

Catalytic Hairpin Assembly-Based Self-Ratiometric Gel Electrophoresis Detection Platform for Reliable Nucleic Acid Analysis

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Scheme S1. Schematic illustration of catalytic hairpin assembly

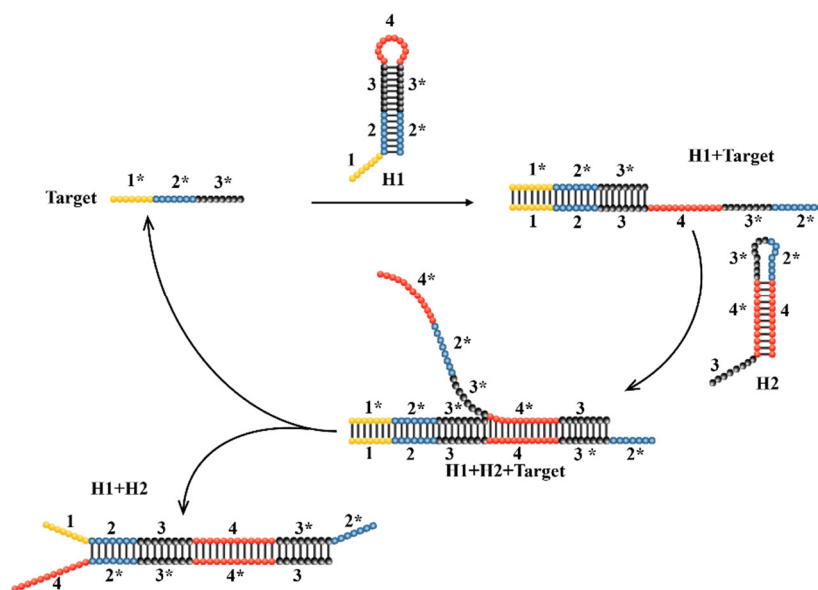


Table S1. Oligonucleotides sequences used in the experiment

Name	Sequence (5'-3')
I	CCCAGGTAACTTAGCTCACTGAC
H1	GTCAGTGAGCTAAGTTAACCTGGGCCATGAGAAGAC CCAGGTAACTTAGC
H2	AAAAAACCTGGGTCTTCTCATGGCCCAGGTAACTTA GCCCATGAGAAGAC
miRNA-141	UAACACUGUCUGGUAAAGAUGG
miRNA-143	UGAGAUGAAGCACUGUAGCUCA
miRNA-21	UAGCUUAUCAGACUGAUGUUGA
miRNA-21-1	UAGCUUAUCAGACUGAU <u>C</u> UUGA
miRNA-21-2	UAGCUUAUCAGACU <u>A</u> AUGUUGA
miRNA-21-3	UAGCUUAUCA <u>T</u> ACUGAUGUUGA
cDNA-21	TCAACATCAGTCTGATAAGCTA
H1-21	TAGCTTATCAGACTGATGTTGACCATGAGAAGATCA ACATCAGTCTGA
H2-21	AAGATGTTGATCTTCTCATGGTCAACATCAGTCTGA CCATGAGAAGAC
HBV	TTGGCTTTCAGTTATATGGATGATGTGGTA
MB	CCCAGGTAACTTAGCTCACTGACTCCATATA ACT <u>X</u> (AP)GAAAGCCAAGTCAGTGAGCTAA

* The underlined bases in miR-21s are mismatched bases. X represents abasic sites.

Table S2. Recovery experiments for HBV detection in 10% human serum

samples	spiked	found	RSD (%, n=3)	Recovery (%)
10% human serum	1.000 pM	1.072 pM	5.35	107.2
	5.000 pM	2.415 pM	3.29	96.6
	10.000 pM	3.163 pM	1.61	105.4

Table S3. Smart phone-combined DARGE assay for HBV detection

samples	spiked	found	RSD (%, n=3)	Recovery (%)
PBS	1.000 pM	1.083 pM	4.42	108.3
	2.500 pM	2.385 pM	3.53	95.4
	3.000 pM	3.174 pM	1.36	105.8

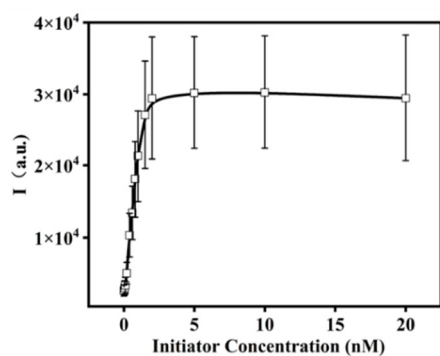
Table S4. Recovery experiments for miRNA-21 detection in 10% human serum

samples	spiked	found	RSD (%, n=3)	Recovery (%)
10% human serum	1.000 pM	0.936 pM	3.81	93.6
	5.000 pM	5.415 pM	1.62	108.3
	10.000 pM	9.435 pM	2.37	94.4

Table S5 Smart phone-combined DARGE assay for miRNA-21 detection

samples	spiked	found	RSD (%, n=3)	Recovery (%)
PBS	0.700 pM	0.680 pM	3.73	97.1
	1.000 pM	1.024 pM	1.53	102.4
	1.500 pM	1.423 pM	2.29	94.8

a)



b)

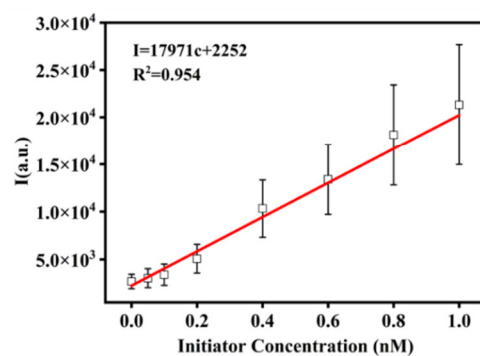


Figure S1. CHA-based non ratiometric gel electrophoresis analysis: (a) Band intensity versus target concentrations. (b) Linear correlation between I and target concentrations range from 0 to 1 nM. Error bars are standard deviations of three repetitive experiments.

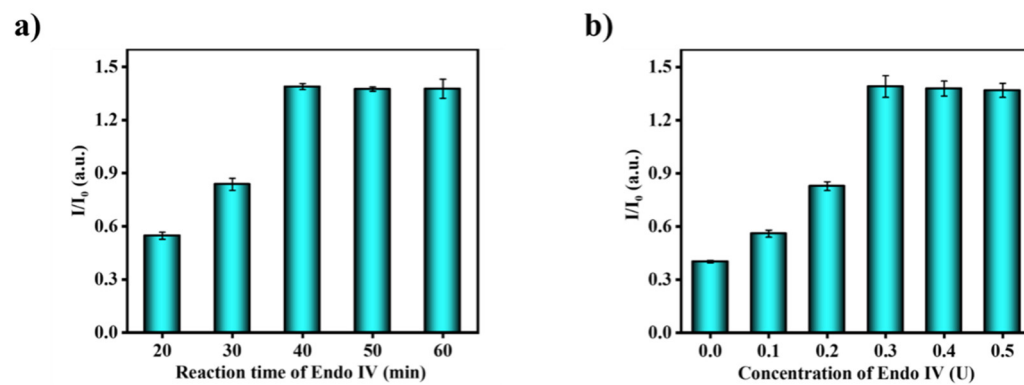


Figure S2. Optimization of experimental conditions on analytical performance. (a) Endo IV reaction time. (b) The amounts of Endo IV.

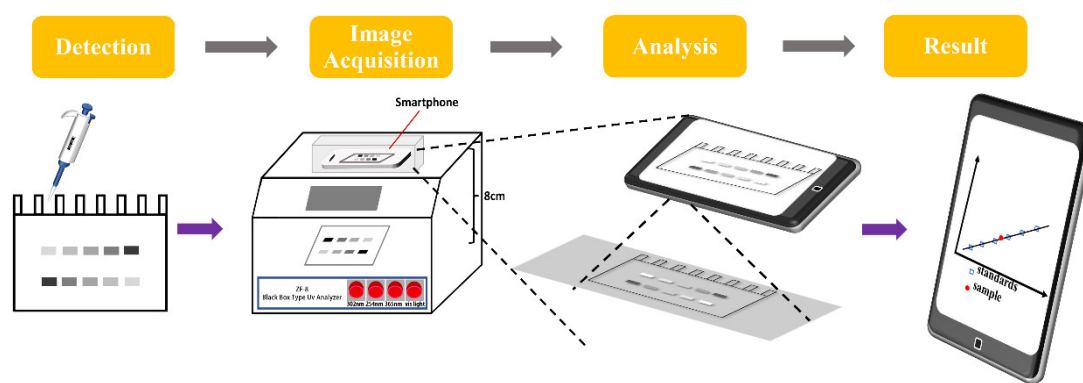


Figure S3. Schematic diagram of smartphone-based gel electrophoresis analysis for quantifying specific target.

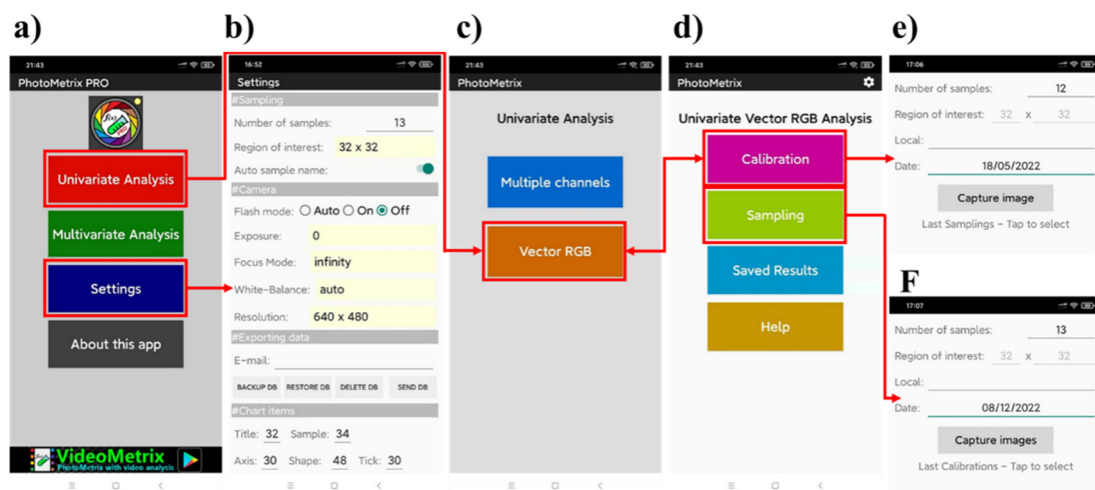


Figure S4. PhotoMetrix® application interfaces: (a) Home screen. (b) Settings screen. (c) Choice of color model for univariate analysis. (d) Interface for univariate analysis. (e) Build the calibration curves and (f) Sampling.

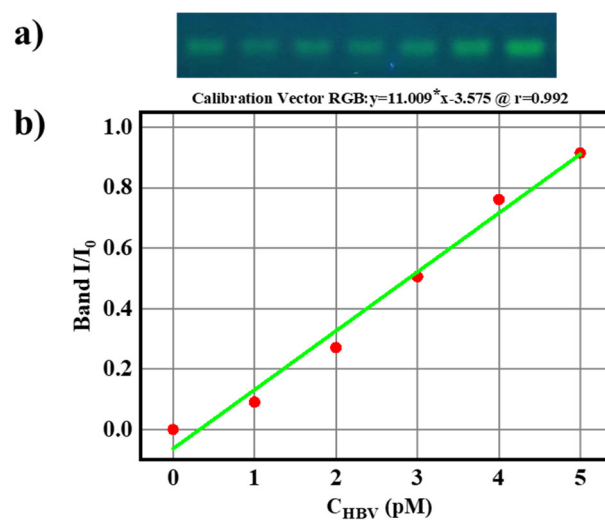


Figure S5. (a) Gel image acquired by smart phone camera. (b): Linear correlation between I/I_0 and HBV concentrations range from 0 pM to 5 pM acquired by PhotoMetrix® software.

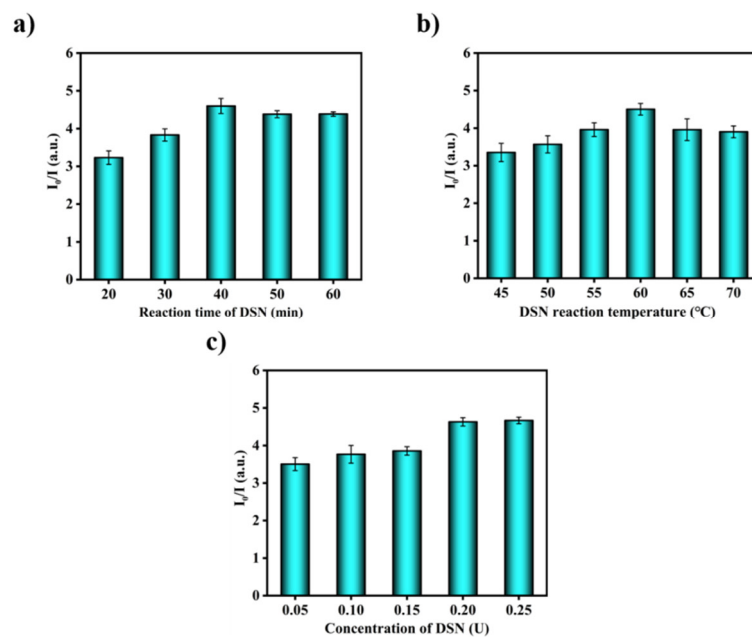


Figure S6. Optimization of experimental conditions on analytical performance. (a) The reaction time of DSN cleavage double-stranded. (b) Reaction temperatures of DSN. (c) The amount of DSN.

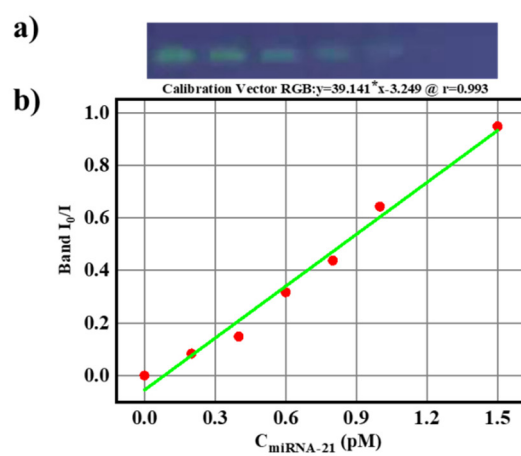


Figure S7. (a) Gel image acquired by smart phone camera for miRNA assay. (b) Linear correlation between I/I_0 and miRNA concentrations range from 0 pM to 1.5 pM acquired by PhotoMetrix® software.