Supporting Information

Silver nanoparticle@DNA tetrahedron based colorimetric detection of HIV-related DNA with cascade strand displacement amplification

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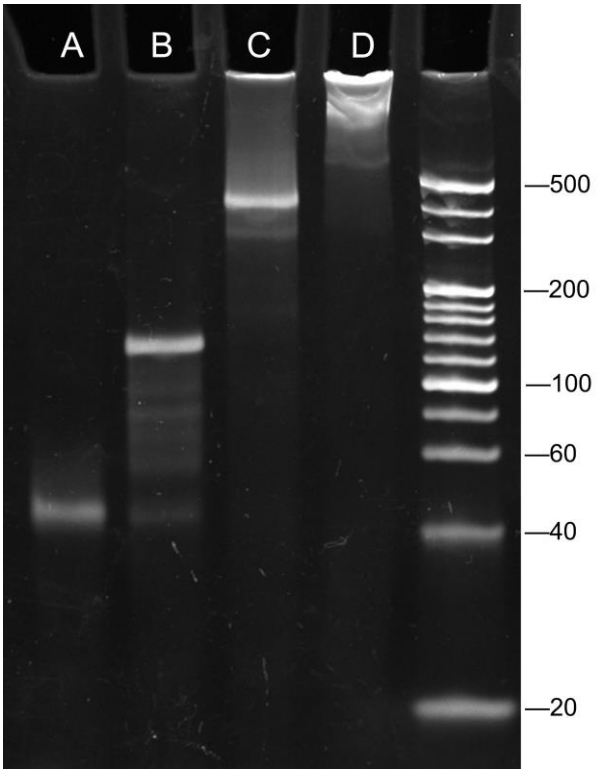

Fig. S1 Polyacrylamide gel electrophoresis analysis of the formation of TDNA: (A) probe T-B, (b) probe T-B and T-C, (c) probe T-B, T-C and T-D, (d) probe T-A1, T-B, T-C and T-D.

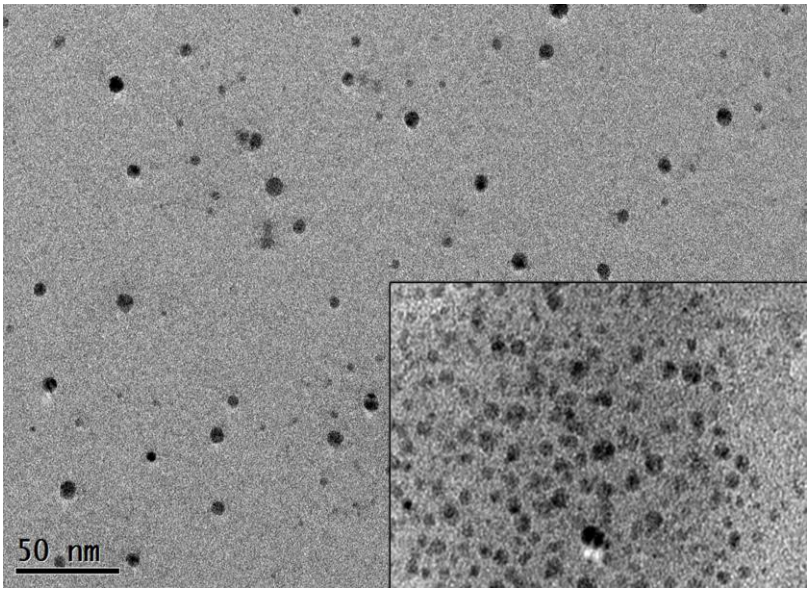

Fig. S2 TEM image of AgNP@DNA tetrahedron. Inset shows Target DNA induced aggregation of AgNP@DNA tetrahedrons.

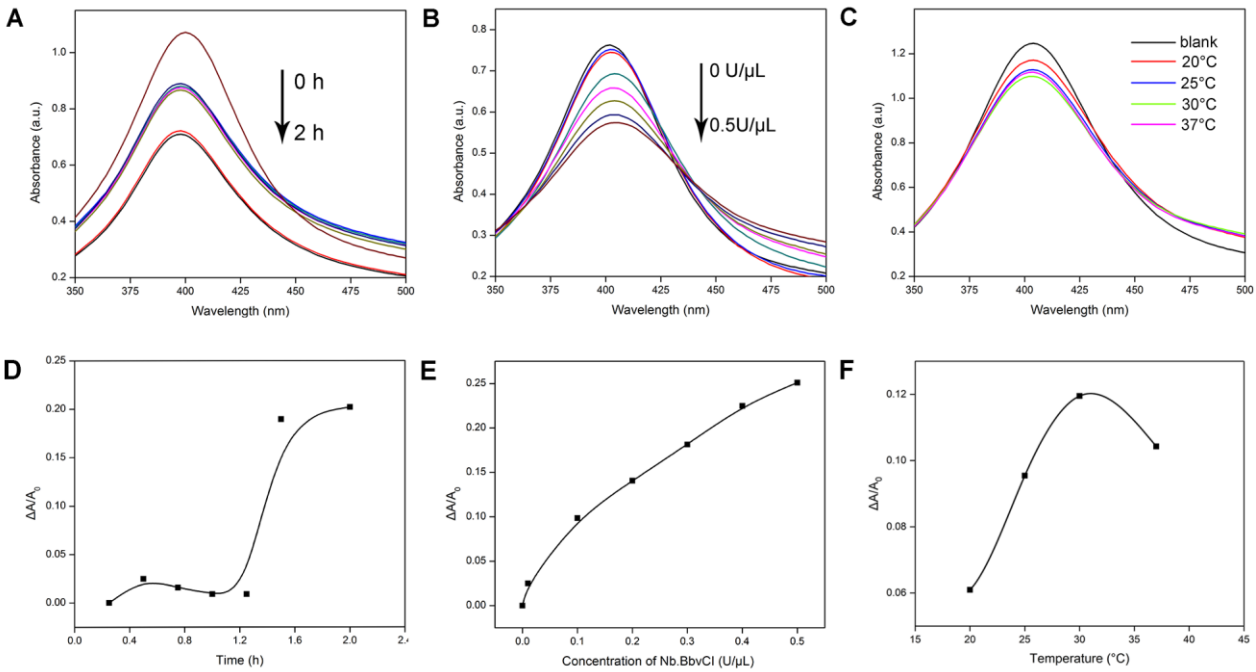

Fig. S3 UV-vis absorption spectra of AgNP@DNA tetrahedron for DNA detection (A) with different reaction time; (B) with different concentrations of enzymes ($c_{\text{Nb.BbvCI}}$: $c_{\text{Klenow fragment}}$ = 5 : 1); (C) at different temperatures for extension and nicking reactions. (D-F) show corresponding $\Delta A/A_0$ values with different experimental conditions.

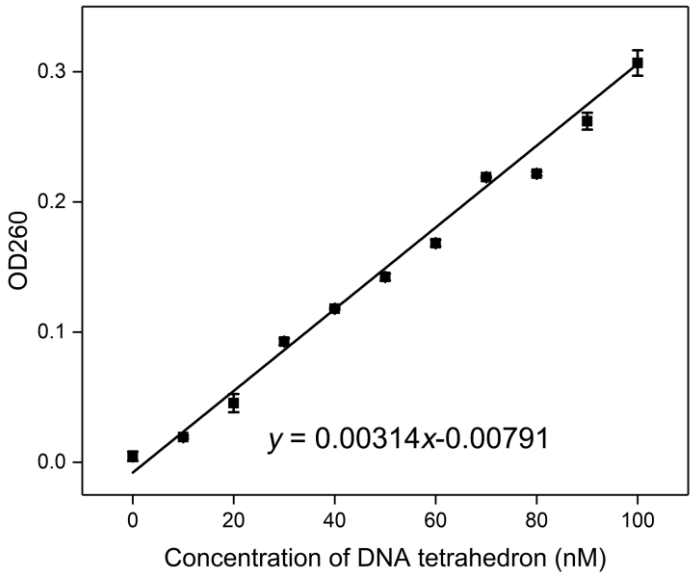

Fig. S4 Calibration plot reflecting the linear relationship between concentration of DNA tetrahedron and UV-vis absorption (260 nm).

Table S1 Comparison of analytical performances of the proposed method with previously developed colorimetric assays.

Strategy	Detection range (M)	LOD (M)	Ref
hybridization-mediated growth of AuNPs	0 to 2×10^{-7}	6×10^{-8}	1
amine-terminated polydiacetylene vesicles	10^{-8} to 10^{-3}	10^{-8}	2
toehold length and temperature adjustments	5×10^{-9} to 3×10^{-8}	5×10^{-9}	3
AuNPs de-aggregation with Exo III-aided amplification	3×10^{-9} to 1.5×10^{-7}	3×10^{-9}	4
aggregation of exonuclease-sheared AuNPs	5×10^{-9} to 4×10^{-8}	2×10^{-9}	5
pyrrolidinyl peptide nucleic acid-induced AgNPs aggregation	2×10^{-8} to 2.5×10^{-6}	1.03×10^{-9}	6
retardation of avidin-induced AuNPs aggregation	10^{-9} to 2.5×10^{-7}	10^{-9}	7
Y-shaped DNA structure	10^{-9} to 2.5×10^{-7}	9.5×10^{-10}	8
peroxidase mimetics of PtNPs on reduced graphene oxide	5×10^{-10} to 10^{-8}	4×10^{-10}	9
catalyzed hairpin assembly and AuNPs	5×10^{-11} to 7×10^{-10}	2.5×10^{-11}	10
AgNP@DNA tetrahedron and cascade SDA	10^{-9} to 1.5×10^{-5}	8.4×10^{-10}	this method

Table S2 DNA sequences used in this work

Name	Sequence (5'-3')
Target DNA	GCTAGAGATTTTCCACACTGACT
Template DNA	GAATCCATGAAAAAAAAGGAAGCTG**CCTCAGC**AGTCAGTGTG GAAAATCTCTAGC**CCTCAGC**AGTCAGTGTGGAAAATCTCTAGC
Linker DNA	TGAGGCAGCTTCCTTTTTTTTCATGGATTC
T-A1	AGGAAGCTGCCTCATTACATTCCTAAGTCTGAAACATTACAGCTT GCTACACGAGAAGAGCCGCCATAGTA
T-A2	GAATCCATGAAATTACATTCCTAAGTCTGAAACATTACAGCTTGC TACACGAGAAGAGCCGCCATAGTA
T-B	NH_2-C_6-TATCACCAGGCAGTTGACAGTGTAGCAAGCTGTAATAGA TGCGAGGGTCCAATAC
T-C	NH_2-C_6-TCAACTGCCTGGTGATAAAACGACACTACGTGGGAATCT ACTATGGCGGCTCTTC
T-D	NH_2-C_6-TTCAGACTTAGGAATGTGCTTCCCACGTAGTGTCGTTTGT ATTGGACCCTCGCAT
M1	GCTAGAGATTTTCCACACTGATT
M2	GTTAGAGATTTTCCACACTGACT
M3	GCTAGAGATTTTCGACACTGACT
M4	GCTAGAGACTTTCCACACTGACT

Bold sequences are the recognition sites of the enzyme. Green and blue sequences are complementary sequences. Underlined parts are the complementary sequences of target DNA.

References

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