Supplementary data

Table S1. Oligonucleotides sequence used in this study

| Oligonucleotide name	sequence (5´ to 3´)
DNA probe	ACC CCT ATC ACG ATT AGC ATT AA
Non complementary DNA target	GAA CAC TTG GGT TAA CAG CCA AA
MiR-21	UAG CUU AUC AGA CUG AUG UUG A
Let-7a	UGA GGU AGU AGG UUG UAU AGU U
MiR-155	UUA AUG CUA AUC GUG AUA GGG GU
MiR-155 with five mismatches	UUA AUG CUA AUC GUG AUA <u>CCA CC</u>
MiR-155 RT	GAAAGAAGGCGAGGAGCAGATCGAGGAAGAAGACGGAAGAATGTGCGTCTCG CCTTCTTTCACCCCTAT
MiR-155 Forward	GCGGTTAATGCTAATCGTGATA
MiR-155 Reverse	CGAGGAAGAAGACGGAAGAAT
U6 small RNA RT	AAAATATGGAACGCTTCACG
U6 small RNA Forward	CGCTTCGGCAGCACATATACTAAAATTGGAAC
U6 small RNA Reverse	GCTTCACGAATTTGCGTGTCATCCTTGC

Characterization of the Fluorescent CdTe QDs

The shape and size of the CdTe QDs were determined by transmission electron microscopy (TEM), and as it can be seen in Fig. S1 A, the results showed that QDs have a size of about 5 nm with negative zeta potential (-25 mV).
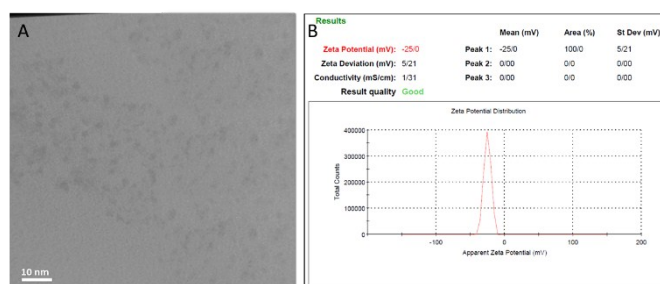

Figure S1. TEM image (A) and Zeta potential (B) for CdTe QDs.
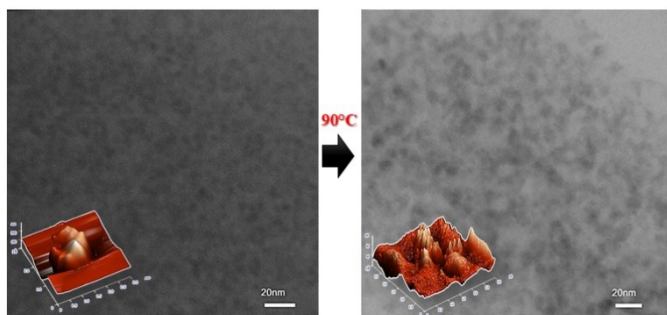
Figure S2. TEM images from double stranded DNA/miR-155@QDs before heat treatment (left) and (D) double stranded DNA/miR-155@QDs after heat treatment (right)
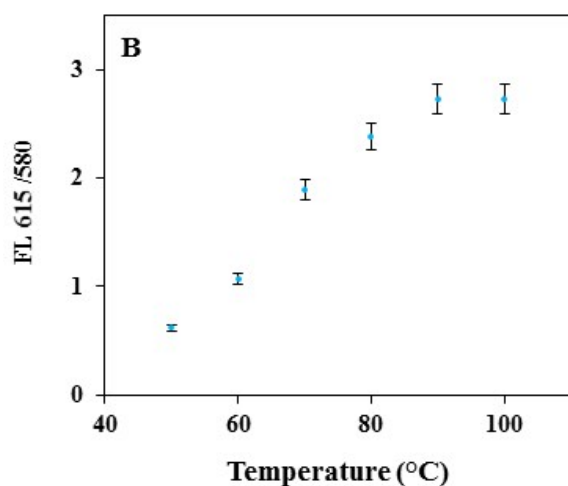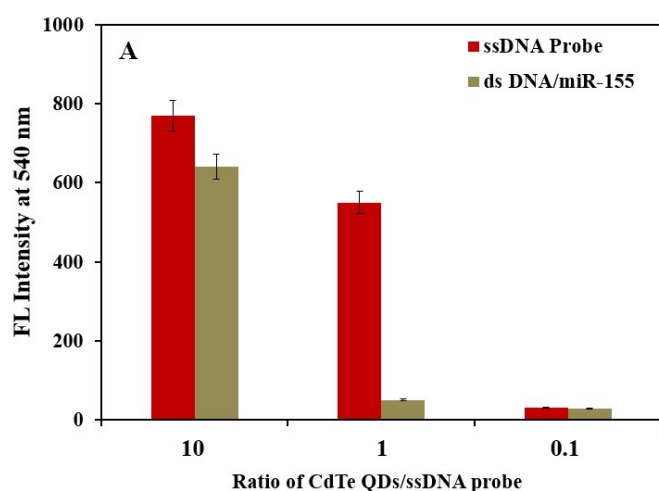
Figure S3. Optimization assay conditions: (A) Effect of different ratios of CdTe QDs to ssDNA (10 , 1, 0.1) (without heating). (B) Effect of different temperature (50, 60, 70, 80, 90, 100°C). (C) Optimization of heating time duration (1, 5, 10, 15 and 20 min)
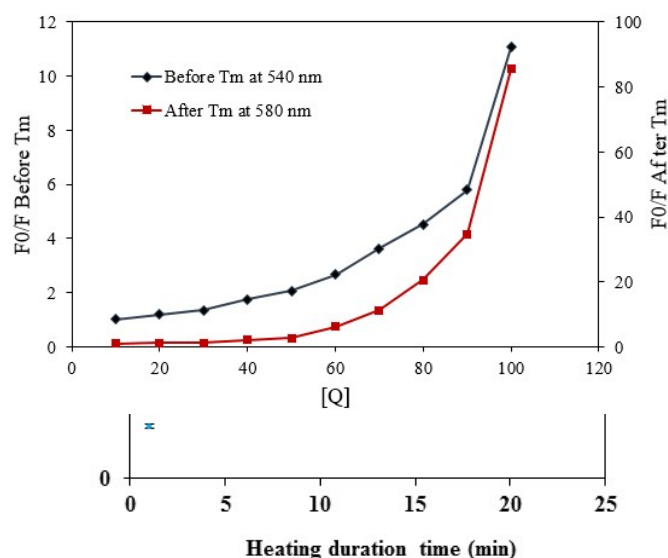
Figure S4 the S-V plot obtained before and after heating.

qRT-PCR analysis

In qRT-PCR analysis, U6 small nuclear RNA (snRNA) was employed as the universal endogenous control and the relative expression was calculated by the equation: Fold change = $2^{-\Delta Ct}$. The sequences of primers for qRT-PCR were listed in Table S1. And in this method, the expression amount was calculated by the equation:

$$\left[HEK-293 \ or \ SK-BR-3 \ or \ MCF-7 \right] = \frac{[probe]-[HEK-293 \ or \ SK-BR-3 \ or \ MCF-7]}{[probe]}$$