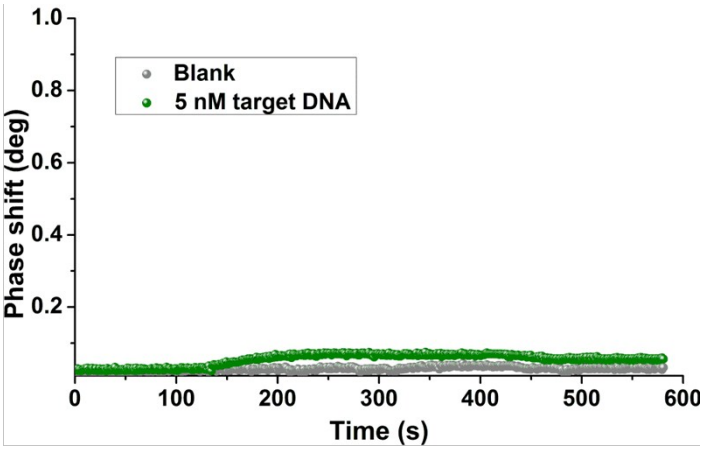

Figure S4. The phase shift of the SAW sensor in response to 5 nM target DNA without signal amplification

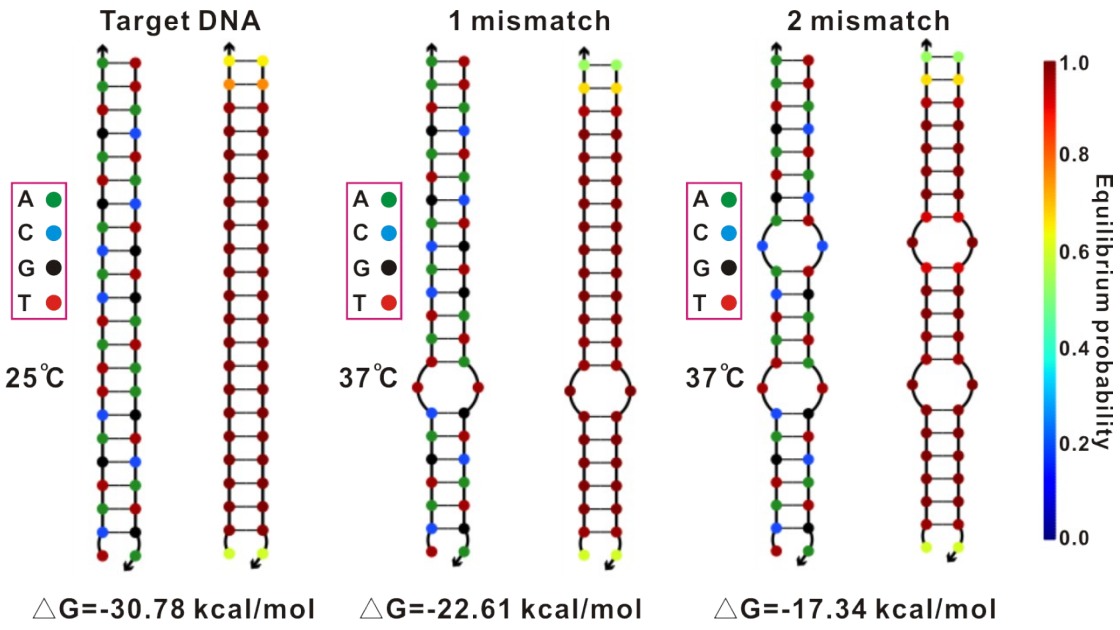

Figure S5. The optimal conformation and free energy of secondary structure (ΔG) of the capture probe in hybridization with the target DNA, 1 mismatch and 2 mismatch sequence, respectively, by NUPACK analysis. The structure of target-capture duplex with free energy of -30.78 kcal/mol at 25°C; The structure of 1 mismatch-capture duplex with free energy of -22.61 kcal/mol at 37°C; The structure of 2 mismatch-capture duplex with free energy of -17.34 kcal/mol at 37°C;

Table S1 Recovery of target DNA spiked into human serum.

Sample	Target DNA added/nM	Target DNA found/nM	Recovery (100%)	RSD(%)
1	0	0	--	--
2	0.05	0.042 [a]	84.0	15.6
3	0.5	0.46 [a]	92.0	18.2
4	5.0	4.4 [a]	88.0	17.5

[a] mean values of three measurements.