Supporting Information

Metal-DNA coordination based bioinspired hybrid nanospheres for in situ amplification and sensing of microRNA

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Table of Contents

Results and Discussion

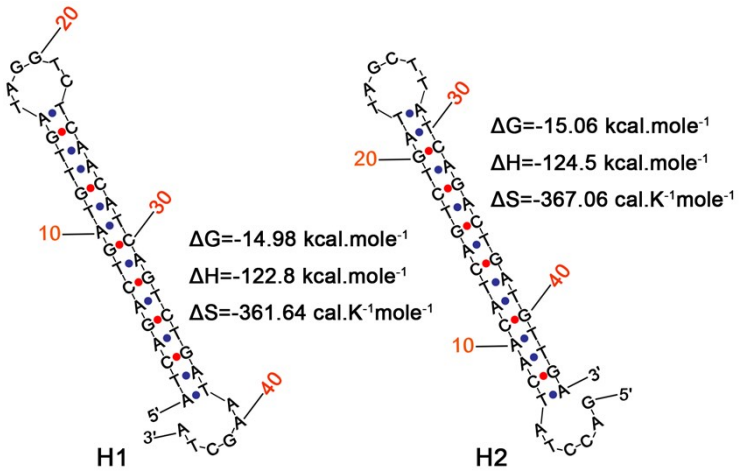

Fig. S1. Ideal hairpin structure and thermal kinetic parameters of H1 and H2.

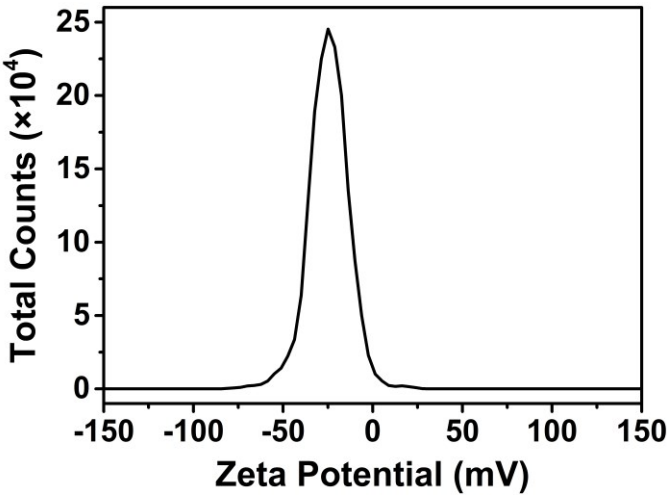

Fig. S2. Zeta potential of NWs.

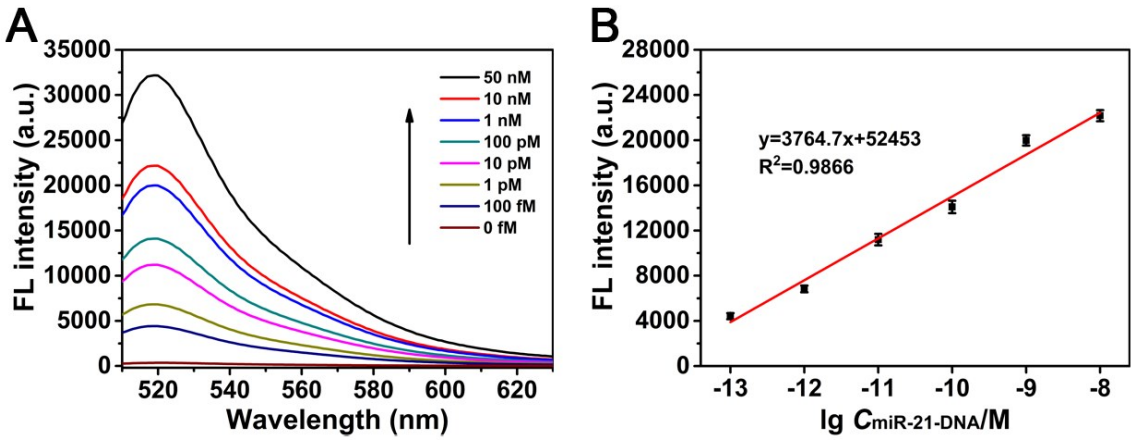

Fig. S3. Detection of miR-21-DNA by NWs-based method. (a) In vitro FL spectra for different concentrations of DNA: 0, 100 fM, 1 pM, 10 pM, 100 pM, 1 nM, 10 nM, and 50 nM, respectively. (b) The linear relationship between the fluorescence signal and the logarithm of concentrations of miR-21-DNA. The illustrated error bars represented the standard deviation of three independent measurements.

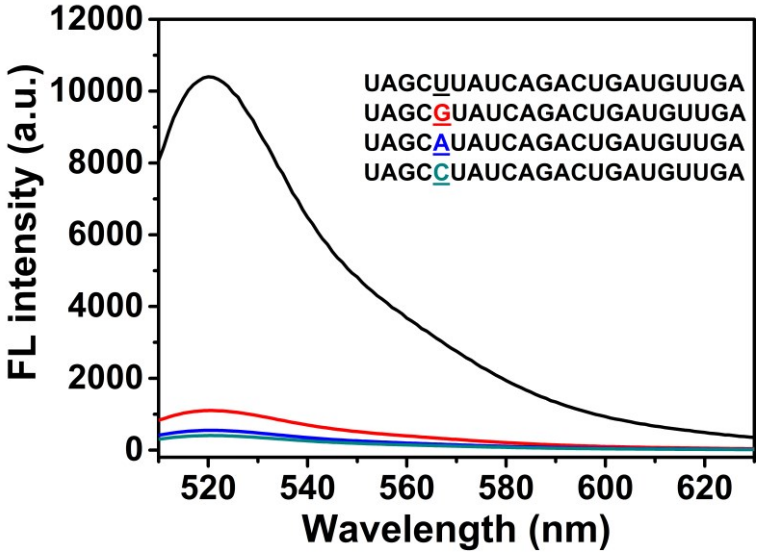

Fig. S4. Specificity investigation of the proposed strategy for miR-21. The assays were carried out in the reaction buffer for a fixed primer concentration of 10 nM.

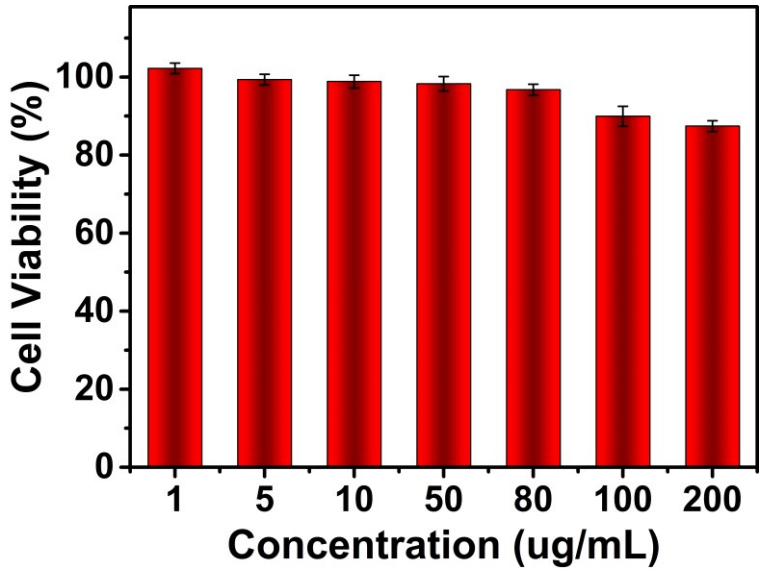

Fig. S5. Cell viability of NWs against HepG2 cells with different treatments after 24 h incubation. Error bars denote the standard deviation (n = 3).

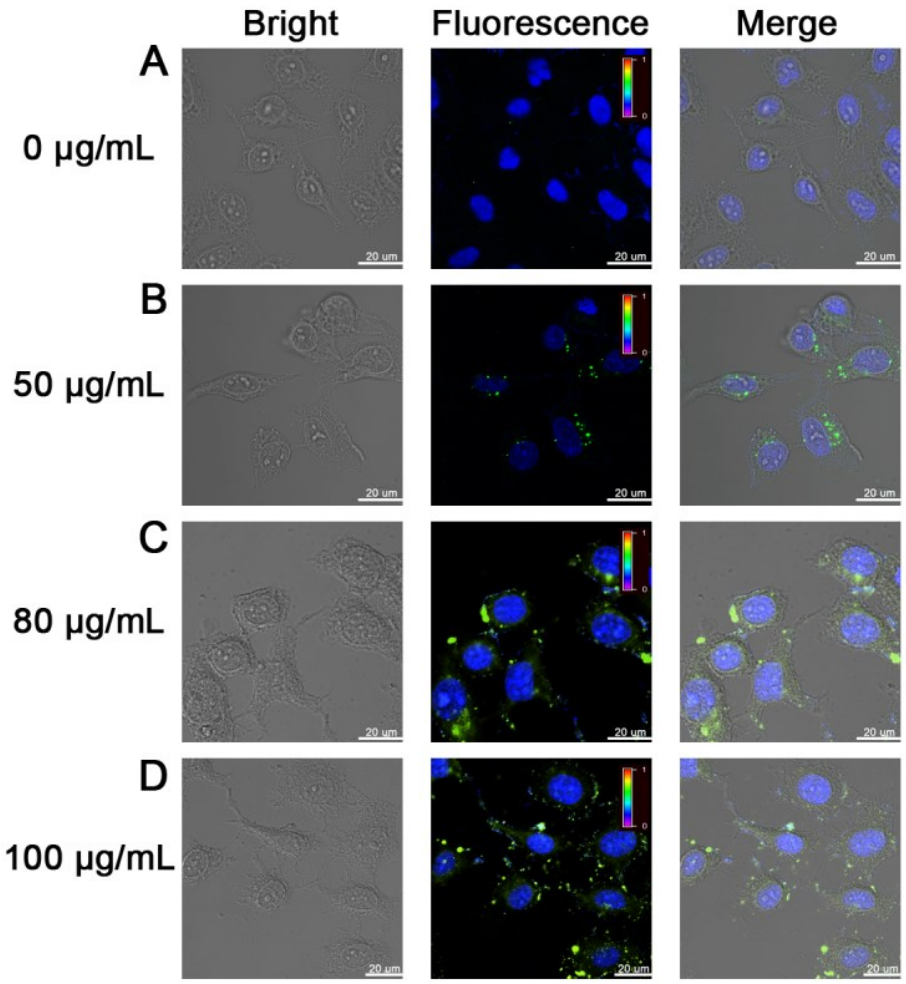

Fig. S6. Confocal microscopy images of HepG2 cells treated with different NWs concentration. Scale bars = 20 μm.

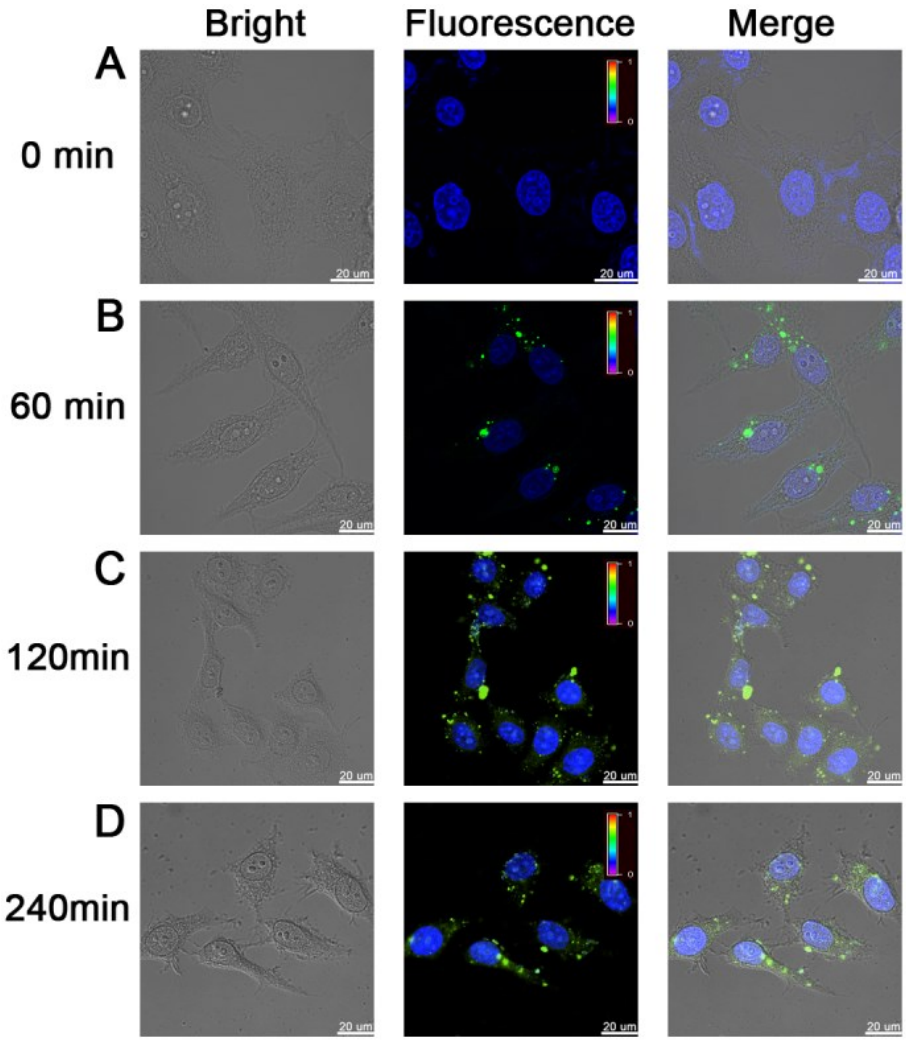

Fig. S7. Confocal microscopy images of HepG2 cells treated with NWs after different incubation times. Scale bars = 20 μm.

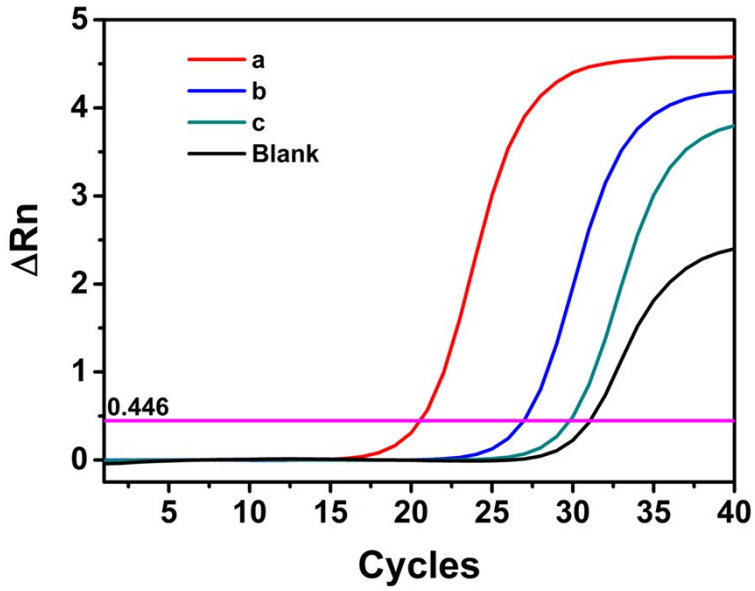

Fig. S8. RT-PCR detection of cell extracts from (a) HepG2 cells, (b) CCC-HEL-1 cells, (c) HepG2 cells treated with miR-21 inhibitor oligonucleotide, and blank control group without target treatment.

Table S1. Oligonucleotide sequences designed in the current study.

Name	Detailed sequence information (from 5′ to 3′)
H1	ATCAGACTGATGTTGATAGGTCTCAACATCAGTCT GATAAGCTA
H2	GACCTATCAACATC-FAM-AGTCTGATTAGCTTATCA GACT-BHQ1-GATGTTGA
miR-21	UAG CUU AUC AGA CUG AUG UUG A
miR-21-a	UAG CGU AUC AGA CUG AUG UUG A
miR-21-b	UAG CAU AUC AGA CUG AUG UUG A
miR-21-c	UAG CCU AUC AGA CUG AUG UUG A
miR-21-DNA	TAG CTT ATC AGA CTG ATG TTG A
miR-21 inhibitor	UCA ACA UCA GUC UGA UAA GCU A
miR-141	UAA CAC UGU CUG GUA AAG AUG G
miR-155	UUA AUG CUA AUC GUG AUA GGG GU
Let-7a	UGA GGU AGU AGG UUG UAU AGU U
RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTG GATACGACTCAACA
Forward primer	GCCCGCTAGCTTATCAGACTGATG
Reverse primer	GTGCAGGGTCCGAGGT

The hairpin structures for H1and H2 are labelled in the same color as it illustrated in the Scheme 1. The miR-21-a, miR-21-b, miR-21-c are single-base mismatched strand of the miRNA-21.

Table S2. Recovery results for the assay of microRNA in 10% human serum.

NO.	Target miRNA spiked (10^{-12} M)	Target miRNA detected (10^{-12} M)	Recovery (%)	RSD% (n=5)
1	10	9.6	96.0	5.3
2	20	20.5	102.5	4.1
3	50	49.3	98.6	3.8
4	100	103.2	103.2	4.7
5	200	190.8	95.4	6.4
6	500	486.5	97.3	5.2
7	1000	1068.1	106.8	4.3