

Supporting Information

Real-Time Monitoring of Enzyme-Free Strand Displacement

Cascade by Colorimetric Assays

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1.Sequences

Table S1. The first set of oligonucleotides' sequences:

Name	Sequence (from 5' to 3')
C1	AACCACCAAACCTTAT <u>CTCT</u> CCAAACAAAACCTAT
C2	<u>AGAG</u> ATAAGTTTGGTGGTT <u>AGAG</u>
C3	CCTAACACAATCACT <u>CTCT</u> AACCACCAAACCTTAT
C4	CCACAAAACAAAACCT <u>CTCT</u> AACCACCAAACCTTAT
C3-TAMRA	CCTAACACAATCACT <u>CTCT</u> AACCACCAAACCTTAT-(TAMRA)
C2-DABCL	<u>AGAG</u> A-(DABCYL) TAAGTTTGGTGGTT <u>AGAG</u>
blue GNP1	HS-TTTTATAAGTTTGGTGGTTAGAGAGTGATTGTGTTAGG
blue GNP1 poly15	HS-TTTTTTTTTTTTTTTTATAAGTTTGGTGGTTAGAGAGTGATTGTGTTAGG
blue GNP1 poly25	HS-TTTTTTTTTTTTTTTTTTTTTTTTATAAGTTTGGTGGTTAGAGAGTGATTGTGTTAGG
blue GNP2	HS-TTTTCCTAACACAATCACTCTCTAACCA
blue helper	HS-TTTTA
SNP5	AACC <u>C</u> CAAACCTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP6	AACCA <u>T</u> CAAACCTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP7	AACCAC <u>A</u> AAACCTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP8	AACCAC <u>C</u> CAACCTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP9	AACCACCA <u>C</u> ACTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP10	AACCACCA <u>T</u> CTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP11	AACCACCAA <u>A</u> TTTAT <u>CTCT</u> CCAAACAAAACCTAT
SNP12	AACCACCAAAC <u>A</u> TAT <u>CTCT</u> CCAAACAAAACCTAT
SNP13	AACCACCAAAC <u>T</u> CAT <u>CTCT</u> CCAAACAAAACCTAT
SNP14	AACCACCAAAC <u>T</u> <u>T</u> <u>CTCT</u> CCAAACAAAACCTAT
SNP15	AACCACCAAAC <u>T</u> <u>A</u> <u>CTCT</u> CCAAACAAAACCTAT
SNP16	AACCACCAAACCTTAT <u>A</u> <u>T</u> <u>C</u> <u>T</u> CCAAACAAAACCTAT
SNP17	AACCACCAAACCTTAT <u>C</u> <u>C</u> <u>C</u> <u>T</u> CCAAACAAAACCTAT
SNP18	AACCACCAAACCTTAT <u>C</u> <u>T</u> <u>T</u> CCAAACAAAACCTAT
SNP22	AACCACCAAACCTTAT <u>CTCT</u> CC <u>C</u> AACAAAACCTAT
SNP27	AACCACCAAACCTTAT <u>CTCT</u> CCAAACA <u>T</u> AACCTAT

Table S2. The second set of oligonucleotides' sequences:

Name	Sequence (from 5' to 3')
2-C1	CAACTCTTTAAA <u>CTCA</u> TACTAAACAAAACCC TTAAATT
2-C2	<u>TGAG</u> GGGTTTTGTTTAGTA <u>TGAG</u>
2-C3	TACTAAACAAAACCC <u>CTCA</u> CATCTTCTAACATCA
2-C4	TACTAAACAAAACCC <u>CTCA</u> CACACTATAATTCCA
2-blue GNP1	HS-TTTTTGATGTTAGAAAGATGTGAGGGGTTTTGTTTAGTA
2-blue GNP2	HS-TTTTTACTAAACAAAACCCCTCACATCT
blue helper	HS-TTTTA
2-SNP4	CAACTCTTTAAA <u>CTC</u> <u>C</u> TACTAAACAAAACCCTTAAATT
2-SNP5	CAACTCTTTAAA <u>CTCA</u> <u>C</u> ACTAAACAAAACCCTTAAATT
2-SNP8	CAACTCTTTAAA <u>CTCA</u> TAC <u>C</u> AAACAAAACCCTTAAATT
2-SNP10	CAACTCTTTAAA <u>CTCA</u> TACTA <u>C</u> ACAAAACCCTTAAATT
2-SNP13	CAACTCTTTAAA <u>CTCA</u> TACTAAAC <u>C</u> AAACCCTTAAATT

2. Materials

Ultrapure water with 18.2 M Ω cm (Heal Force) is used in all experiments. All of the chemical reagents are of analytic grade and are used without further purification. The 10 nm gold nanoparticles, Tris(2-carboxyethyl) phosphine hydrochloride (TCEP) are purchased from Sigma. All the DNA oligonucleotides purified via HPLC are synthesized by TaKaRa Bio Inc. (Dalian, China) DNase I is purchased from TaKaRa Bio Inc. (Dalian, China)

3.Reversible assembly (Figure S1)

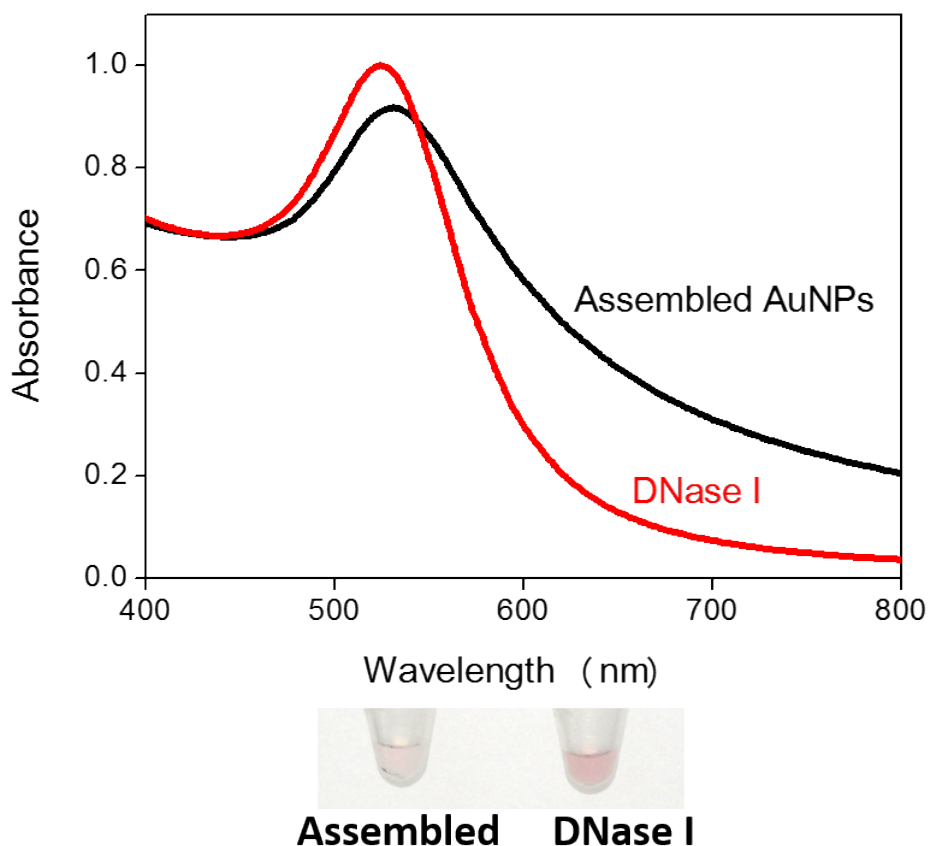


Figure S1. (a) UV-vis spectra of aggregated AuNPs and disassembled AuNPs by DNase I. The reaction time is 1 h at 37°C. After adding DNase I, the wavelength of absorbance peak decreases, proving the disassembly of AuNPs. (b) Corresponding bar graphs and photographs of AuNPs before and after adding DNase I.

4.The effects of the number of polyT (Figure S2)

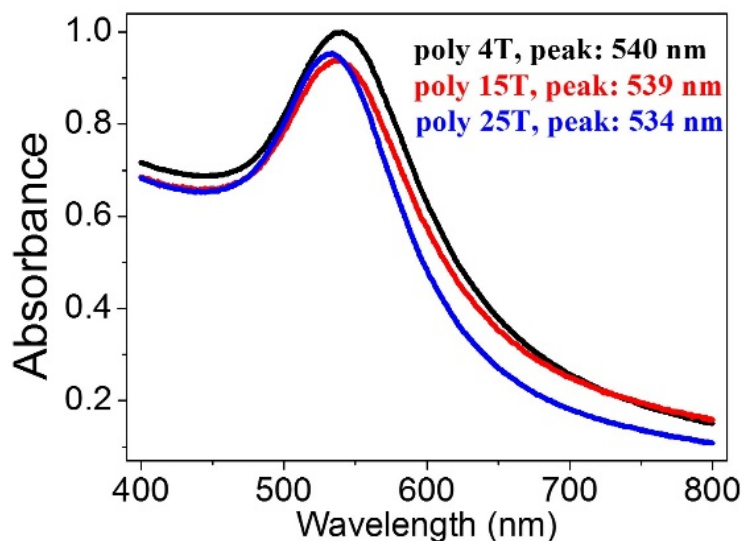


Figure S2. The effects of the number of poly T of the effective oligonucleotides on making AuNPs aggregate. The absorbance peaks of aggregated AuNPs modified with 4-base, 15-base and 25-base poly T are 540 nm, 539 nm and 534 nm respectively.

5. Average diameter (Figure S3)

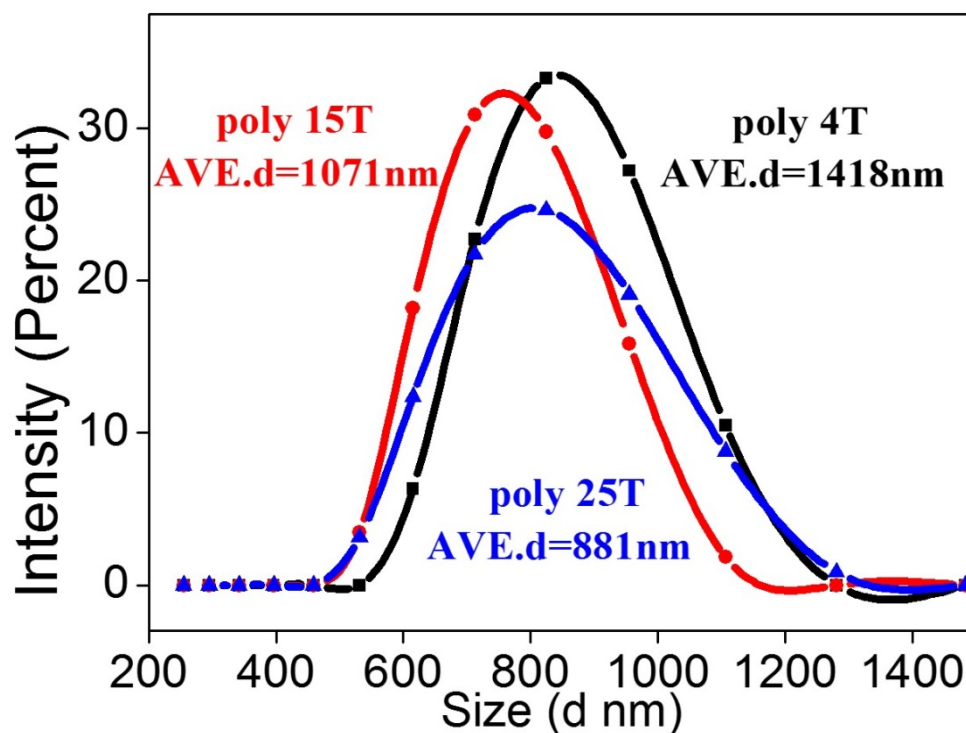


Figure S3. The scattering data shows the average diameter of each kind of AuNPs after annealing. The average diameters of aggregated AuNPs modified with 4-base, 15-base and 25-base poly T are 1418 nm, 1071 nm and 881 nm respectively.

6. Not producing 'false mismatch signal' (Figure S4)

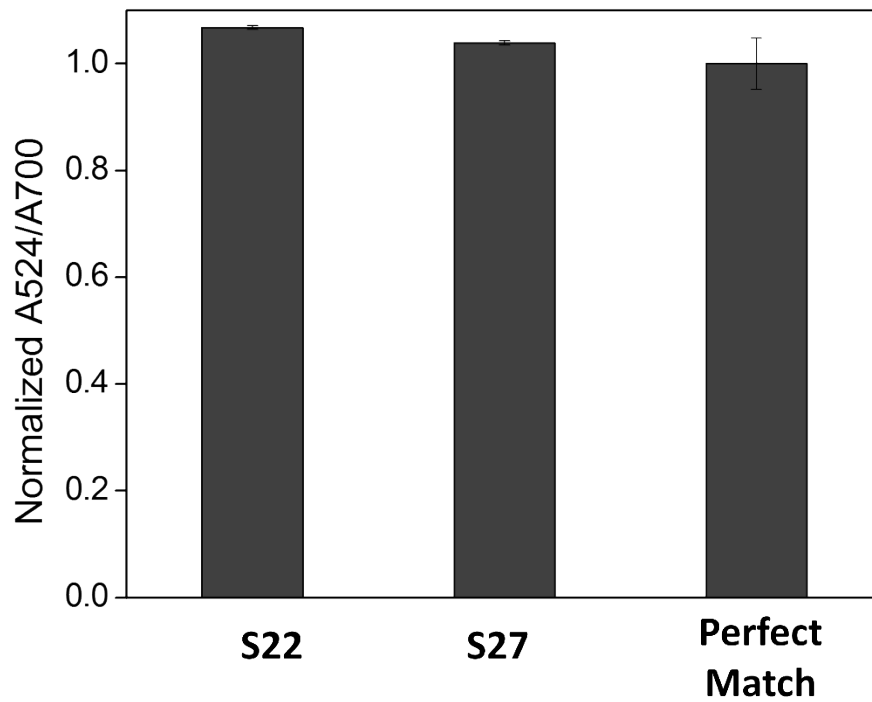


Figure S4. The values of A524/A700 of mismatch positions belonging to the part not participating hybridization are close to that of perfect match sequence, indicating the part not participating hybridization will not produce 'false mismatch signal'.

7. Another set of mismatch experiment (Figure S5)

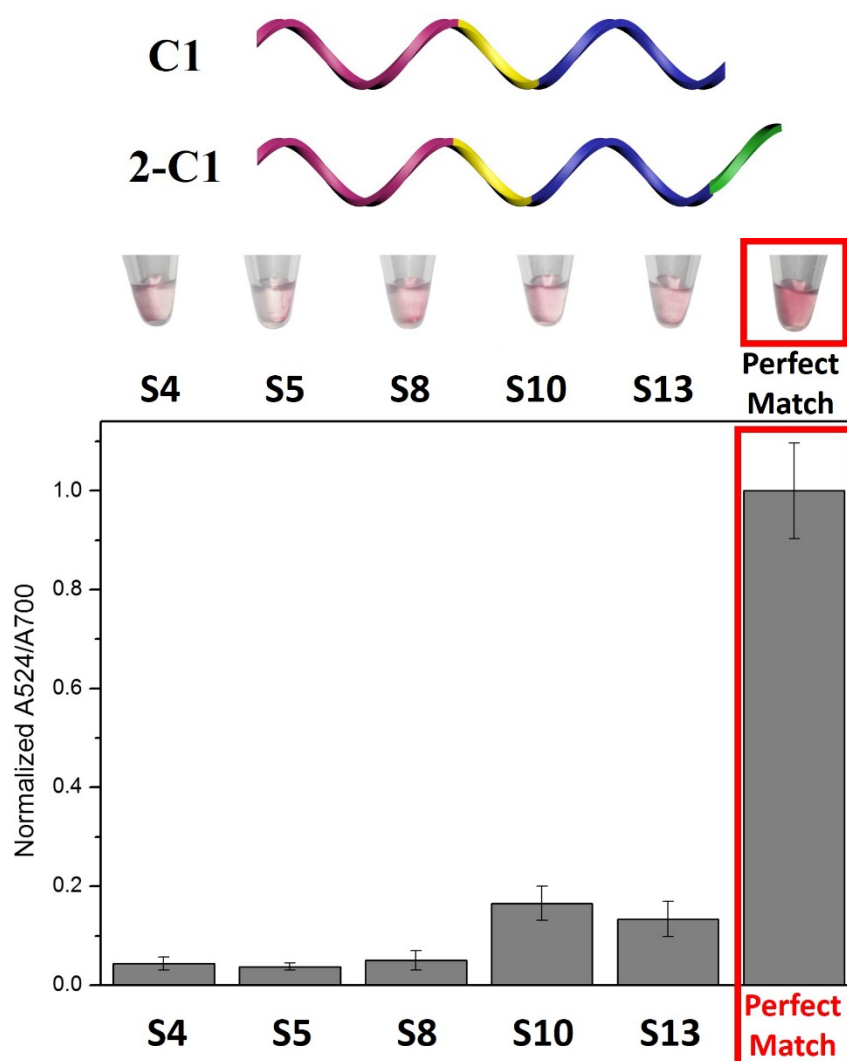


Figure S5. (Upper) Compared with **C1**, **2-C1** has two hang out parts (purple and green) on each side of hybridization part (yellow and blue). (Bottom) Another set of sequences for single-base mismatch detection also work well. The bar graph shows the value of A524/A700 of each sample.

8. References

1. Qian, L. & Winfree, E. Scaling Up Digital Circuit Computation with DNA Strand Displacement Cascades. *Science* **332**, 1196-1201 (2011).
2. Song, S.P. et al. Gold-Nanoparticle-Based Multicolor Nanobeacons for Sequence-Specific DNA Analysis. *Angew. Chem. Int. Ed.* **48**, 8670-8674 (2009).