Electronic Supplementary Material (ESI) for Nanoscale Advances.

Supplementary Materials

Section 1. SEM identification

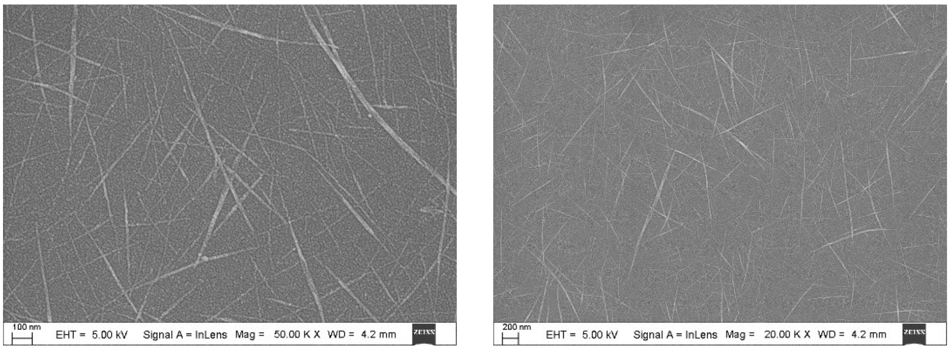


Figure. S1a. SEM images of CNT-TFT before modification and washing steps.

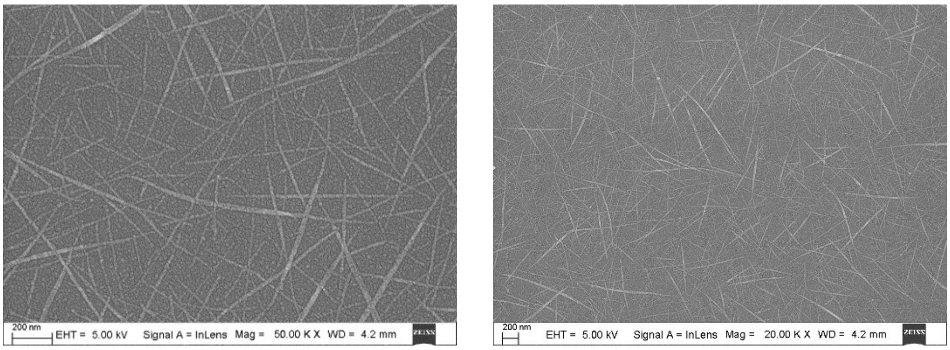


Figure. S1b. SEM images of CNT-TFT after modification and washing steps.

Section 2. AFM identification

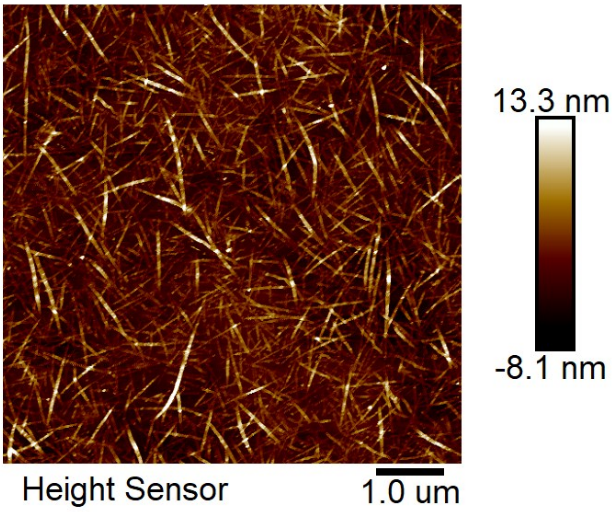


Figure. S2a. AFM images of CNT-TFT before modification and washing steps.

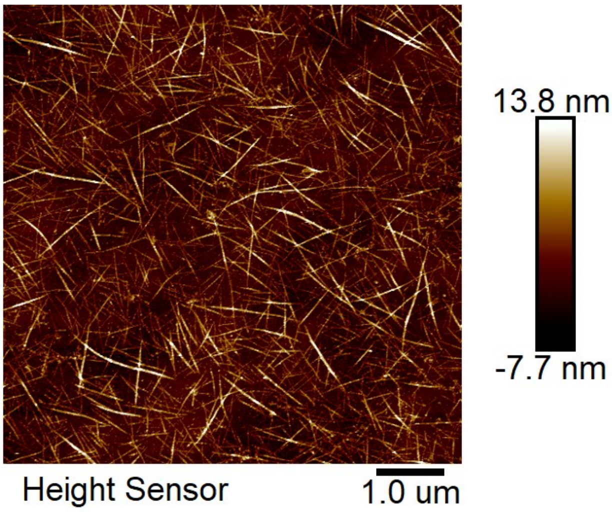


Figure. S2b. AFM images of CNT-TFT after modification and washing steps.

Section 3. Responses of incubation time

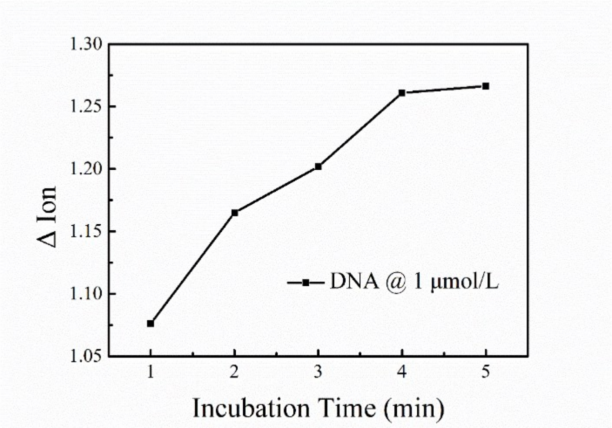
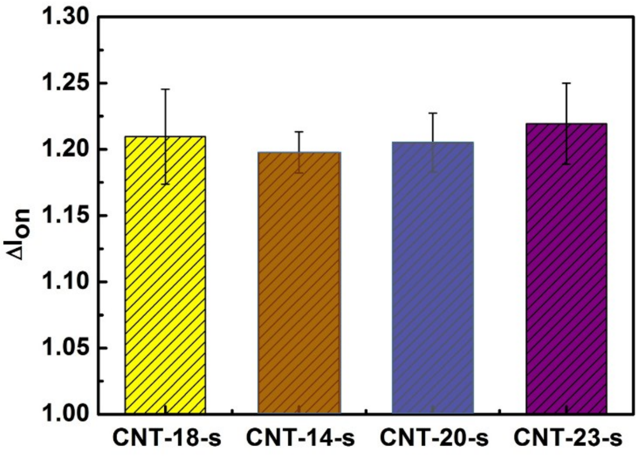


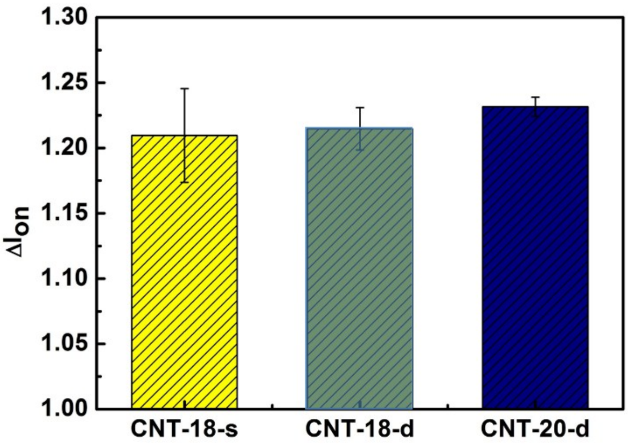
Figure. S3. The relationship between ΔIon signal and incubation time (1 μmol/L). When the incubation time increased to 4 minutes, the response signal approached saturation.

Section 4. Responses of different type of DNA



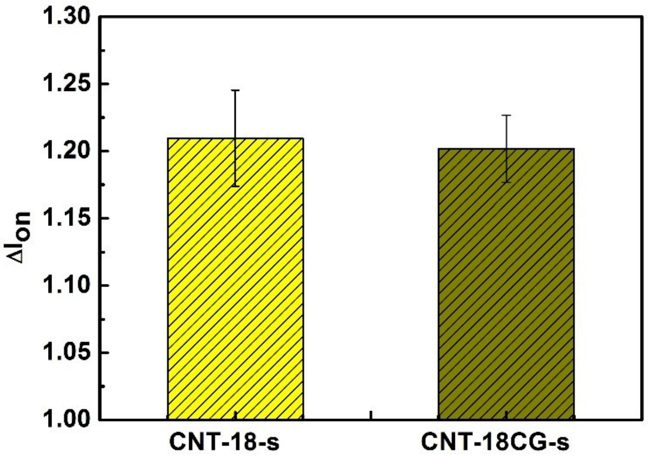
DNA sample	Sequence	Single/double strand	GC%
CNT-18-s	GAAATGTGGCAACTCGTC	Single strand	50%
CNT-14-s	TAGATCGTGTGCGA	Single strand	50%
CNT-20-s	TGACAAGTGTGAGCAGAGGT	Single strand	50%
CNT-23-s	TGACAGGAGTGTGAGCTCTAGAG	Single strand	52%

Fig. S4 ΔIon responses of different length of single DNA.



DNA sample	Sequence	Single/double strand	GC%
CNT-18-s	GAAATGTGGCAACTCGTC	Single strand	50%
CNT-18-d	TAGGATCGTAGTGCCGAG	Double strand	56%
CNT-20-d	TCAGCATCTGGTGTGACGAT	Double strand	50%

Fig. S5 ΔIon responses of single/double strand DNA.



DNA sample	Sequence	Single/double strand	GC%
CNT-18-s	GAAATGTGGCAACTCGTC	Single strand	50%
CNT-18CG-s	TGGCACGTGCTGCAGAGG	Single strand	67%

Fig. S6 ΔIon responses of single strand DNA with different CG content.

Section 5. Limit of detection in nonlinear calibration

The limit of detection using the normal distribution is formulated as following:

$$LOD = \bar{y}_b + k_D s^{n-1}_b$$

Here $\bar{y}_b$ is the average blank signal value, s^{n-1}_b is the standard deviation of the blanks, n is the number of blanks, and k_D=3.[1] In our experiment, the average blank signal was 1.018 and standard deviation was 0.0066, respectively. The corresponding concentration was obtained by substitute LOD of 1.0378 into fitting Hill-Langmuir equation and the value of LOD concentration was 1.6×10^{-4} µmol/L (the molecular weight of DNA was 5524.6, corresponding LOD was 0.88µg/L).

Reference

1. J. Mocak, A.M. Bond, S. Mitchell, G. Scollary, *Pure Appl. Chem.*, 1997, **69**(2), 297-328.

Section 6. RNA detection

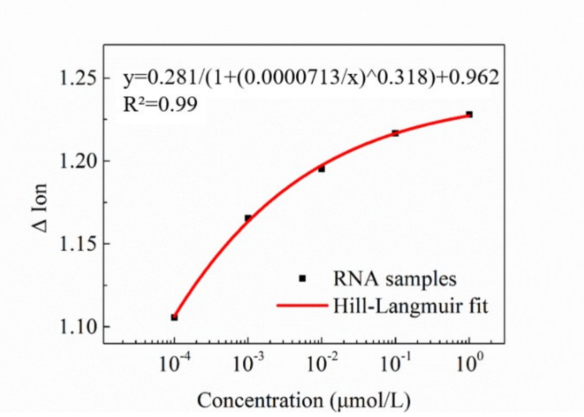


Figure. S7. The ΔIon signal responses to RNA concentrations from 1×10^{-4} to 1 µmol/L. The relationship between ΔIon and RNA concentration could be fitted with the Hill-Langmuir model with the fitting correlation coefficient R^2 approximately to 0.99. The maximum response A, response offset Z, and Hill coefficient n were almost same with DNA detection fit parameters.

Section 7. CW peptide

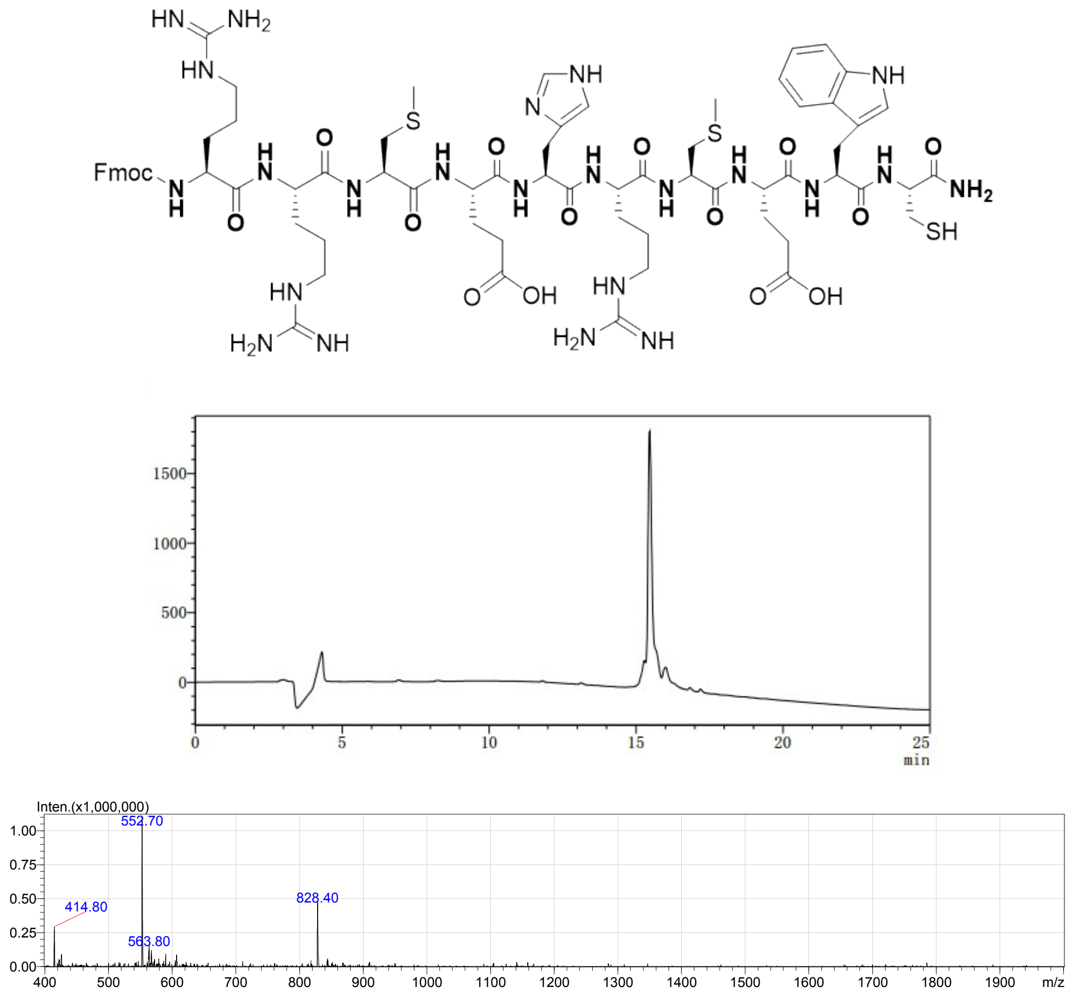


Figure. S8. LC-MS identification of CW peptide.