Electronic Supplementary Material (ESI) for Analyst.

Supporting Information

Table S1. Details of targets

ID	Target	Gene	NCBI accession	Amplicon length (bp)
1	*E. coli*	*malB*	NC_019072.1	204
2	*P. aeruginosa*	*oprL*	Z50191.1	176
3	*K. pneumoniae*	*rcsA*	NC_012731.1	191
4	*P. mirabilis*	*ureR*	Z18752.1	235
5	*E. faecalis*	*Ef0027*	NC_004668.1	199

Table S2. LAMP primers

Gene	Sequences (5' to 3')	References
malB		1
F3	GCCATCTCCTGATGACGC	
B3	ATTTACCGCAGCCAGACG	
FIP	CATTTTGCAGCTGTACGCTCGCAGCCCATCATGAATGTTGCT	
BIP	CTGGGGCGAGGTCGTGGTATTCCGACAAACACCACGAATT	
LF	CTTTGTAACAACCTGTCATCGACA	
LB	ATCAATCTCGATATCCATGAAGGTG	
oprL		2
F3	GCGTTGCCGCCAACAATG	
B3	GGATCTGGTTCTGCTGCT	
FIP	GTTGTCACCCCACCTCCGGGCGGCAACGTTCCTCC	
BIP	CTCCGTGCAGGGCGAACTGCAGGCGAGCCAACTC	
LF	ACCTGCCGTGCCATACC	
LB	GTTCATGCAGCTCCAGCAG	
rcsA		3
F3	GGATATCTGACCAGTCGG	
B3	GGGTTTTGCGTAATGATCTG	
FIP	CGACGTACAGTGTTTCTGCAGTTTTAAAAAACAGGAAATCGTTGAGG	
BIP	CGGCGGTGGTGTTTCTGAATTTTGCGAATAATGCCATTACTTTC	
LF	GAAGACTGTTTCGTGCATGATGA	
ureR (P.m-3)		This study
F3	TGGTGCAAAAGGTGAGAT	
B3	ATAATCTGGAAGATGACGAGTA	
FIP	TGTCACATCACAAGAAACTTGACTAGTATTAATGGGCAAA	

	CTATCACAG	
BIP	TTCCCGACCAAACCGATTGAATTA-TAATGGTTTGAGTAAAGAGAACAC	
LF	TCAACGTGAGATTAGTGGTGA	
LB	CATACCTTAGTACTGTCTGAAACTG	
Ef0027		4
F3	ACAGAAAGCGATAGTCGTAGT	
B3	CCTAAAAATGTTAGCTTTCGTGC	
FIP	TGGCTTCATCCATTTGTTGAAAACTTTTCAAGCTATTACGCAACAGT	
BIP	AAGTCGCGGAAATGCTTAAAATG-GTACAAATAGGAAAACTGCCAC	
LF	ATCTTGCACATTGGCAATCA	
LB	CGATTGAAGTGTTCGGTGT	

Table S3. Primer screening for *Proteus mirabilis*

Primer	Sequences (5' to 3')
P.m-1	
F3	CGCCGATTACTCGTCATC
B3	TTTGGCTCATCATAATTAAAACG
FIP	GGTAGACATTGCTGAAGTAACGTAATTCCAGATTATCATCTATCAACAC
BIP	CCTCTCAAGAGACCCTGTTTATGCTATCGACCCCTTCGTGAT
LF	AGCCTCTTTTTTATTTTGCTGGCGG
LB	CGCCGATTACTCGTCATC
P.m-2	
F3	CAACACCTGAGGTGGTTA
B3	CGGATCTTGTGTTATTAGATGAG
FIP	CAGGGTCTCTTGAGAGGGGGCTAATTTTACGTTACTTCAGCAATG
BIP	TGCTGGCGGTTTATCACGAA-GCCTGATTTTTTGGCTCAT
LF	TGCCATGTTCAAGCGGTAGA
LB	CAACACCTGAGGTGGTTA
P.m-3	
F3	TGGTGCAAAAGGTGAGAT
B3	ATAATCTGGAAGATGACGAGTA
FIP	TGTCACATCACAAGAAACTTGACTAGTATTAATGGGCAAACTATCACAG
BIP	TTCCCGACCAAACCGATTGAATTA-TAATGGTTTGAGTAAAGAGAACAC
LF	TCAACGTGAGATTAGTGGTGA
LB	CATACCTTAGTACTGTCTGAAACTG
P.m-4	
F3	TGACAAATTTTTTCCCGACC
B3	TGTTGCATAAACAGGGTCT
FIP	CGCCCCTGATTTTATTAATGGTTTG-GAATTACATACCTTAGTACTGTCT

BIP	TATCATCTATCAACACCTGAGGTGG-CCATGTTCAAGCGGTAGAC
P.m-5	
F3	GGGTCGATATTCTTAATATTTTTCG
B3	TAATTTAATGCGATGGGGATT
FIP	ATGCCATTTACGTTGCGGATCTGATGAGCCAAAAAATCAGGC
BIP	AACGCTCTATACTACACCATCAACACTGACATCCAACAGTAATTGG
LF	CGCCATTTAAGTAAAGAGGGCGT

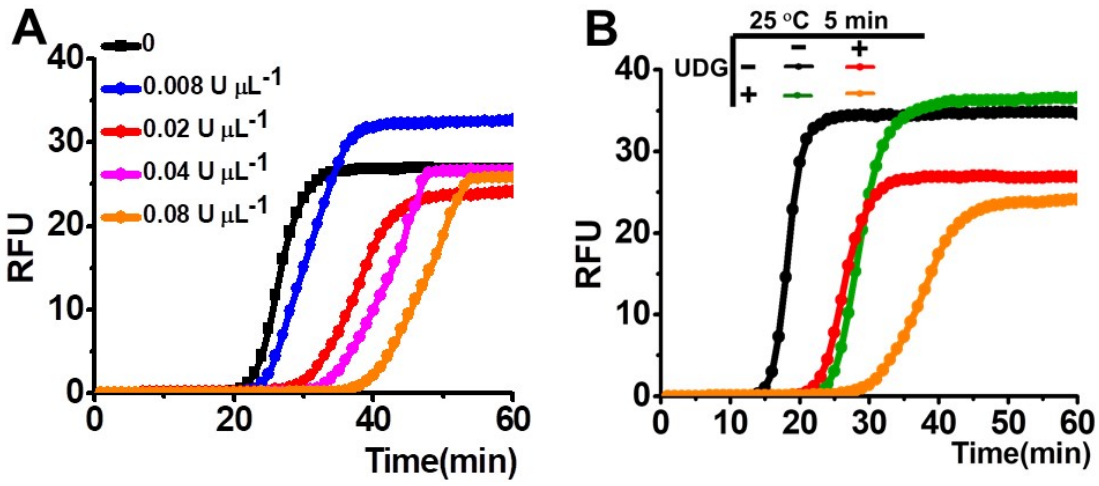

Figure S1. (A) Optimizing the concentration of UDG. (B) Reaction efficiencies were compared in case of two factors: room temperature placement and UDG.

We carried out an experiment to optimize the concentration of UDG (Figure S1(A)). Except for different final concentrations of UDG, the other compositions of the reaction were the same as described in Figure 2A. The stock concentration of UDG was 1 U μL^{-1}. We added 0, 0.2, 0.5, 1, and 2 μL of UDG respectively to the 25 μL of reaction mixture.

Table S4. Comparison of the performances of commercial kits for nucleic acid extraction.

Material	Molecule	Commercial products	Sample	Application	Advantage	Disadvantage	Reference
1.FTA cards	DNA, RNA	Whatman	1.2 mm punches	5-20 ng DNA	Easy to use and store	limited amount of nucleic acid	5
2.Silica matrices	DNA, RNA	QIAamp	Blood (200 μL)	4-12 μg DNA	High-purity DNA	Unable to recover small DNA fragments	6
3.Magnetic bead	DNA, RNA	TIANGEN	Blood (100-250 μL)	4-8 μg DNA	No centrifugation, best choice for automation	Interference in PCR amplification	6, 7
4.Alkaline extraction	Plasmid	TaKaRa	1-4 mL of fresh bacteria	1-20 μg Plasmid DNA	High-purity plasmid DNA	Containing high concentration of alkaline solutions and denaturant	8

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