Supplementary Information

Diagnosing the miR-141 Prostate Cancer Biomarker Using Nucleic Acid-Functinoalized CdSe/ZnS QDs and Telomerase

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Optimization on the performance of the sensing platform

Toinvestigate the optimal amount of **(1)**-modified QDs participated in the amplified detection of miR-141, the fluorescence spectra were recorded after 1 hr interaction of variable concentrationsof **(1)**-modified QDs (0, 2.1, 4.2, 8.4, 16.7, 33.3, and 50 nmol) withmiR-141, 100 nM. As shown in Fig. S1A, the fluorescence responses intensify with the increased amount of (**1**)-modified QDs, leveling off to a saturationvalue ca. 33.3 nmol. Moreover,the effect of DSN on the DSN-stimulated catalyticcleavage was conducted. The fluorescence responses were recorded while 0, 12.5, 25, 50, 100, 250 U/mL of DSN were added to interact with 100 nM miR-141 for 1 hour. Fig. S1B depicts comparable fluorescence response in groups containing 100, 150 U/mL and 250 U/mL of DSN ($P>0.02$), suggesting 100 U/mL of DNS issufficientto implement our analytical procedure. In addition to (**1**)-modified QDs and DSN, the reaction temperature plays a crucial role in achieving efficient biocatalytical cleavage. Combinations consisting of variable **(1)**-modified QDs, DSN, and the reaction temperature were evaluated for theirsensing effectiveness. As shown in Fig. S1C, the combinations of 33.3 nmol of **(1)**-modified QDs and 100 U/mL of DSN at three different reaction temperatures(50 ℃, 55 ℃ and 60^{o}C) validate the premier fluorescence responses, suggestingthat 33.3 nmol of **(1)**-modified QDs and 100 U/mL of DNS representthe optimized concentrations to be used. Furthermore, 55^{o}C was found to be the best reaction temperature, and thus it was chosen as optimum and used throughout the study.

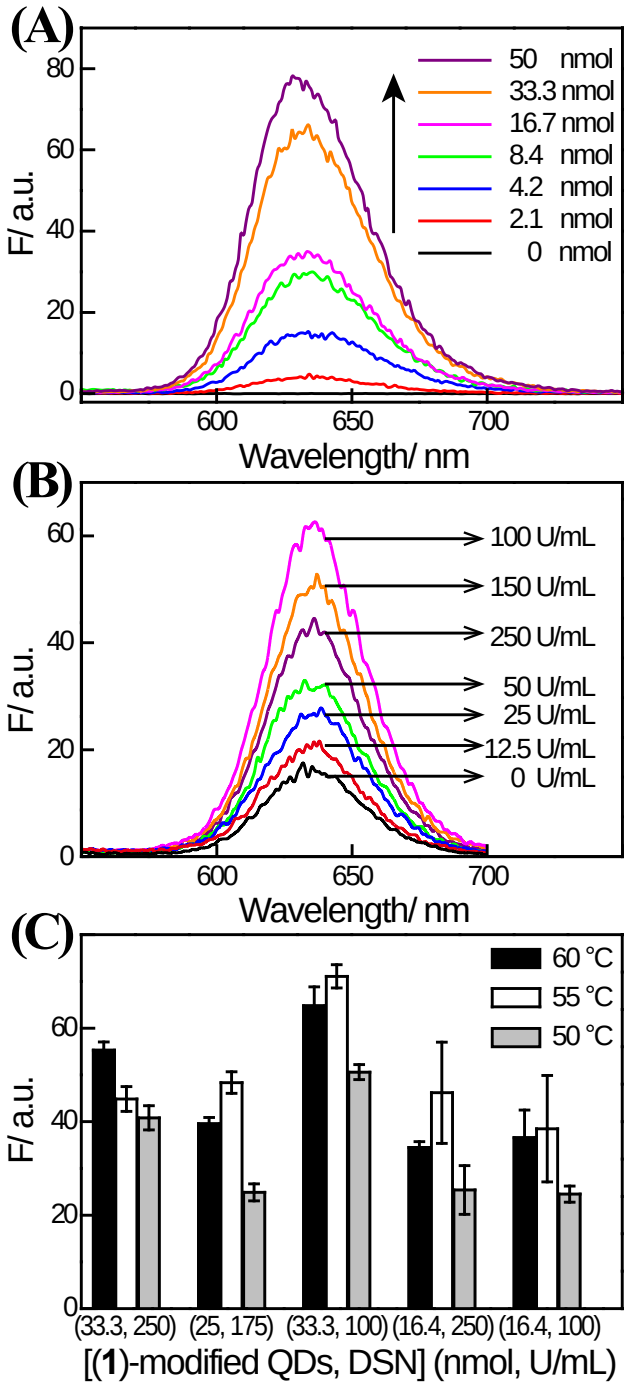
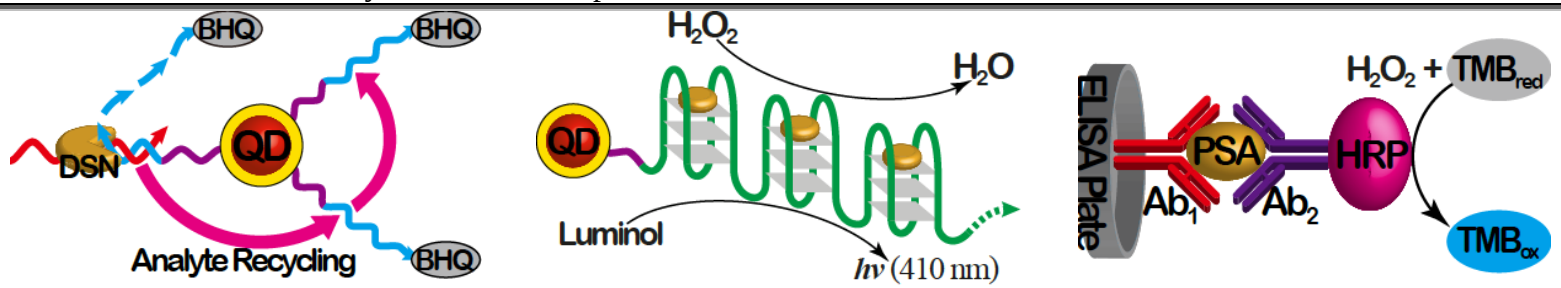


Fig. S1. The effects of the amount of the (**1**)-modified QDs, the concentration of DSN, and the reaction temperature, on the performance of the sensing platform. **(A)** Fluorescence spectra observed upon interacting different amounts of **(1)**-modified QDs with miR-141, 1×10^{-7} M, and DSN, 0.2 U. **(B)** Fluorescence spectra corresponding to the **(1)**-functionalized QDs system upon interacting different concentrations of DSN with **(1)**-modified QDs, 33.3 nmol, miR-141, 1×10^{-7} M. **(C)** Fluorescence spectra corresponding to the **(1)**-functionalized QDs system upon reacting with different combinations of **(1)**-modified QDs and DSN under varied reaction temperatures with miR-141, 1×10^{-7} M. All error bars in the figures indicate standard deviations using N = 3 experiments.

Table S1. miR-141 and PSA levels in healthy individuals and prostate cancer carriers.



	Healthy	Patient	Healthy	Patient	Healthy	Patient
Subject 1	5.1×10^{-12} M	6.4×10^{-10} M	4×10^{-13} M	8.1×10^{-12} M	< LOD[b]	2.5×10^{-10} M
Subject 2	8×10^{-12} M	3.8×10^{-11} M	3.9×10^{-13} M	5.3×10^{-13} M	< LOD[b]	1.8×10^{-9} M
Subject 3	< LOD[a]	9.4×10^{-11} M	3.4×10^{-13} M	6.8×10^{-13} M	1.2×10^{-10} M	2.0×10^{-9} M
Subject 4	5.3×10^{-12} M	3.2×10^{-10} M	4.0×10^{-13} M	1.9×10^{-12} M	< LOD[b]	1.7×10^{-9} M
Subject 5	< LOD[a]	1.3×10^{-7} M	3.8×10^{-13} M	2.2×10^{-9} M	8.1×10^{-11} M	2.7×10^{-10} M
Subject 6	< LOD[a]	3.1×10^{-10} M	3.5×10^{-13} M	1.0×10^{-12} M	1.8×10^{-10} M	2.0×10^{-9} M
Subject 7	< LOD[a]	2.0×10^{-8} M	4.1×10^{-13} M	7.8×10^{-11} M	9.0×10^{-11} M	1.7×10^{-9} M
Subject 8	< LOD[a]	1.1×10^{-7} M	3.9×10^{-13} M	1.3×10^{-9} M	7.5×10^{-11} M	4.7×10^{-10} M
Subject 9	< LOD[a]	1.7×10^{-7} M	3.8×10^{-13} M	3.9×10^{-9} M	1.4×10^{-10} M	4.0×10^{-10} M
Subject 10	< LOD[a]		3.5×10^{-13} M		7.1×10^{-11} M	
Average concentration in serum	4.3×10^{-13} M[c]	3.4×10^{-9} M[c]	2.6×10^{-14} M[c]	5.8×10^{-11} M[c]	1.1×10^{-10} M	8.6×10^{-10} M
Standard deviation in serum	1.1×10^{-13} M	4.9×10^{-9} M	1.6×10^{-15} M	9.7×10^{-11} M	4.1×10^{-11} M	8.0×10^{-10} M

[a]Detection limit for fluorescence assay is calculated to be 1.7×10^{-12} M, [b]Detection limit for PSA immunoassay is calculated to be 3.5×10^{-11}M, [c]Average concentration in serum samples is calculated by dividing (the mean of all the subjects) by (a concentration factor of 14.3).