Fluorescent recognition of double-stranded DNA based on the quenching of gold nanoparticles to fluorophore labeled DNA probe

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Experimental

CD measurement

For the CD spectroscopy measurements, target dsDNA (5.0 μM), MB (5.0 μM) solution and the mixture of them (5.0 μM) were prepared in 20 mM of PBS buffer (pH 7.0, with 50 mM of NaCl). Subsequently, the samples were measured in a 0.1 cm path length cuvette by using a spectropolarimeter at RT. The average value of the spectra was recorded between 200 and 350 nm at a scanning rate of 50 nm/min, with a response time of 1.0 s and a bandwidth of 1.0 nm.

Samples preparation for TEM images and DLS analysis

For TEM images, the AuNPs and DNA-AuNPs probe samples (20 μL) were dropped onto a carbon-coated copper grid. Then, the samples were kept and dried in a desiccator prior to use. For DLS analysis, 20 μL of AuNPs and DNA-AuNPs probe were diluted to 200 μL respectively. The sizes of AuNPs reported were based on the number average, and each reported particle size was the average of three measurements.

Table S1 Sequence of different oligonucleotides

Name	Sequence (5'-3')
MB	TCAGCTGCGAGTTCTTTCTTTCTTCCTCCCTCGCA
DP	FAM-GCTGCAGCTGAGAGC-$(CH_2)_3$-SH
Target dsDNA (T)	AAGAAAGAAAGAAGGAGG (Ta) CCTTCTTCTTTCTTTCTT (Tb)
Control dsDNA 1 (T_1)	AAGGAAGAAAGAAGGAGG (T_1a) CCTCCTTCTTTCTTCCTT (T_1b)
Control dsDNA 2 (T_2)	AAGGAAGAAAGGAGGAGG (T_2a) CCTCCTCCTTTCTTCCTT (T_2b)

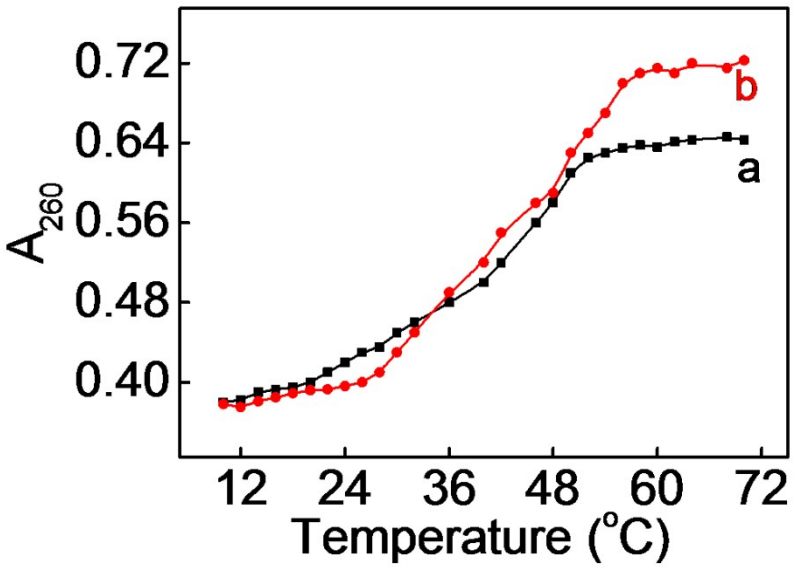

Fig. S1 Melting curves of triplex DNA in the absence (a) and presence (b) of Ag+.

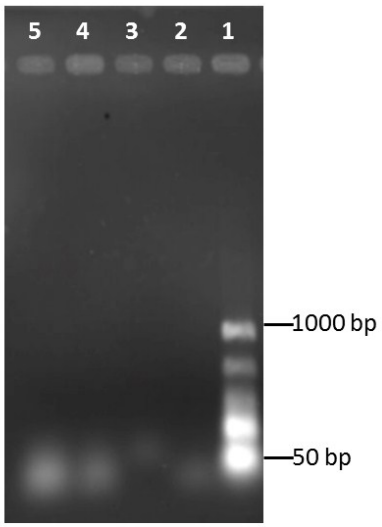

Fig. S2 Gel analysis of 4 μM of DNA strands: 1) DNA marker, 2) DNA probe that used for AuNPs modification, 3) MB/dsDNA/DNA probe, 4) dsDNA and 5) MB.

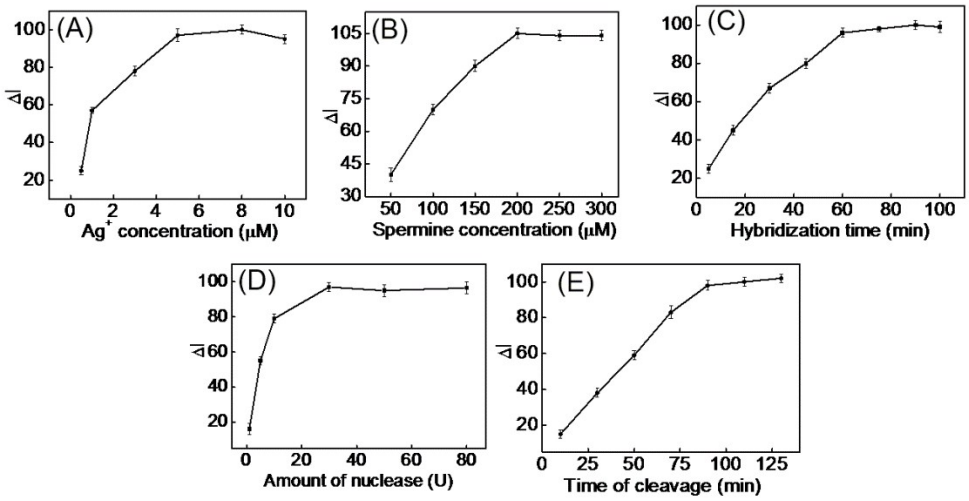

Fig. S3 Effect of Ag^{+} concentration (A), spermine concentration (B), the hybridization time between MB and dsDNA (C), the amount of nicking nuclease (D) and the cleavage time of DNA-AuNPs probe (E). Experiments were conducted in 20 mM of PBS buffer (pH 7.0, with 50 of mM NaCl).

Table S2 Recovery detection of dsDNA in serum samples

Serum samples	Added (nM)	Found (nM)	Recovery (%)	RSD (%)
1	0.5	0.53	106	2.76
2	1.0	0.96	96	3.81
3	1.5	1.46	97.3	2.83