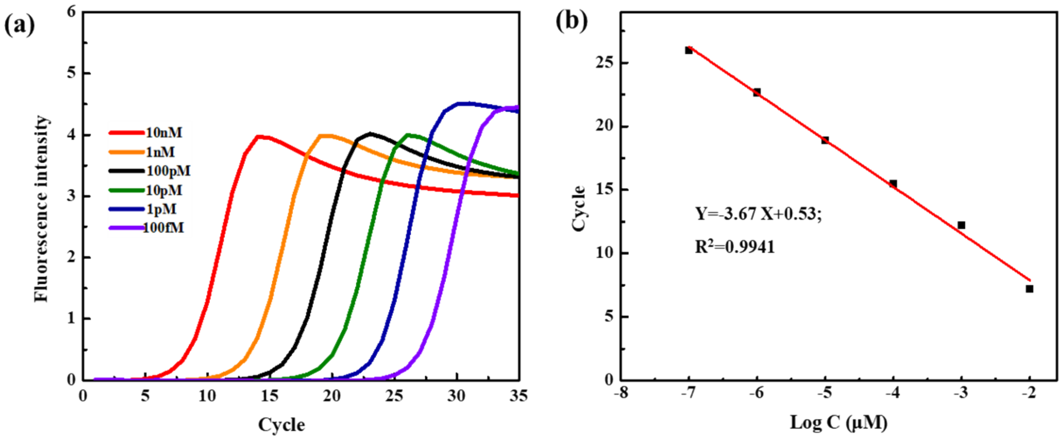

Figure S1 The standard curve plotting of library. (a) Amplification curves of Library at 10 nM, 1 nM, 100 pM, 10 pM, 1 pM and100 fM, respectively; (b) Linear fitting graph between Ct values and logarithmic values of concentration for library.

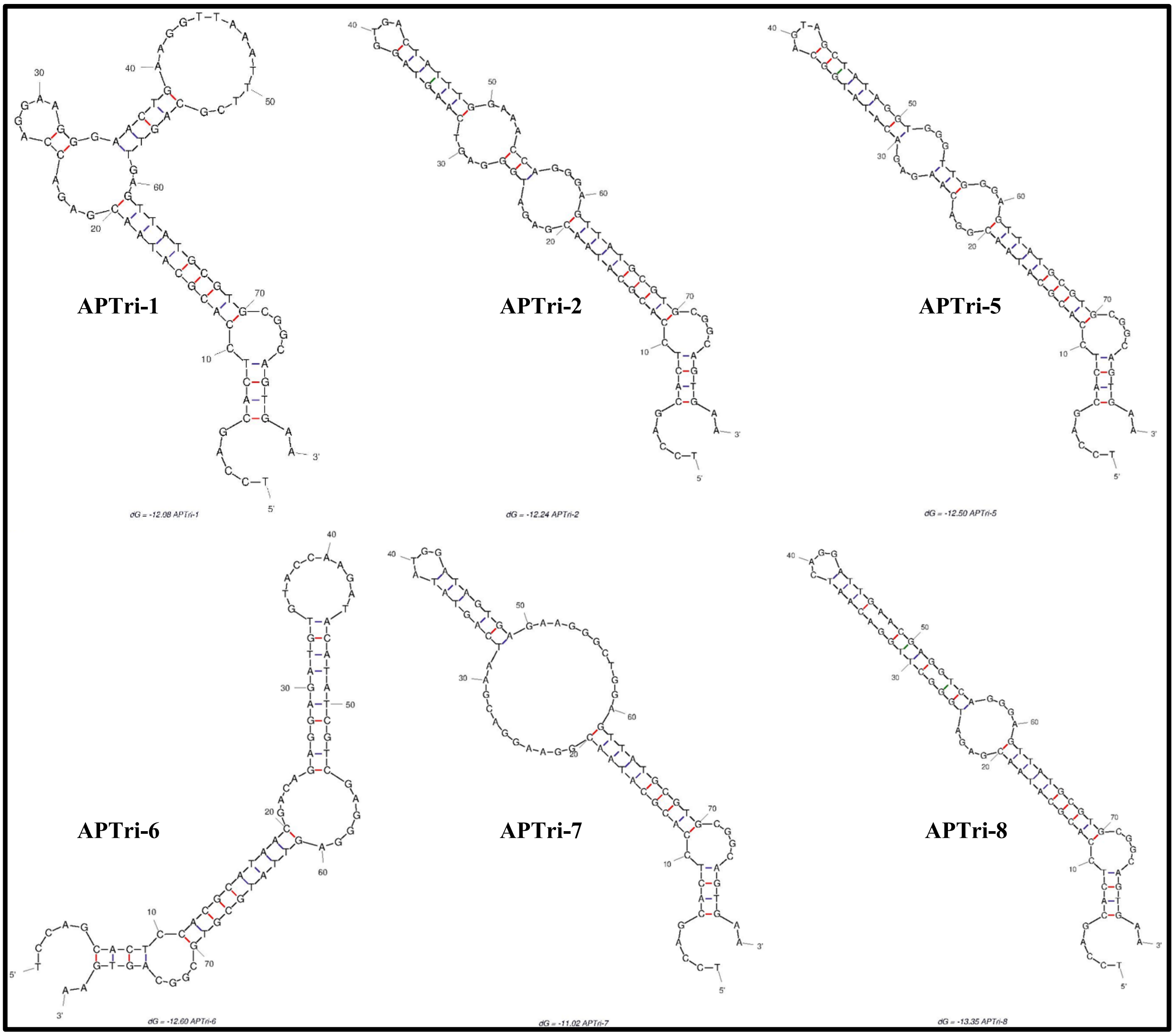

Figure S2 Secondary structure diagram of six candidate aptamers.

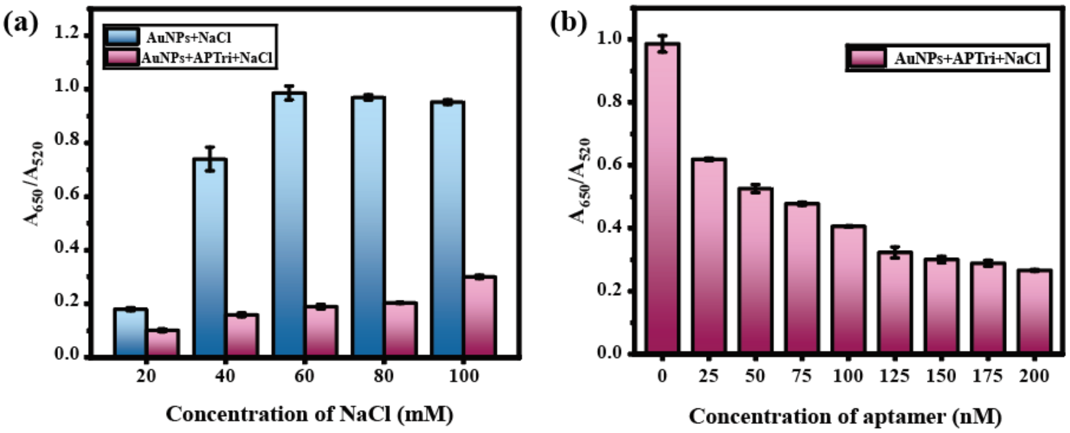

Figure S3 Optimization of experimental parameters for colorimetric assay using AuNPs. (a) Optimization of NaCl concentration; (b) Optimization of aptamer concentration.

Table S1 List of DNA sequences

Name	Sequence（5′→3′）
Library 3	TCCAGCACTCCACGCATAAC-(N)40-GTTATGCGTGCGGCAGTGAA
P5	TCCAGCACTCCACGCATAAC
P6	TTCACTGCCGCACGCATAAC
Lib3-biotin	GTTATGCGTGGAGTGCTGGA-biotin
Lib3-polyA	AAAAAAAAAAAAAAAAAAAAAAAAA/iSp18/TTCACTGCCGCACGCATAAC
Lib3-FAM	FAM-TCCAGCACTCCACGCATAAC

Table S2 Thirteen sequence information with the highest degree of enrichment

APTri-n	Sequence information（5′→3′）	△G (kcal/mol)
APTri-1	TCCAGCACTCCACGCATAACGAGACCAGGAAGGGAACTGAAGGTTAAATTTCGCAGTTGAGTTATGCGTGCGGCAGTGAA	-12.08
APTri-2	TCCAGCACTCCACGCATAACGAGATGGGAGTCAAGTAGGTGACTATTTGGAAACCAGGGAGTTATGCGTGCGGCAGTGAA	-12.24
APTri-3	TCCAGCACTCCACGCATAACGACAGAGACACGATTGGCGAAAAGCAATGGGGATGATGGAGTTATGCGTGCGGCAGTGAA	-9.53
APTri-4	TCCAGCACTCCACGCATAACGAGGGACGTAGACTGAAGGAACTGAGAGGGTATGGCGTGAGTTATGCGTGCGGCAGTGAA	-9.12
APTri-5	TCCAGCACTCCACGCATAACGGACAAGAGACATATGGCAGTAGCTATAGGTGGGTTGGGAGTTATGCGTGCGGCAGTGAA	-12.50
APTri-6	TCCAGCACTCCACGCATAACGACAGAGGAGATGTGTACCAAGATACATATCGTCGAGGGAGTTATGCGTGCGGCAGTGAA	-12.60
APTri-7	TCCAGCACTCCACGCATAACGGAAGGACGAATCAGTATATGGATAGTGAGAAGGGCTGGAGTTATGCGTGCGGCAGTGAA	-11.02
APTri-8	TCCAGCACTCCACGCATAACGAGATGGGCTTGGACAATCAGGATTGAACGAGGTCAGGGAGTTATGCGTGCGGCAGTGAA	-13.35
APTri-9	TCCAGCACTCCACGCATAACGGAGACGACAACAATACAAGGGGTATGGGAAGGAGATGTAGTTATGCGTGCGGCAGTGAA	-9.87
APTri-10	TCCAGCACTCCACGCATAACGACAACGGAACACGATGGTTTTAACAGAGAGGACCTTGGAGTTATGCGTGCGGCAGTGAA	-11.49
APTri-11	TCCAGCACTCCACGCATAACGACAGACAGCCAGAGATAGTTAATCCGTGTGGTGTTTGGAGTTATGCGTGCGGCAGTGAA	-12.17
APTri-12	TCCAGCACTCCACGCATAACGAAAGACCGAGACAGACCGATAGTGATGTTGAGTTCTGGAGTTATGCGTGCGGCAGTGAA	-9.35
APTri-13	TCCAGCACTCCACGCATAACGAGCAGGCTCAGCTGAAATAGGTTGAAGTGGGGGTTGTGAGTTATGCGTGCGGCAGTGAA	-10.30