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

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Table S2. The ZIKV genomes used in this study.

Lineage	Accession Number
Asian	KF993678, KJ776791, JN860885, EU545988, HQ234499
African	NC_012532, LC002520, HQ234498, AY632535, KF383121, KF383119, KF383118, KF268950, KF268948, KF268949, KF383115, DQ859059, KF383116, HQ234501, HQ234500, KF383117