Supporting Information

Nanostructuring-Synergetic Base-Stacking Effect: An Enhanced Versatile Sandwich Sensor Enables Ultrasensitive Detection of MicroRNAs in Blood

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Table of contents

Involved oligonucleotides and corresponding sequences (Table S1)
T_m of CPs with different lengths and the corresponding SPs (Table S2)
Free energy of prehybridized mixtures and direct CP-TS hybridization complexes (Table S3)
Comparison between our sensor and other miRNA sensors (Table S4) S6
SWV signals of different CPs with DNA21-MB of Bsee-miR sensor (Figure S1)S7
CV and EIS characterization for stepwise modification of Bsee-miR sensor (Figure S2)
Feasibility of Bsee-miR sensor in HRP-TMB amplification system (Figure S3) S9
Optimizing the assembly concentration of CP of Bsee-miR sensor (Figure S4)S10
CV characterization for stepwise modification of nanostructuring-enhanced Bsee-miR sensor (Figure S5)
SWV curves of AuNS-SPCE based Bsee-miR sensor (Figure S6) S12
Detection total RNAs from cells by nanostructuring-enhanced Bsee-miR sensor (Figure S7)
The difference of nanostructuring-enhanced Bsee-miR sensor in detection total RNA from different cells (Figure S8)

Name	Sequence (5'-3')	
9 nt CP ^⁵	HS-(CH ₂) ₆ -TCAACATCA	
13 nt SP ^⁵	GTCTGATAAGCTA	
10 nt CP ⁸	HS-(CH ₂) ₆ -TCAACATCAG	
12 nt SP ⁸	TCTGATAAGCTA	
11 nt CP ⁸	HS-(CH ₂) ₆ -TCAACATCAGT	
11 nt SP ^⁵	CTGATAAGCTA	
12 nt CP ⁸	HS-(CH ₂) ₆ -TCAACATCAGTC	
10 nt SP ^⁵	TGATAAGCTA	
13 nt CP ⁸	HS-(CH ₂) ₆ -TCAACATCAGTCT	
9 nt SP ^⁵	GATAAGCTA	
14 nt CP ⁸	HS-(CH ₂) ₆ -TCAACATCAGTCTG	
8 nt SP ⁶	ATAAGCTA	
22nt CP ^⁵	HS-(CH ₂) ₆ -TCAACATCAGTCTGATAAGCTA	
DNA21-MB ⁸	TAGCTTATCAGACTGATGTTGA-MB	
miR21	UAGCUUAUCAGACUGAUGUUGA	
miR21-Biotin-SP	TCTGATAAGCTA-TTTTT-Biotin	
miR223	UGUCAGUUUGUCAAAUACCCCA	
miR223-CP	HS-(CH ₂) ₆ -TGGGGTATTT	
miR223-Biotin-SP	GACAAACTGACA-TTTTTT-Biotin	
miR141	UAACACUGUCUGGUAAAGAUGG	
miR141-CP	HS-(CH ₂) ₆ -CCATCTTTAC	
miR141-Biotin-SP	CAGACAGTGTTA-TTTTT-Biotin	
miR10b	UACCCUGUAGAACCGAAUUUGUG	
miR10b-CP	HS-(CH ₂) ₆ -CACAAATTCG	
miR10b-Biotin-SP	GTTCTACAGGGTA-TTTTTT-Biotin	

 Table S1. Involved oligonucleotides and corresponding sequences

Name	Sequence (5'-3')		
SM-miR21	UAGCUUAUCAGACUGAUAUUGA		
TM-miR21	UAG <mark>A</mark> UUAUCAGACUGAU <mark>A</mark> UUGA		
Random-RNA	UUGUACUACACAAAAGUACUG		

CP: capture probe

SP: stacking probe

MB: methylene blue

⁸labeled sequences were used in optimal HS-DNA CP selection.

The mismatched bases were marked in red.

Name	T_{m}	Name	T_{m}	ΔT_m
9 nt CP	12.5	13 nt SP	32.0	16.5
10 nt CP	22.5	12 nt SP	27.2	4.7
11 nt CP	27.3	11 nt SP	23.2	4.1
12 nt CP	32.0	10 nt SP	17.0	15.0
13 nt CP	35.1	9 nt SP	10.8	24.3
14 nt CP	38.8	8 nt SP	0.9	37.9

Table S2. T_m of different length of CPs (9 nt to 14 nt) and corresponding SPs (13 nt to 8 nt).

Name	Free energy (F)	Name	Free energy (F)	ΔF
13nt SP+D-21	-10.41	9 nt CP+D-21	-13.4	2.99
12nt SP +D-21	-17.12	10 nt CP +D-21	-15.7	1.42
11nt SP +D-21	-16.4	11 nt CP +D-21	-16.75	0.35
10nt SP +D-21	-14.06	12 nt CP +D-21	-18.51	4.45
9nt SP+D-21	-13.29	13 nt CP +D-21	-19.59	6.3
8nt SP +D-21	-10.8	14 nt CP +D-21	-27.78	16.98

Table S3. Free energy of prehybridization mixtures (SP and DNA21) and direct hybridization mixtures (CP and DNA21)

D-21: DNA21;

The unit of free energy is kcal/mol.

Methods	Targets	Linear range	Sensitivity	Ref ^a
		C C		
Fluorescence	miR21	0-16 nM	47 pM	1
SERS	miR21	1 pM-10 nM	1 pM	2
Colorimetric	miR21	150 fM-3 nM	70 fM	3
Photoelectrochemistry	miR21	1 pM-100 nM	31 fM	4
Electrochemical	miR21	140 pM-10 nM	40 pM	5
FRET	miR21	100 pM-200 nM	100 pM	6
Fluorescence	let-7a	100 fM-1 nM	58 fM	7
Chemiluminescence	miR122	80 pM-100 nM	49.6 fM	8
Electrochemical	miR21	10 fM-1 nM	79.3 aM	This work

Table S4. Comparison between our sensor and other similar sensors for miRNA detection.

SERS: surface-enhanced Raman scattering

FRET: fluorescence resonance energy transfer

^aReferences at the end of SI

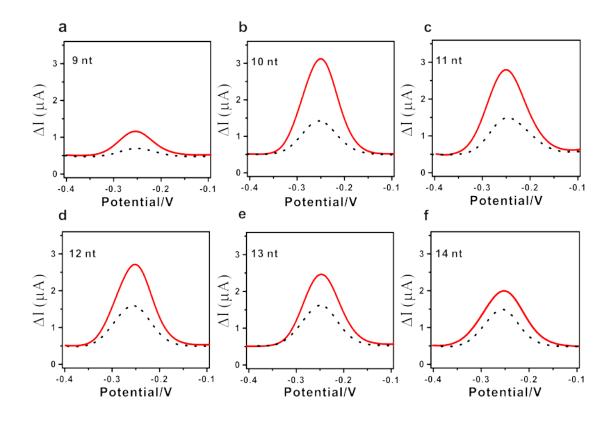


Figure S1. Square wave voltammetry (SWV) curves of the sensor assembled with 0.5 μ M 9-14 nt HS-DNA CPs (a: 9 nt; b: 10 nt; c: 11 nt; d: 12 nt; e: 13 nt; f: 14 nt), in response to 1 μ M DNA21-MB with (sandwich structure (I_S): red line) or without 2 μ M corresponding reporter probes (direct CP-TS hybridization (I_H): dark dot) in 10 mM PBS (pH = 7.4) at room temperature.

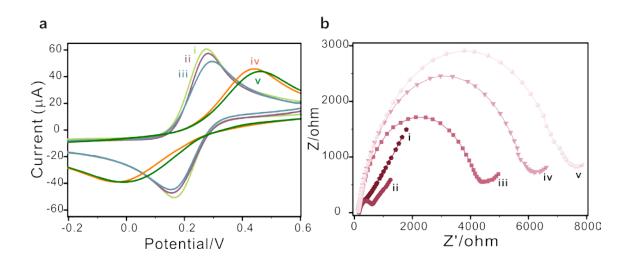


Figure S2. To verify the successful assembly of probes on the sensor, cyclic voltammetry (CV) and electrochemical impedance spectroscopy (EIS) were employed to characterize the step by step construction of the sensing interface using the redox pair of [Fe(CN)₆]^{3-/4-}. A typical CV response of bare gold electrode (GE) was obtained (line i in a) with minimal electro-transfer resistance (Ret) (curve i in b), reflecting the barrier-free diffusion of $[Fe(CN)_6]^{3-/4-}$ to the bare gold electrode. After the immobilization of HS-DNA CPs, there is an increment in peak separation of CV (line ii in a), owning to the negatively charged phosphate backbone in DNA probes. Similarly, Ret also increased because of the improved repulsion between charged DNA and $[Fe(CN)_6]^{3-/4-}$ (curve ii in b). After blocking by MCH, there were further changes of CV (line iii in a) and Ret (curve iii in b). As the prehybridized duplex was captured on the interrogating electrode, the peak current continued to reduce and an increase in peak separation emerged (line iv in a). There is also an increment for Ret (curve iv in b). Finally, when we apply avidin-HRP, we can also see changes of CV and EIS (line v in a, and curve v in b). Overall, these results indicated the successful preparation of our sensor. Electrochemical measurement in 0.1 M KCl solution containing 5 mM $[Fe(CN)_6]^{3-/4-}$ by scanning the potential from -0.2 to 0.6 V at a scan rate of 100 mV/s.

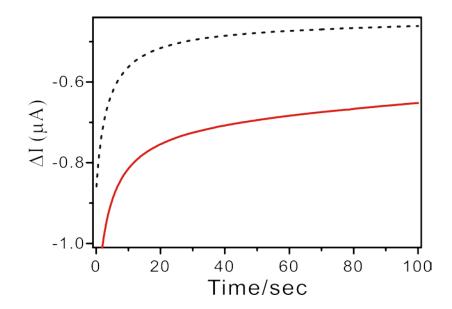


Figure S3. The feasibility of Bsee-miR sensor implemented HRP-TMB signal amplification. Amperometric i-t curve of 1 pM 10 nt HS-DNA CP incubation with miR21-Biotin-SP (2 μ M)-miR21 (1 pM) prehybridization complexes and SA-HRP (red line) or miR21-Biotin-SP (2 μ M)-PBS complexes and SA-HRP (dark dot) in TMB at room temperature.

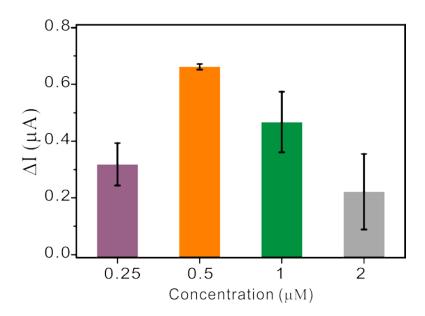


Figure S4. Assembly concentrations of HS-DNA CP ranging from 0.25 μ M to 2 μ M in Bsee-miR sensor were optimized (in the presence of 10 nM target miR21 and 20 nM biotin stacking probe) to obtain the maximal hybridization efficiency and the minimal steric hindrance, as well as to maintain highly ordered molecular orientation at biointerface. Error bars show the standard deviations of measurements taken from at least three independent experiments.

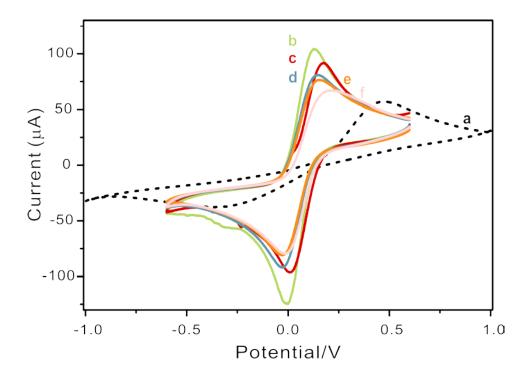


Figure S5. Cyclic voltammetry characterization of stepwise modification of nanostructuring-enhanced Bsee-miR sensor. (a) bare SPCE; (b) SPCE decorated with gold nanostructures (AuNS-SPCE); (c) HS-DNA CPs assembled on AuNS-SPCE via Au-S bond; (d) Passivation by MCH; (e) Target miR21 and biotinylated stacking probe complexes were captured on AuNS-SPCE; (f) Introduction of 1% BSA to block the nonspecific sites. The CV was carried out in 0.1 M KCl solution containing 5 mM $[Fe(CN)_6]^{3-/4-}$ at a scan rate of 100 mV/s.

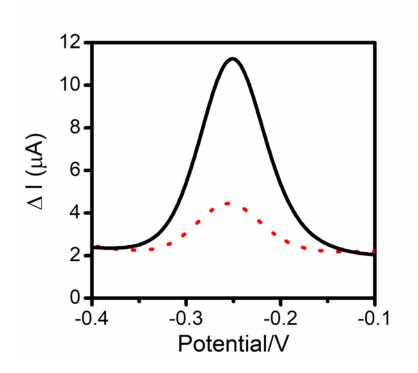


Figure S6. Square wave voltammetry (SWV) curves of AuNS-SPCE based Bsee-miR sensor incubating with 0.5 μ M 10nt HS-DNAs 1 μ M DNA-21-MB and 2 μ M corresponding probes (experimental group: black line) or PBS (control group: red dot) in 10 mM PBS (pH = 7.4) at room temperature.

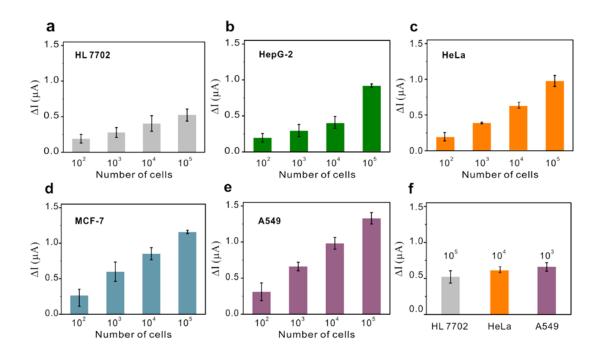


Figure S7. Nanostructuring-enhanced Bsee-miR sensor allows for detection of the target miR21 from total RNA extracted from A549 (a), MCF-7 (b), HeLa (c), HepG-2 (d) cells and HL7702 cells (e) with different numbers $(10^2, 10^3, 10^4 \text{ and } 10^5 \text{ cells})$, respectively. (f) Comparison of signal changes in response to HL7702, HepG-2 and A549 with distinct cell numbers. Error bars represent the standard deviations of measurements (n = 3).

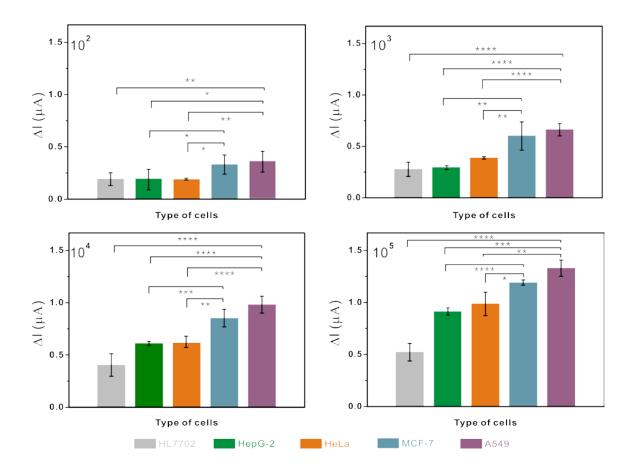


Figure S8. The difference of nanostructuring-enhanced Bsee-miR sensor in detection of total RNA from different cells. T test was used to prove the over-expression of miR21 in A549 and MCF-7 cells relative to HepG-2 and HeLa, as well as HL7702.

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