

FIGURE S1. Nucleotide sequence of the *H. influenzae* capsulation locus genes used to design the non-Hib LAMP primers. The sequences used for the LAMP primers are indicated by arrows. (A) to (E) in the figure are the sequences of *H. influenzae* capsulation locus genes for serotypes a, c, d, e, and f, respectively.

Fig. S1(A)

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3001                                                    3070
TTGACGATGG TTCAAAGAT AACACTGTTA ATAATGCAAA ATTAGCCGTT GCTAACGATA AAAGATTTAC

3071                                                    3140
TATTCTTCGA AAAGAAAATT CTGGTGTTTC CTCTACTAGA AACTTTGGAA TAAAAAAGG AAAAGGAGAA

3141                                                    3210
TTCATTTTTT TCTGTGATTC TGATGACATT TTAGAAGGAA ATGCTATTGA TAACTACTC ATTGCAGCAT
                                                    |-----F3-----

3211                                                    3280
TTGCTGAAAA TGCGGATTAT ATTTACGGTG GCATCAAAAA ATTTAATAAA GAAAAAGAGT GGACTATTCC
---> |-----F2-----><-----LF-----| <-----F1-----

3281                                                    3350
TGTTACGAC AAAAATAATC TATTCCTACA AGGAACAAAG ACCATCGATA AGAATACAGA ACTATTTTTA
-----| |-----B1-----> |-----

3351                                                    3420
TCAATGTCTC CTGGGGCAAA ATTAATACAT CGGTCACTGT TAAAGAATAA ATTTTTTCCA GAAGATATTC
----LB-----><-----B2-----| <-----B3-----

3421                                                    3490
ATTGTGTCTA TTGTATCGGT AACTATATCT ACAAATATAC AGAAGATCAG GTCATATTCT TCAATATATT
-----|

3491                                                    3560
TTTAGATGCT AAAAAAATCT ATTGTATCGG TAACTATATC TACAAATATA GAGAGCGAGA TTTAGAAAAC

3561                                                    3600
AATGAACGAT CAATTACACA GCAACGTGAT ATAAAAGCCT

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Fig. S1(B)

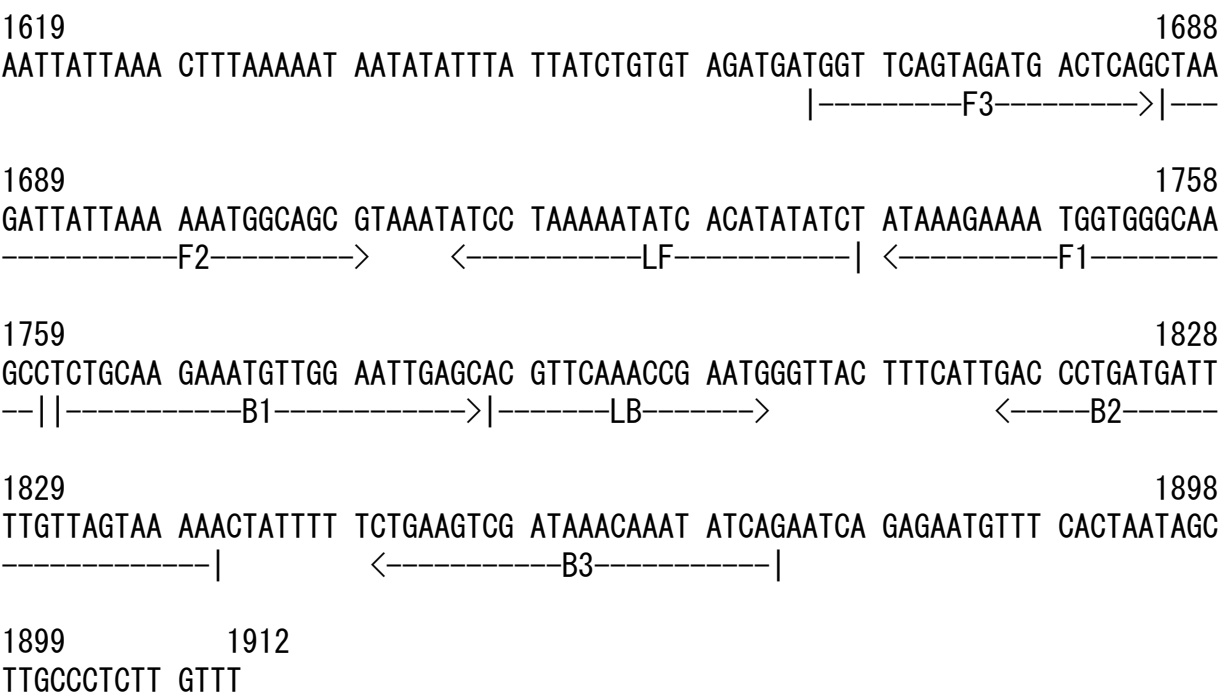


Fig. S1(C)

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1                                     60
GCAAATCATA GTGACAAAGA ACTGACTTTA CTAGACTACC AAGAAAGCTT AAAAAGCTGTA

61                                     120
GATGTAGCTG TATTATTAGT TAACCATAAA GAATTTGTTG AAAATAAACC GCACTTTGGA

121                                    180
ACAATGTTG TAATCGTTGA TACGAAAGGG ATTTGGTAAT TTCACTATT ATAGGAAAAA

181                                    240
ACTAAGTACT GGTAGAATTA ATTTATCTAC CAGTACTTTA TGTATATAAT TAGGTAAAAC

241                                    300
AGATGAAGAT TTTAATTTTT GGTAGCTATG TTACAAGAGA TGCTTTTACT TTTGATAAAT

301                                    360
CAAATGAATT TGAATTAGAT CGATATTTCTG TTAGAACATC TCTAGCAACT GCTTTTAATT
          |-----F3-----> |-----F2-----

361                                    420
CAGAGCCAAT AGAAGATAAT TATACGATGC AATTAACCTC TGCATTTTCTG AAAAAAATTG
-----> <-----F1-----|

421                                    480
TAAATGCTGA GTTAAAAAAA GAATTCAAAG AACTCTTTCT TCTTGGAAG TATGATTACC
          |-----B1----->|-----LB-----

481                                    540
TTGTGATTGA TTTTATTGAT GACCGATACA ACCTGTTTAA ATTTAAGAAT GGTTGTAAAA
-----> <-----B2-----| <-----B3-----

541                                    600
CTCTTCTTAG TGCTGAATTA AAAAATACTG ATTTCTTAGA TAAAAATCAA CATAACGGAG
-----|

601                                    645
AAATAATTC TGGATTCTCT GAAGAATGGT TTGAAGAGTG GAAAA
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Fig. S1(D)

3139 3208
AAAAGCTCTT AGTTATGAGC ACTCAATGTC ATTTGCGATTG GGATACGCCC TCATTTTTGG TTTTAAATCA

3209 3278
TGGACAGGCT TTAAACATTT AATTAAAAACA CTTTACACAC TACCTTTTGA GAAGAGAACT AAAAAACAAC

3279 3348
AAGGTACAGA AATATCAGTT ACACTTCGCA AACCTGATTA TTAACTATT AATTGGAAAG GTCGCCGTAC
|-----F3----->

3349 3418
TATTACTCAA TGGACAAGTC TACCTCAAAA AGAGTTTAAG GATTTTATTG AGCTTTTCGC AGTGGAGCGG
|-----F2-----> <-----F1-----|

3419 3488
CTTGAATTAA GAAACAGAGG GTTCTTTCAA ACTATTGCTT GCAAAAATAT TGACCAACTT GTCTTATCAA
|-----B1-----> |-----LB-----

3489 3558
TCAACATTGA TAGTGAAGAA ACCCCTAAGC AGACTAAACA AGCACTGGCA GCTATTACAT TCTTAGATAA
--> <-----B2-----| <-----B3-----|

3559 3628
AGATAATAAT AACTAGAACT CTAGTATTGA ATTACCACAA AGTAAAAAAC TGGGGAAATA CTATTTCTAC

3629 3698
CTTAATACAG AGAAAGATCA ACAGGATAAT TTATTTATTA TCCACCTTT AGATTGTGAA AATATAAAAT

3699 3768
TAGATATTGT TCCTTGGGAT ATAAAAGGAA AAATATCTGT ACATAATAAA GTAGGCATAT CTCACTATAC

3769 3838
AAATGGTATT AGTATCATTC TTCCAACATA TAAAGGAGTT AATACTATTA AGAAATGCTT AGATTCTTTA

Fig. S1(E)

11861 11930
TTATTTTAAA GCCTGACGTT ATTATATACT CTCAACCTTC CTGTGATTTT TCTGCTTTAC TATATGAAAA

11931 12000
TGGATATTAT AACAATAGTA AATATTTTTTC TAATATTATT CCATCAGTAG AAAGTGATGT TTTTAGATTG

12001 12070
AAAACTATTC AAGATAATTT AATTCAGATA CAGAATAATA TTATTATGCT ATCTAAACTA TGTGAGTTAT
|-----

12071 12140
ACAGTATCGA TCTCTTTATA TCAACTTGCT GTTCAAATTC ATCTAAACGC CAACTTAAAA TGATGAATGA
-----F3-----> |-----F2-----> <-----LF-----|

12141 12210
TATTATTAGA GAGAATTCTT ATCTTGGGTA TAAGGTTATT GATTGGACT TGATAGTACC AAAACAGAG
<-----F1-----| |-----B1-----> |

12211 12280
GCCTATTTTT ATGATAAACA ACACTTAAAT GAATATGGTA GTAATTTAGT TGCTAATATT TATCTATATA
-----LB-----> <-----B2-----|

12281 12350
ACGTTAGAAA TTTTTCAGAT GACATGCCAA AAAAAACAAT ACAAAAACAT CATATACAAA AAATAAATGG
<-----B3-----|

12351 12420
CGTCTTTGAA ATACCTCAA ACACTTAGA AAAAGAGAGC AACTCTATTT TGTTAAAAAT AAAAAACAAT

12421 12490
GAAAAACAAA ATCAAGATTT TGAAATAAAA ATAACATATT TCAATGAAGG AGAAATAATA AAGAATGATG

12491 12560
TAAAAAAAAT ATTATTGTTA CCATTGCATA GTATAGAATG CTCATATTTT ATAGAAGAAC TACATCAGAC

12561 12600
TAAAGTACTT ATAGAACCAA TTTCTATATC AAAAAATATT