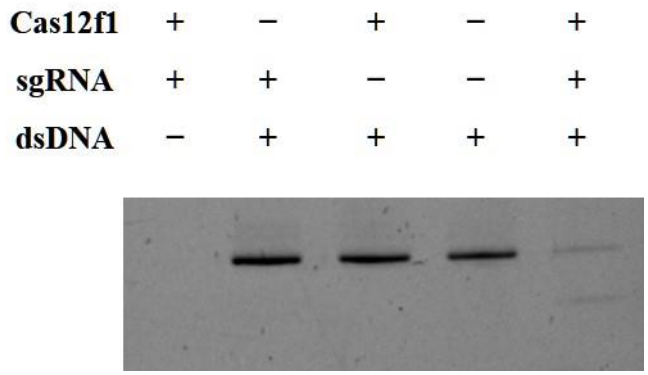
Supplementary Table S1. Sequences of Engineered sgRNAs for HBV Detection

Name	Sequence（5′-3′）
HBV-sgRNA1	ACCGCUUCACUUAGAGUGAAGGUGGGCUGCUUGCAUCAGC CUAAUGUCGAGAAGUGCUUUCUUCGGAAAGUAACCCUCG AAACAAAGAAAGGAAUGCAACCUAGUGCCAUUUGUUCAG UGUUUUAUUUU
HBV-sgRNA2	ACCGCUUCACUUAGAGUGAAGGUGGGCUGCUUGCAUCAGC CUAAUGUCGAGAAGUGCUUUCUUCGGAAAGUAACCCUCG AAACAAAGAAAGGAAUGCAACUUCAGUGGUUCGUAGGGC UUUUUUAUUUU

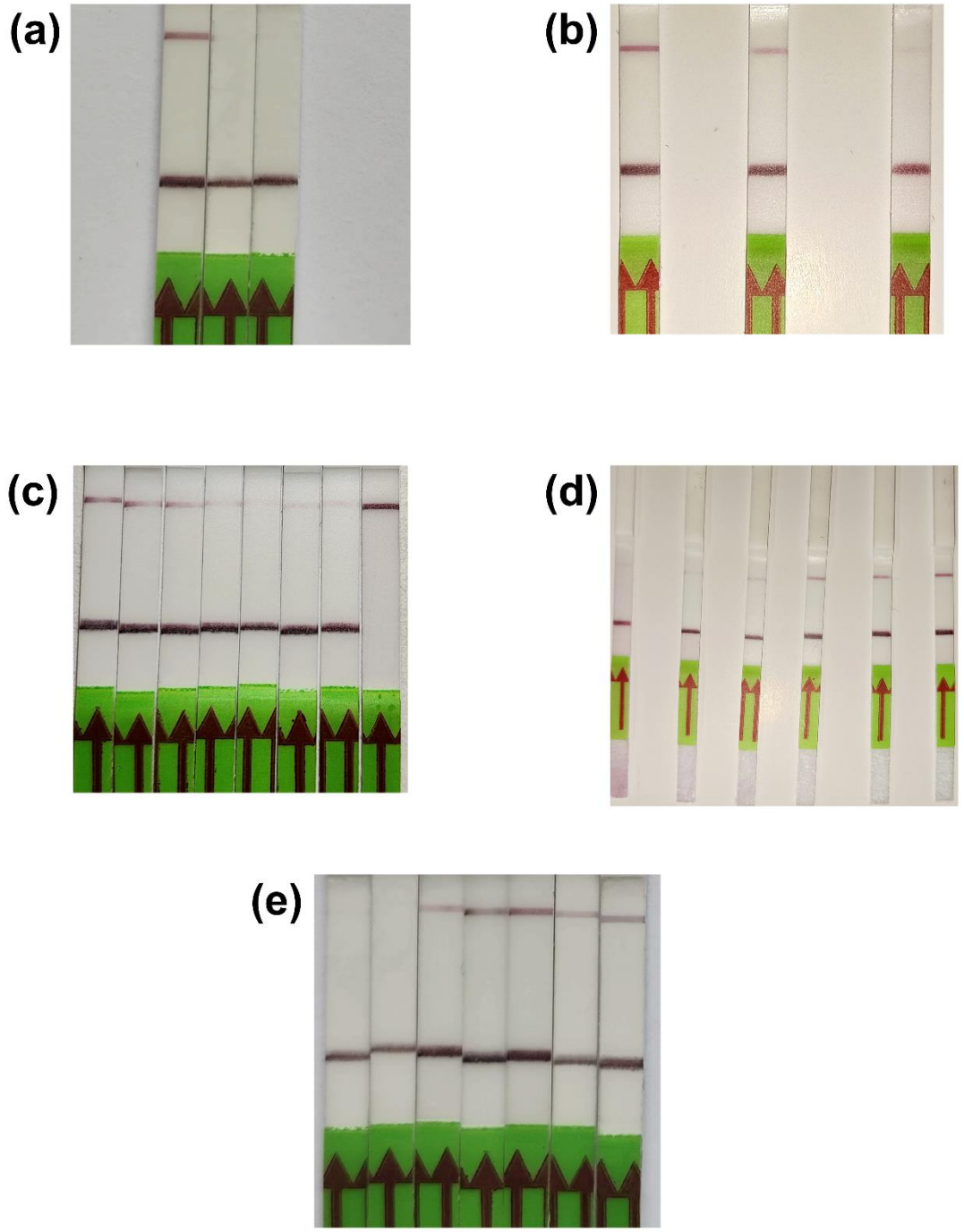
Supplementary Table S2. Nucleotide Sequences of Candidate Primers for HBV Detection

Name	Sequence（5′-3′）	Length（bp）
F1	CCTGCACGACTCCTGCTCAAGGCAACTCT A	30
R1	GACTTGGCCCCCAGTACCACATCATCCAT A	30
F2	AACCTGCACGACTCCTGCTCAAGGCAACT C	30
R2	CTTGGCCCCCAGTACCACATCATCCATATA	30

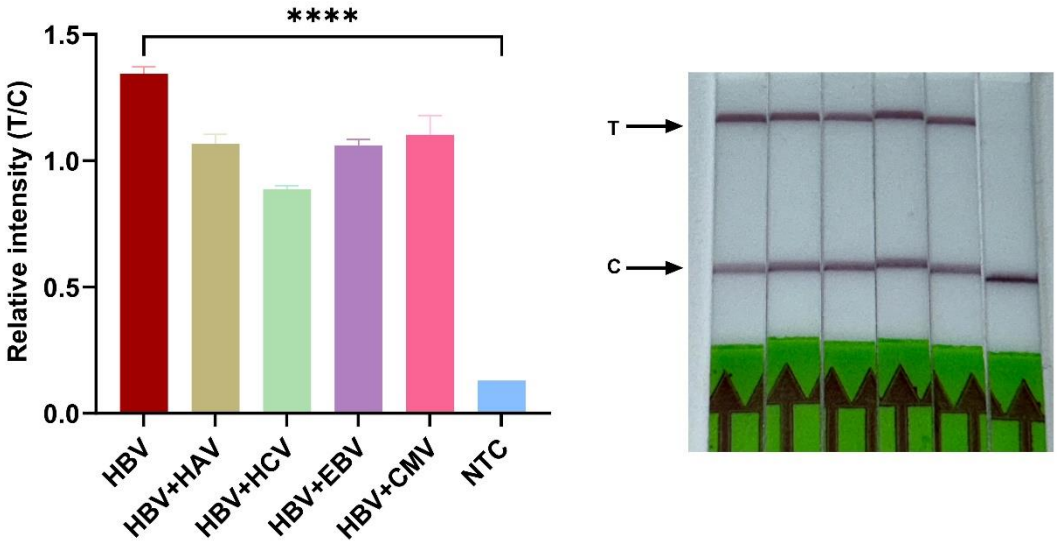
Note: The primer pairs F1/R1 and F2/R2 are designed specifically for sgRNA1/2 to target the conserved regions of HBV for amplification in the ERA/CRISPR-Cas12f1_ge4.1 system.



Supplementary Fig. S1. The electrophoresis process of DNA hybridization and cleavage. The Lateral Flow Assay System was analyzed using a 10% TBE-Urea-PAGE gel. The presence and absence of the system are denoted by "+" and " − ", respectively.



Supplementary Fig. S2. (a) Selection of the Optimal sgRNA. (b) Optimization of ERA Primer Pairs. (c) Optimization of the F-B Reporter Probe Concentration in the Lateral Flow Assay. (d) Optimization of the Best Cleavage Time for the Lateral Flow Assay. (e) Optimization of the Best Cleavage Temperature for the Lateral Flow Assay.



Supplementary Fig. S3. Interference analysis of the Lateral Flow Assay System against different types of viruses.