Supplementary text

Links to publicly available data used in methods

Hybrid capture probes that target Zika and chikungunya viruses

https://storage.googleapis.com/sabeti-public/hybsel_probes/zikv-chikv_201602.fasta [2.25 MB]

(*Note*: Probe sequences are 140 nt. They contain 20 nt adapters on each end for PCR amplification; the middle 100 nt targets the virus.)

Kraken database built for identifying viruses in samples by unbiased sequencing

https://storage.googleapis.com/sabeti-public/meta_dbs/kraken_full-and-mosquito-and-all_human_viral.tar.gz [185.25 GB]

Sequences used for taxonomic filtering or analyses

Sequences against which reads from unbiased and hybrid capture approaches were taxonomically filtered

GenBank accessions: KX087101.2 KX198135.1 KX101066.1 KU501215.1 KX197192.1 KU365779.1 KU991811.1 KU681082.3 KU955589.1 KU926309.1 KU321639.1 KX087102.1 KX253996.1 HQ234500.1 KF383115.1 KU955591.1 KF383117.1 KU955593.1 KF383119.1 KX156775.1 KU922923.1 KU729218.1 KF268950.1 KU820899.2 KU866423.1 NC_012532.1 KU365777.1 KU955590.1 KF268948.1 KU501216.1 KU647676.1 KX198134.1 KU963574.1 KU527068.1 KU937936.1 KX101062.1 KX262887.1 DQ859059.1 KX051563.1 KU820897.2 KU497555.1 KU926310.1 KU681081.3 KU707826.1 KU509998.3 AY632535.2 KX156774.1 KX247646.1 KU820898.1 KU365780.1 HQ234501.1 KU940228.1 HQ234498.1 KU955592.1 KF383118.1 JN860885.1 KU365778.1 KU955595.1 KX185891.1 KU922960.1 KX156776.1 KJ776791.1 KU853013.1 KU744693.1 KX056898.1 KF383116.1 KU761564.1 KU963796.1 KU853012.1 KU312312.1 LC002520.1 HQ234499.1 KU963573.1 KU729217.2 KU870645.1 KF993678.1 KU501217.1 KF383120.1 KF268949.1 KX117076.1 EU545988.1 KU955594.1

Sequences used in molecular clock phylogenetic analyses and SNP analyses

We used all sequences generated in this study, as well as:

- 32 published sequences from the Americas. *GenBank accessions*: KU312312.1 KU321639.1 KU365777.1 KU365778.1 KU365779.1 KU497555.1 KU501216.1 KU501217.1 KU509998.3 KU527068.1 KU647676.1 KU707826.1 KU729217.2 KU729218.1 KU820897.5 KU853012.1 KU853013.1 KU926310.1 KU940224.1 KU940227.1

KU940228.1 KX051563.1 KX101060.1 KX101061.1 KX101066.1 KX269878.1 KX280026.1 KY317936.1 KY317937.1 KY317938.1 KY317939.1 KY317940.1

- 32 sequences generated in the ZiBRA project, with permission from the authors. *ZiBRA project IDs*: ZBRA105 ZBRC14 ZBRC16 ZBRC18 ZBRC28 ZBRC301 ZBRC302 ZBRC313 ZBRC319 ZBRC321 ZBRD103 ZBRD107 ZBRD116 ZBRX1 ZBRX2 ZBRX4 ZBRX7 ZBRX8 ZBRX11 ZBRX12 ZBRX13 ZBRX14 ZBRX15 ZBRX16 ZBRX100 ZBRX102 ZBRX103 ZBRX106 ZBRX127 ZBRX128 ZBRX130 ZBRX137

Sequences used for maximum likelihood estimation and root-to-tip regression

We used sequences from “Sequences used in molecular clock phylogenetic analyses and SNP analyses” as well as 6 outgroup sequences from Southeast Asia and the Pacific. These outgroup sequences are:

- 6 published sequences. *GenBank accessions*: EU545988.1 JN860885.1 KF993678.1 KJ776791.2 KU681081.3 KU681082.3