

A reverse transcription loop-mediated isothermal amplification for broad coverage detection of Asian and African Zika virus lineages

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**A) F3**

5' → 3'

```

F3      : GGCRGAYATWGAGATGGCTGG 454/463
KX694533 : A.....
KX601167 : A.....
KX377336 : A.....
MF510857 : .A.....
MH513598 : .....G.....
MF574576 : .....G.....
MF574575 : .....G.....
MF574567 : .....G.....
KY785419 : .....C.....
    
```

**B) B3**

3' ← 5'

```

B3      : GGTTC AACACARGTTGGAGTG 454/463
MK241417 : ..G.....
MK241416 : ..G.....
MK241415 : ..G.....
KY785410 : ..C.....
MN473454 : ..C.....
MN025403 : ..C.....
MH061908 : ..C.....
MH061881 : ..C.....
MH061868 : ..C.....
    
```

**C) FLP**

3' ← 5'

```

FLP     : ATGTACATTGAAAGAGCAGGTGAYATCA 433/463
MG807647 : .....C.....T.
KU963574 : .....C.....T.
KU955595 : .....C.....
KU955592 : .....C.....
MG758785 : .....C.....
MG758786 : .....C.....
KU955591 : .....C.....
KX601166 : .....C.....
MK028860 : .....C.....
KY348860 : .....C.....
MF510857 : .....C.....
MN025403 : .....C.....
MF574555 : .....G.....
KY785426 : .....G.....
MH882542 : .....T.....
MH882541 : .....T.....
MH882540 : .....T.....
MH882539 : .....T.....
MH882538 : .....T.....
MH882536 : .....T.....
MH882535 : .....T.....
MH882534 : .....T.....
MH882533 : .....T.....
MH882532 : .....T.....
MH882531 : .....T.....
MH882530 : .....T.....
MH882529 : .....T.....
MH882528 : .....T.....
MH882527 : .....T.....
MN473453 : .....C.....
    
```

**D) BLP**

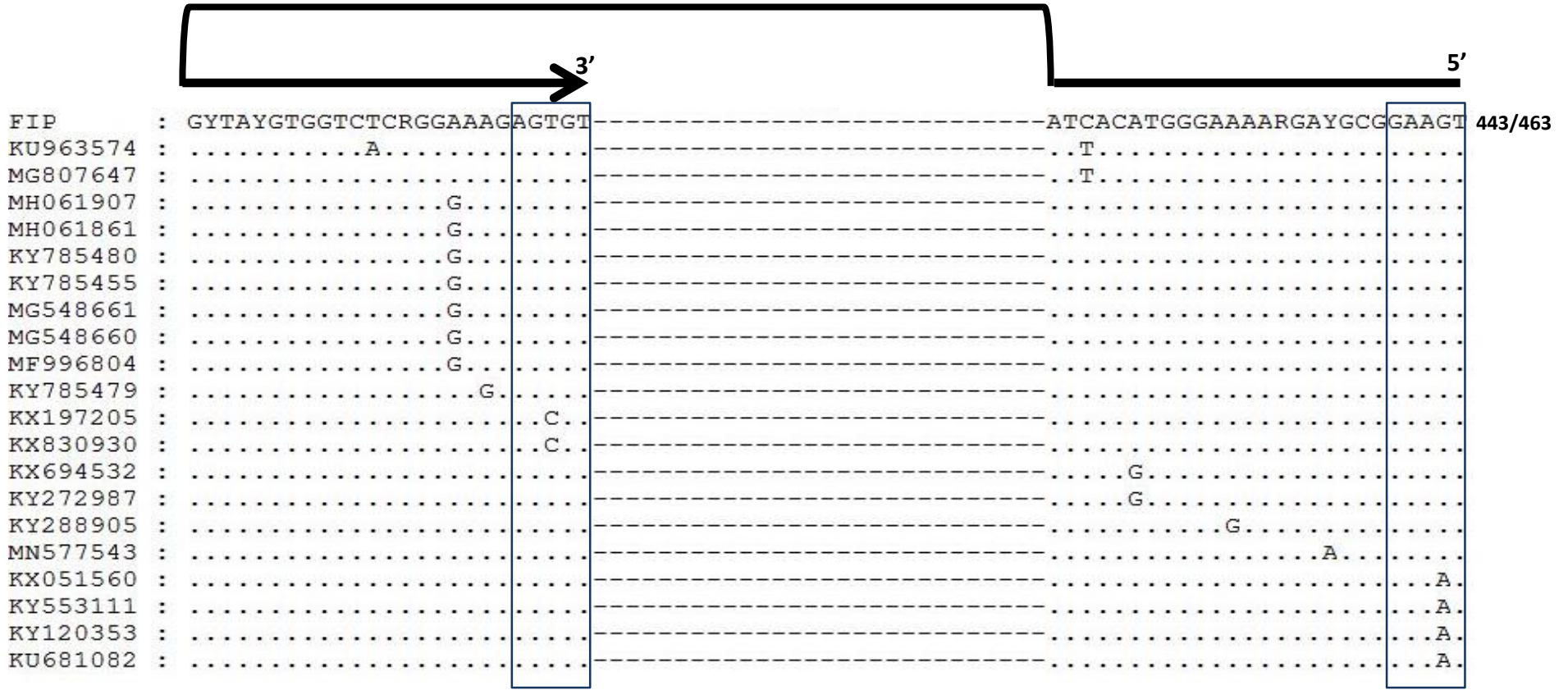
5' → 3'

```

BLP     : TGTGGCATGAACCCAATAGC 450/463
KY553111 : ..C.....
KY120353 : ..C.....
KU681082 : ..C.....
KY693679 : .....A.....
KY693678 : .....A.....
MN611472 : .....T.....
KU365778 : .....T.....
MH882548 : .....G.....
MH882547 : .....G.....
MH882544 : .....G.....
MH882545 : .....G.....
MH882546 : .....G.....
MH882543 : .....G.....
    
```



E) FIP



F) BIP

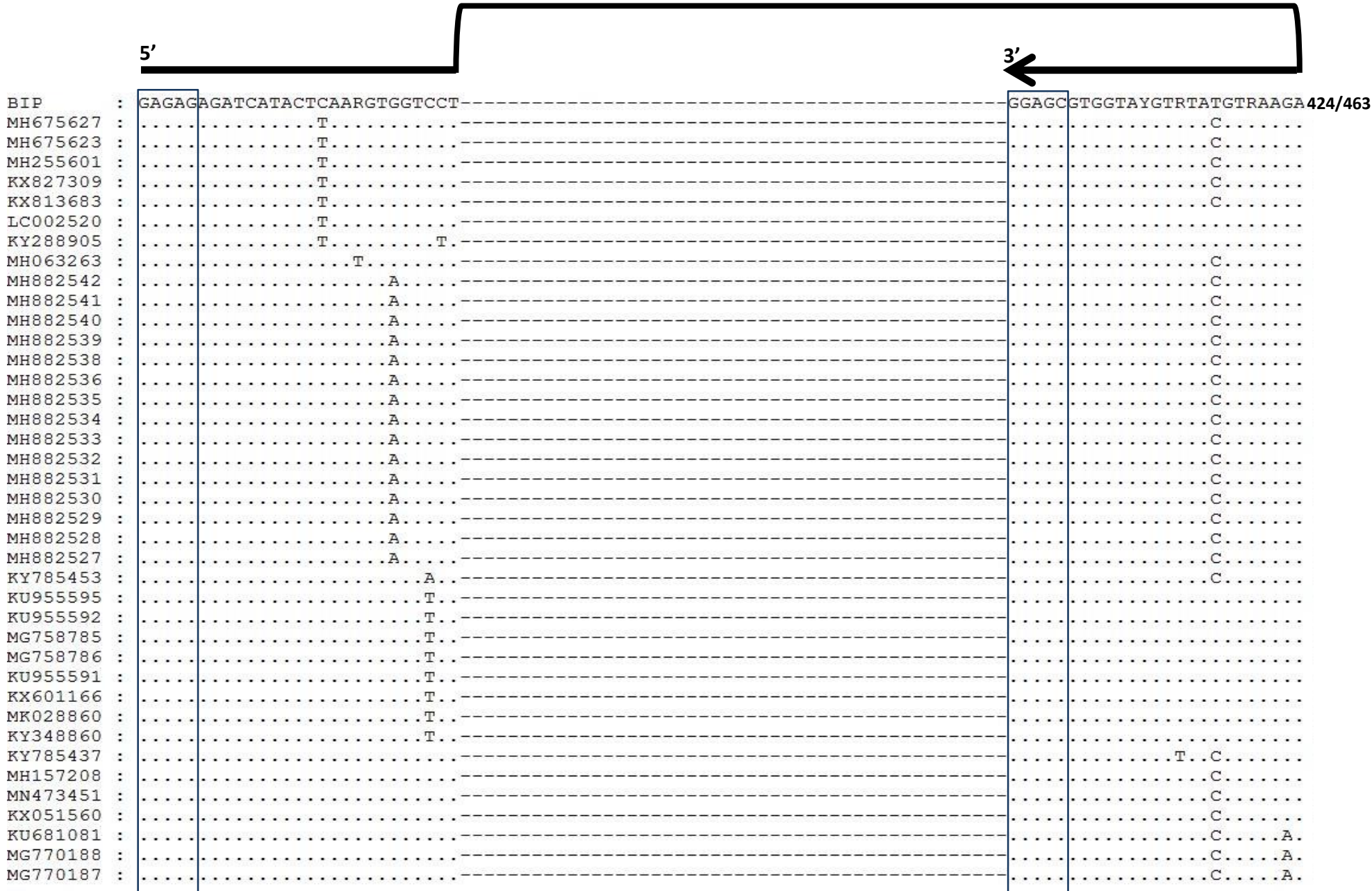


Figure S2. Nucleotide mismatches of the RT-LAMP primers against 463 ZIKV genome sequences. The top sequences are primer sequences. Total numbers of ZIKV genomes with 100% sequence similarity to the primers are shown at 3' end of the primers. Only the ZIKV genomes with nucleotide mismatches to the primer are listed. The dots indicate the same nucleotides as the top sequence. The boxes indicate the nucleotide positions which are critical for priming and amplification.