

Supporting Information

A Visual Protocol for Sensitive *Vibrio parahaemolyticus* Detection Based on Hybridization chain reaction cascaded DNAzyme

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Table S1. DNA sequences used in this work.

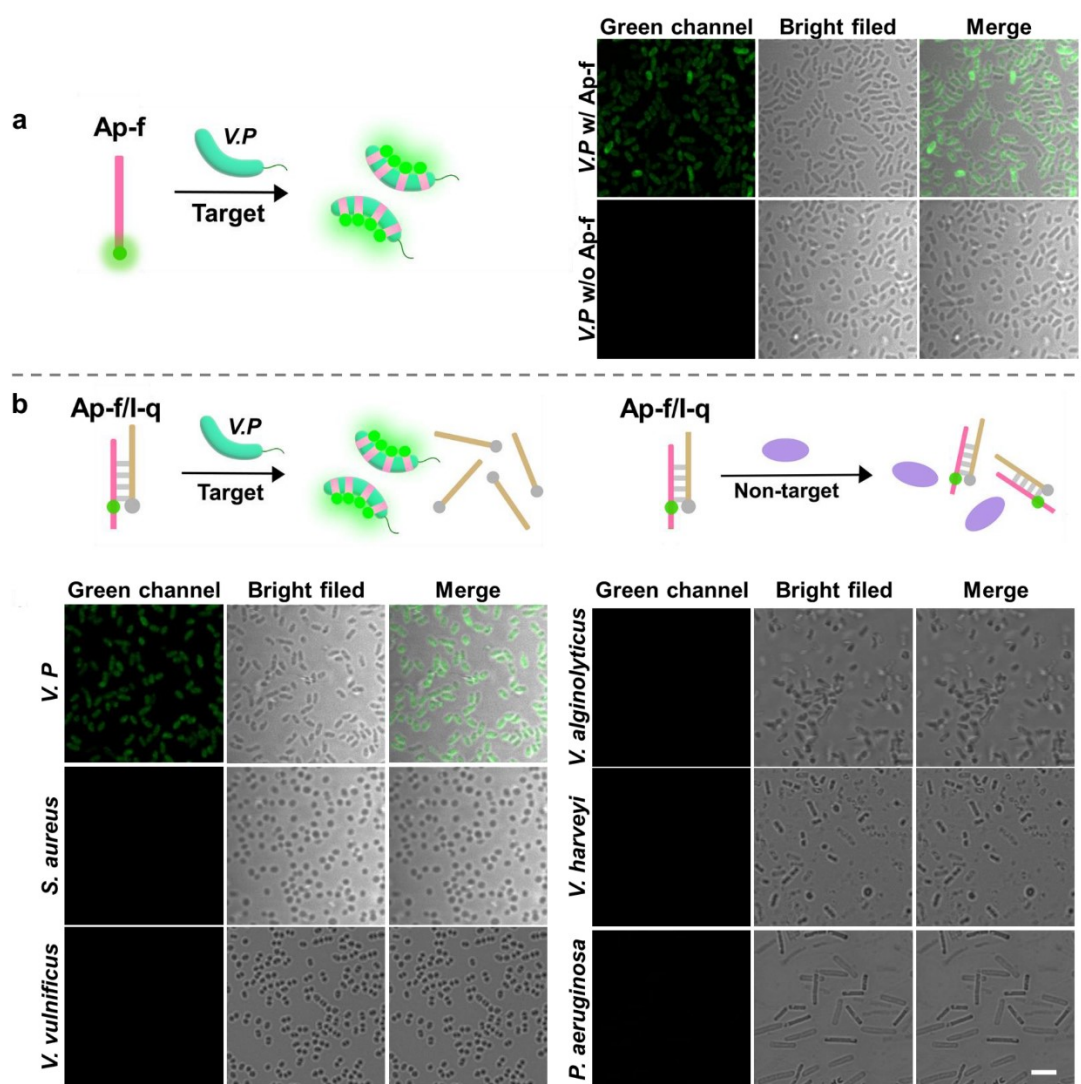
Name	Sequence (from 5' to 3')
Ap-b	Biotin-TTTTTTTTTTCAACGAAACAGTGACTCGTTG
Ap-f	FAM-TTTTTTTTTTCAACGAAACAGTGACT-(FAM)CGTTG
I	GAGTCACTGTTTACACGTTAC
I-q	(BHQ1)-GAGTCACTGTTTACACGTTAC
H1	CTGTTTACACGTTACGGGTAGGGTCCTGGGTAACG TGTAACAGTGACTC
H2	CCAGGACCCTACCCGTAACGTGTAAACAGGAGTCACTGTTTACAC GTTACGGGTAGGGCGGGTTGGGATT

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Table S2. Comparison of this study with other methods.

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Target Strain	Detection Method	Mode	Detection Range (CFU/mL)	LOD (CFU/mL)	reference
<i>V. parahaemolyticus</i>	Aptamer + G4 DNAzyme + HCR	colorimetry	10^0 – 10^6	0.82	this work
<i>V. parahaemolyticus</i>	Aptamer +G4 DNAzyme	colorimetry	10^2 – 10^7	10	1
<i>V. parahaemolyticus</i>	HRPzyme + LAMP	colorimetry	10^1 – 10^7	10	2
<i>V. parahaemolyticus</i>	CuO ₂ @MOF nanozyme	colorimetry + electrochemical	10^2 – 10^8	30	3
<i>V. parahaemolyticus</i>	Dual-aptamer + RCA + G4 DNAzyme	colorimetry	10 – 10^6	10	4
MRSA	Aptamer-assisted M-MXene@CuS nanozyme	colorimetry + electrochemical	10^1 – 10^7	7	5
MRSA	Finger-press microfluidic chip + Au@Pt nanozyme	colorimetry	10^2 – 10^5	350	6
MRSA	RPA + CRISPR/Cas12a	colorimetry	10 – 10^5	8	7
<i>S. aureus</i>	CRISPR/Cas9 + RPA	colorimetry + SERS	10^0 – 10^5	1	8
<i>V. parahaemolyticus</i>	Peptide probe + MnO ₂ nanozyme	colorimetry	20 – 10^4	15	9
<i>V. parahaemolyticus</i>	Fe ₃ O ₄ -ZIF-8@Pt nanozyme + aptamer	colorimetry	10^2 – 10^7	100	10
<i>V. parahaemolyticus</i>	Aptamer + ATP/G4-DNAzyme	colorimetry + microchip electrophoresis	10^2 – 10^7	30	11
<i>S. aureus</i>	Paper-based Au/Pt nanozyme	colorimetry + electrochemical	10^2 – 10^8	80	12
<i>S. aureus</i>	MOF-assisted dual-mode aptasensor	colorimetry + electrochemical	10 – 10^8	48	13
<i>S. typhimurium</i>	Aptamer-triggered CHA	colorimetry + electrochemical	10^2 – 10^6	240	14



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26 **Figure S1.** (a) Illustration the specific binding of aptamer (Ap-f) for *V. parahaemolyticus* (V.P) and
 27 the corresponding images. (b) Illustration the binding Ap-f/I-q complex with *V. parahaemolyticus*
 28 (V.P) and non-target bacteria (*S. aureus*, *V. vulnificus*, *V. alginolyticus*, *V. harveyi*, and *P.*
 29 *aeruginosa*) and (d) their corresponding images. “w/” denotes “with”; “w/o” denotes “without.”
 30 Scale bar: 5 μ m.

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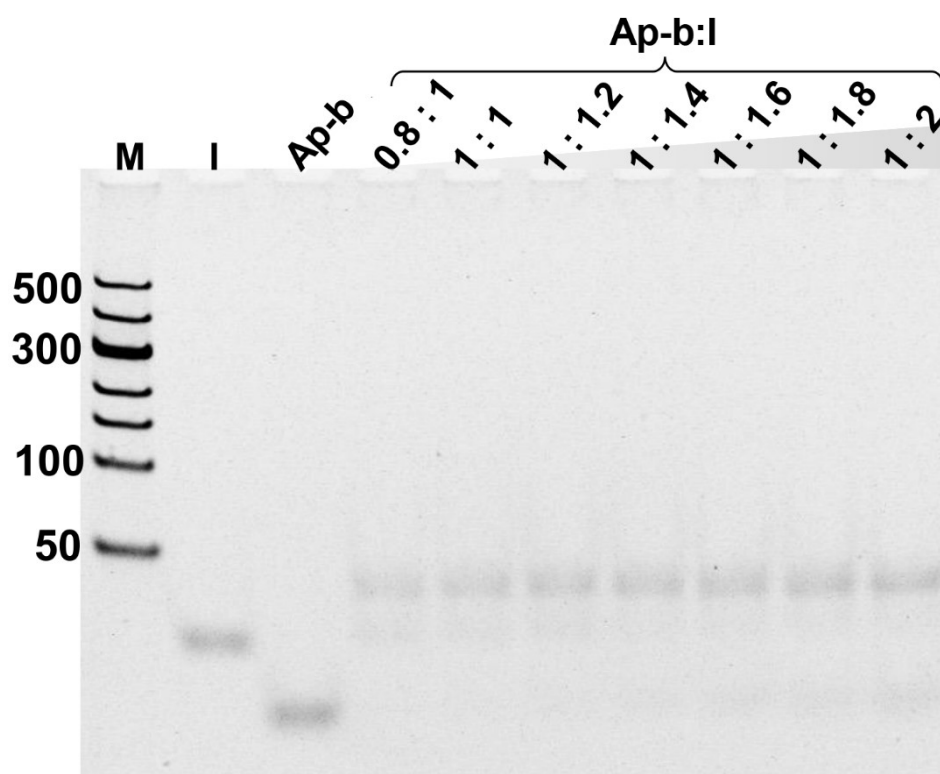
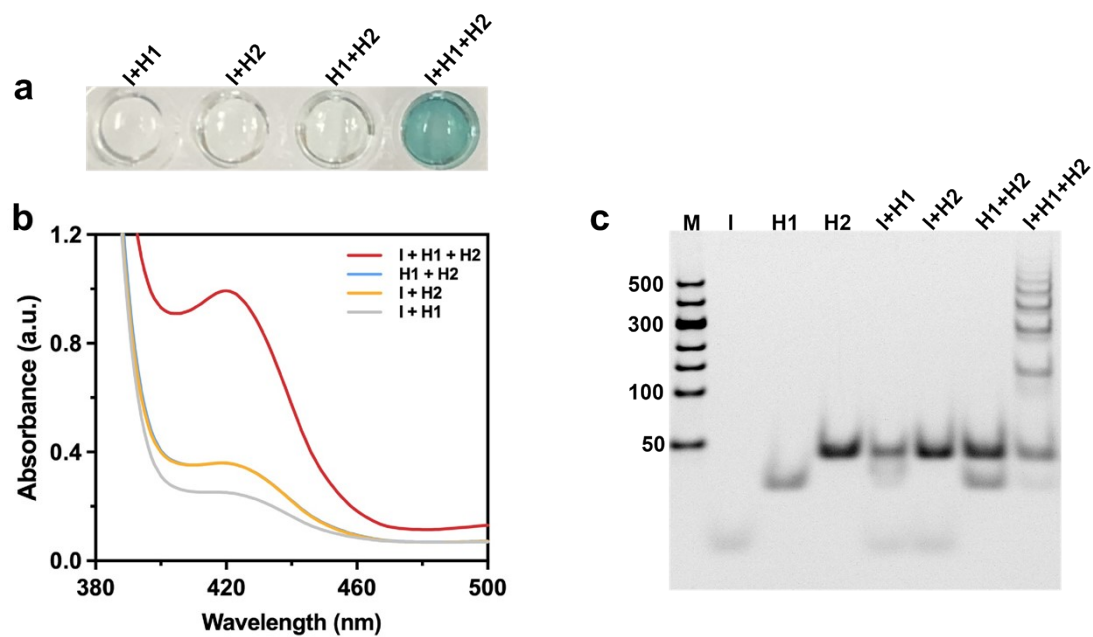


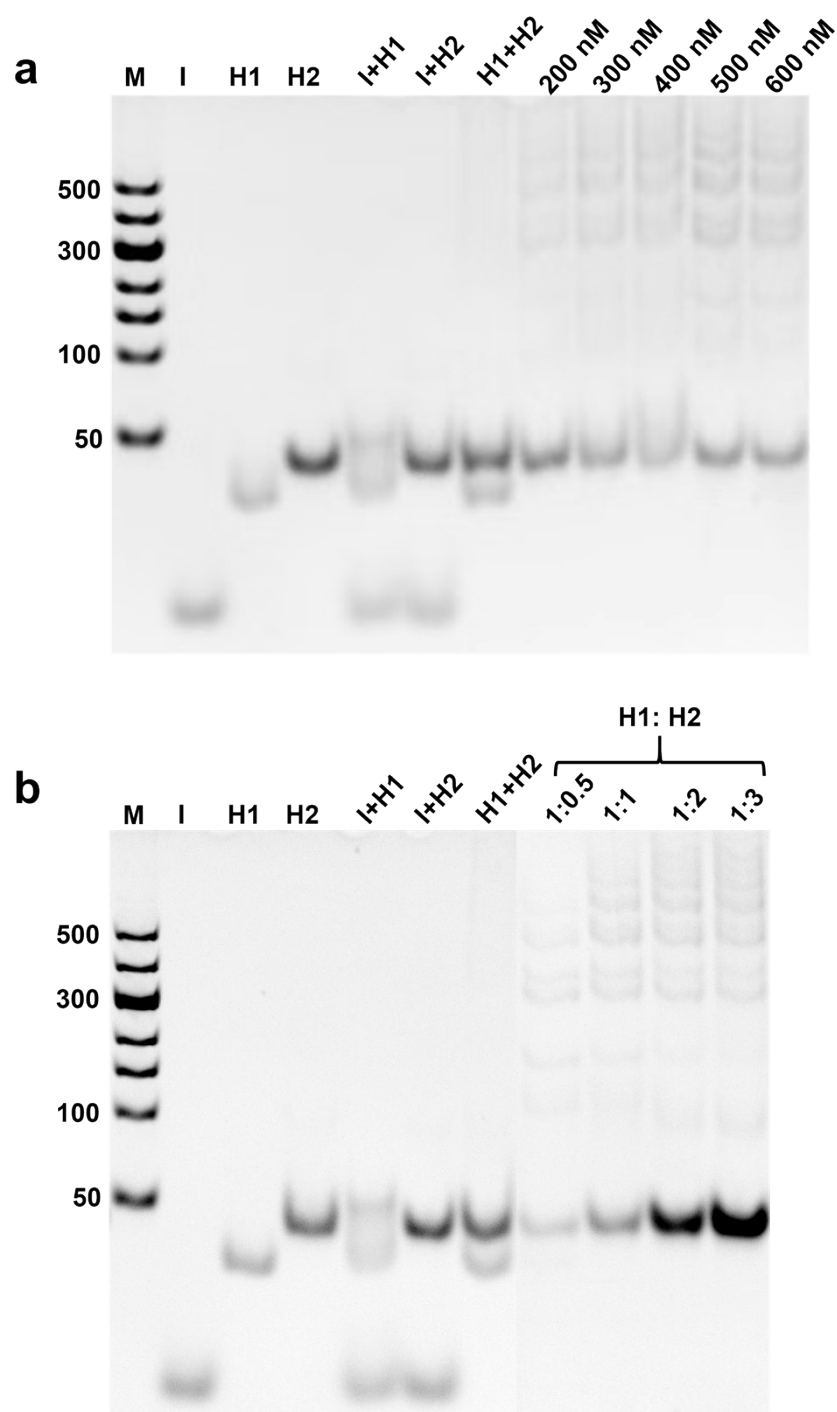
Figure S2. Optimization the ratio of Ap to I strand for Ap/I complex.

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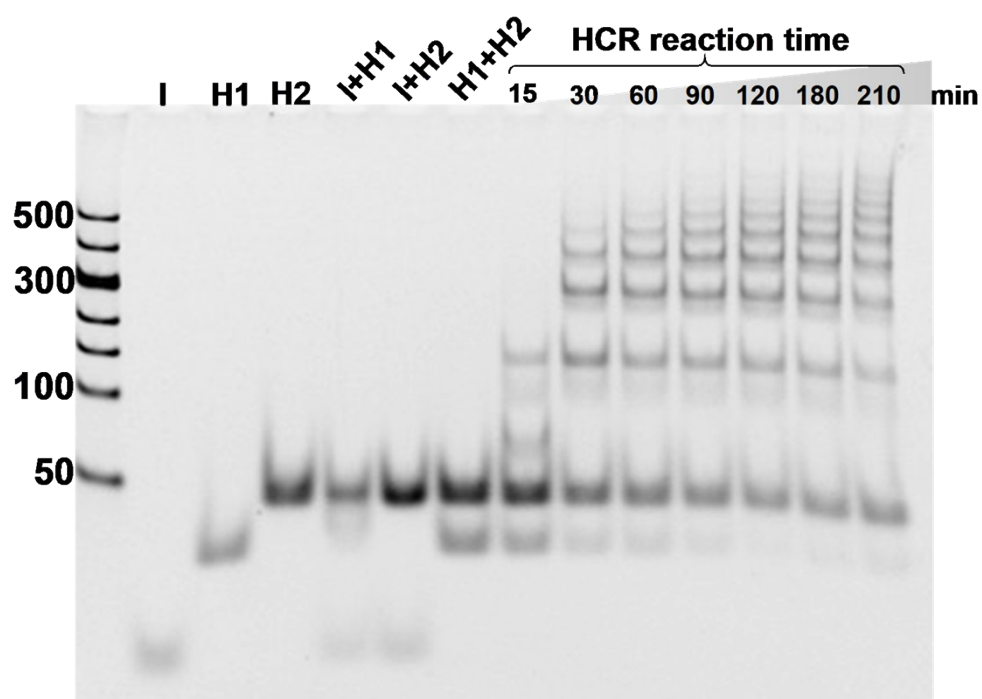
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39 **Figure S3.** Verification of I strand triggered HCR reaction. (a) and (b) are the photograph and the
 40 corresponding absorbance spectra of I strand triggered HCR reaction. (c) Characterization of HCR
 41 reaction with 8% native PAGE.



44 **Figure S4.** Optimization of (a) the concentration of H1 and (b) the ratio of H1 to H2 used in HCR.

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Figure S5. 8% PAGE to verify the HCR reaction products at different reaction times.

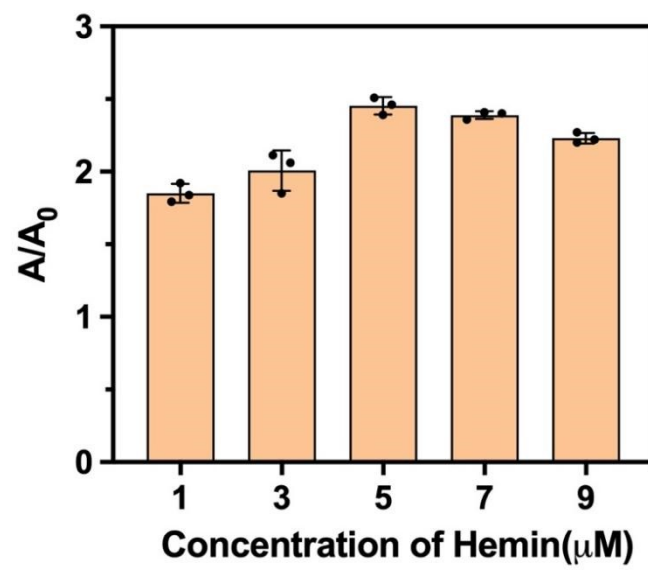
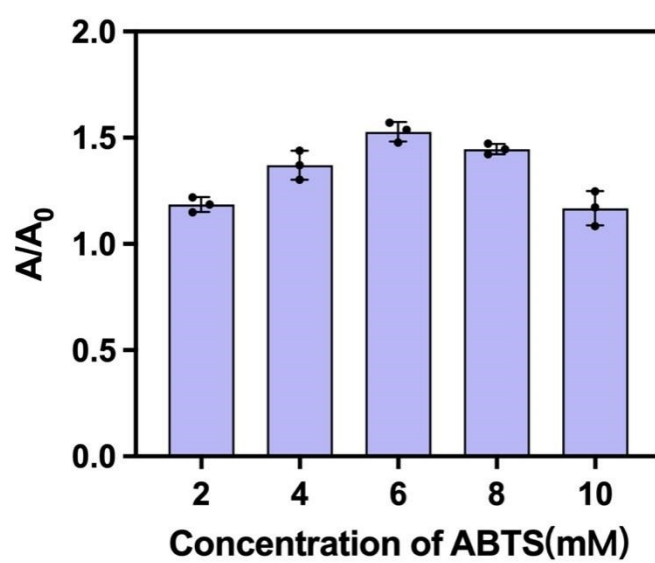


Figure S6. Optimization of Hemin concentration.

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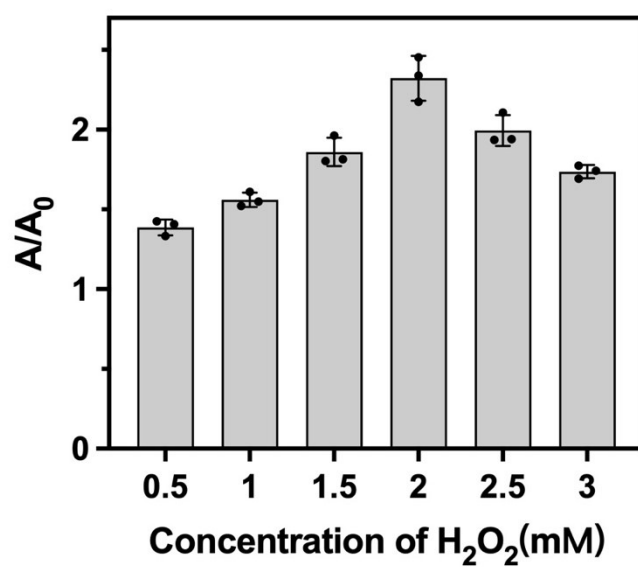
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Figure S7. Optimization of ABTS concentration.

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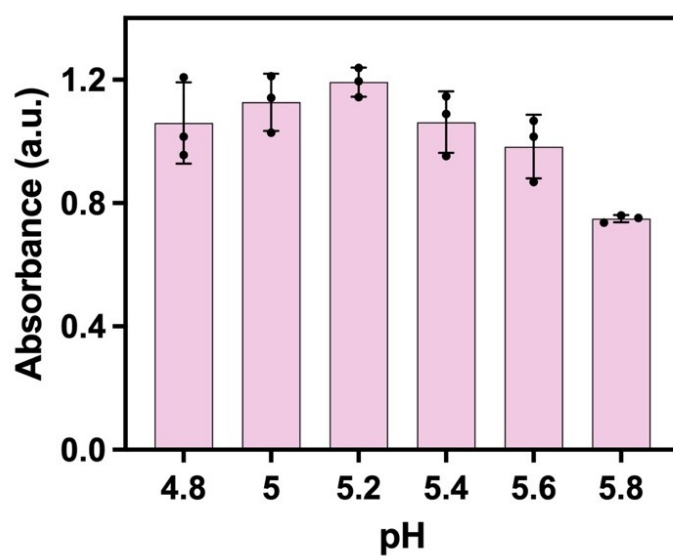


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Figure S8. Optimization of H₂O₂ concentration.

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Figure S9. Optimization of the reaction buffer pH.

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