# SUPPLEMENTARY INFORMATION

# High-quality resolution of outbreak-related Zika virus genome and discovery of new viruses using Ion Torrent-based metatranscriptomics

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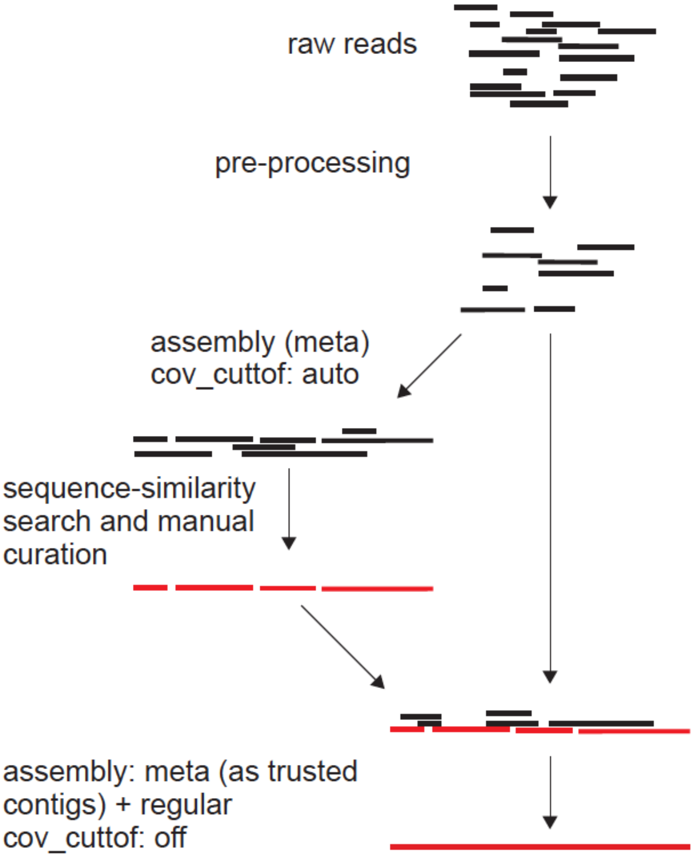
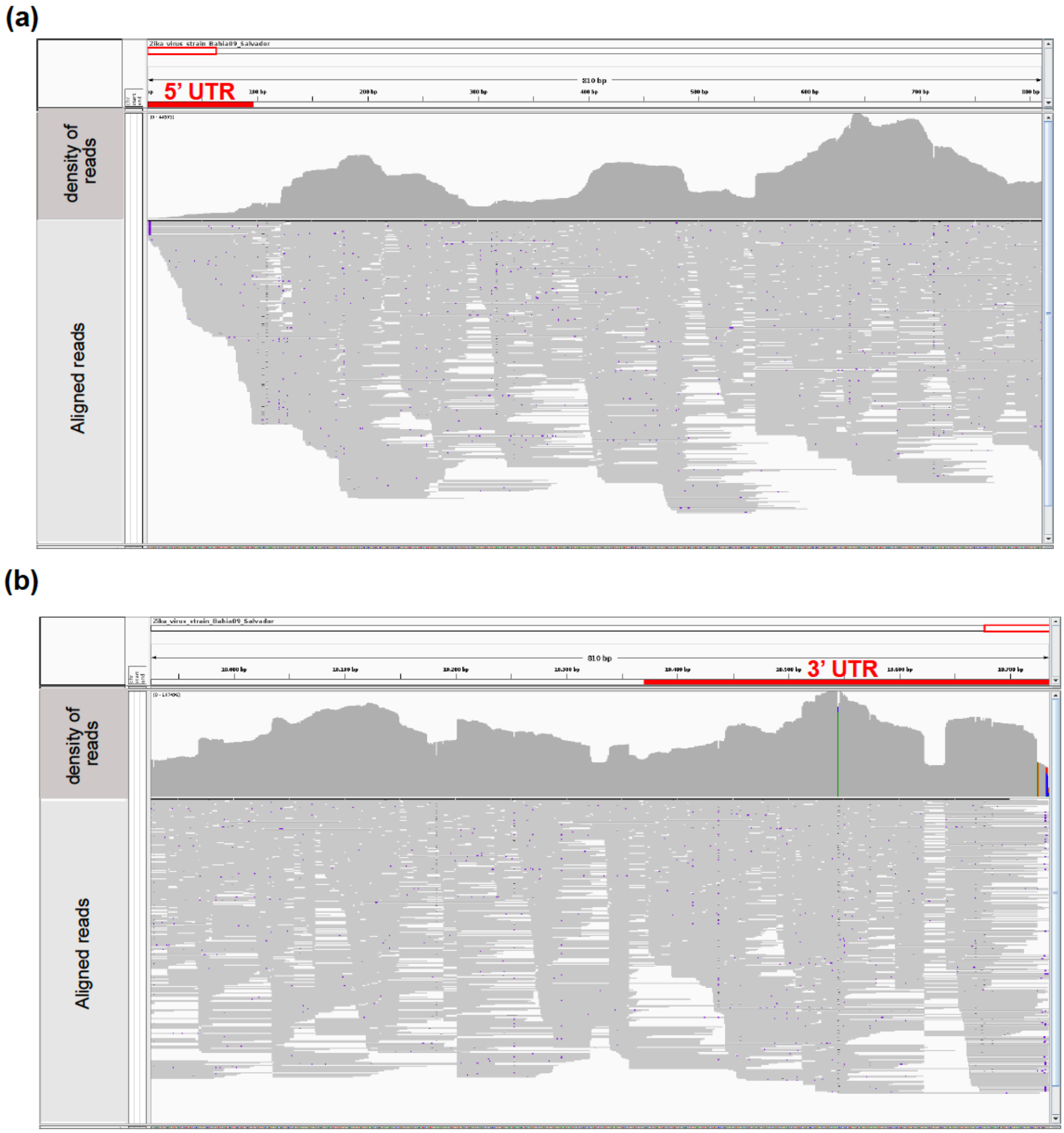
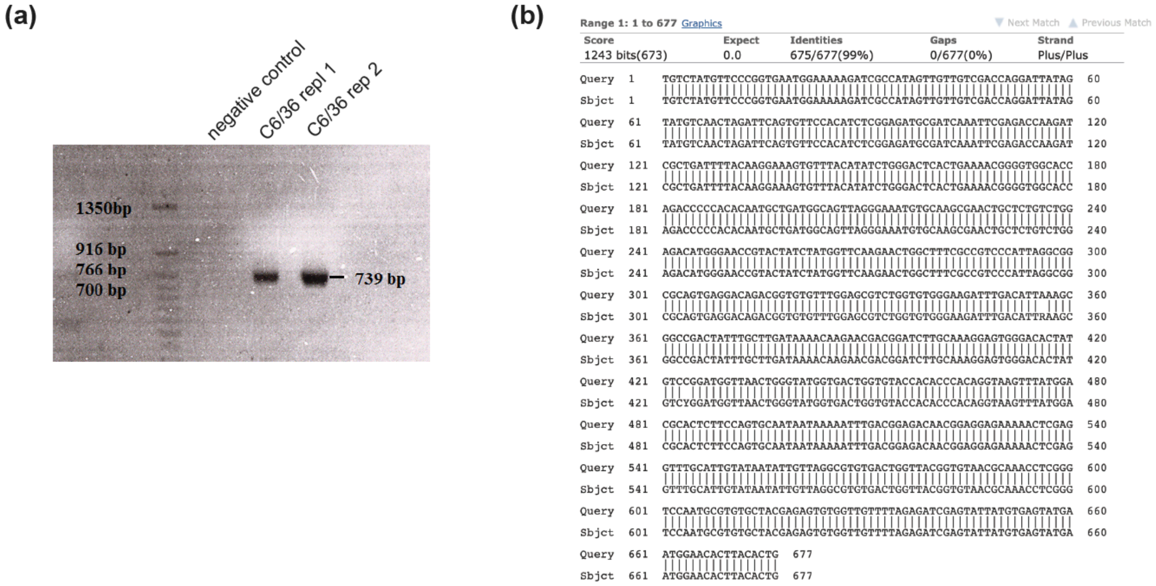


**Supplementary Figure 1. Bioinformatics approach to reconstruct viral genomes based on ION torrent data.** Raw reads are pre-processed in order to remove low quality reads, reads containing ambiguous bases and smaller than 70nt. Reads that passed in quality control were submitted to contaminants removal, which reads that matched host or bacterial genomes are filtered out. Pre-processed reads were used to *de novo* assembly contigs using "*meta*" strategy with automatic definition of coverage cuttof. Assembled contigs were characterized based on sequence-similarity searches and manually curated. Then, high quality viral contigs were used as anchors (trusted contigs) to perform posterior *de novo* assembly using regular "strategy" with coverage cuttof turned off.



**Supplementary Figure 2. Overview of reads aligned to UTR regions of the Zika virus genome assembled using IGV genome browser.** Density and alignment profile of reads derived from 5′ (a) and 3′ (b) UTR regions of Zika virus genome. Red bars indicate UTR regions. A total of 6,784 reads were aligned to 5′ UTR and 250,906 reads to the 3′ UTR.



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Range 1: 1 to 677
Score             Expect  Identities      Gaps         Strand
1243 bits(673)    0.0     675/677(99%)    0/677(0%)    Plus/Plus

Query  1    TGTCTATGTTCCCGGTGAATGGAAAAAGATCGCCATAGTTGTTGTCGACCAGGATTATAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGTCTATGTTCCCGGTGAATGGAAAAAGATCGCCATAGTTGTTGTCGACCAGGATTATAG  60

Query  61   TATGTCAACTAGATTCAGTGTTCCACATCTCGGAGATGCGATCAAATTCGAGACCAAGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  121  CGCTGATTTTACAAGGAAAGTGTTTACATATCTGGGACTCACTGAAAACGGGGTGGCACC  180
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Query  181  AGACCCCCACACAATGCTGATGGCAGTTAGGGAAATGTGCAAGCGAACTGCTCTGTCTGG  240
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Sbjct  181  AGACCCCCACACAATGCTGATGGCAGTTAGGGAAATGTGCAAGCGAACTGCTCTGTCTGG  240

Query  241  AGACATGGGAACCGTACTATCTATGGTTCAAGAACTGGCTTTCGCCGTCCCATTAGGCGG  300
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Sbjct  661  ATGGAACACTTACACTG  677
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**Supplementary Figure 3. Amplification of RdRp fragment of the new totivirus-like identified in *A. albopictus* C6/36 cell lines.** A) RT-PCR of RdRp fragment of the new totivirus-like in uninfected C6/36 stock or water (negative control). B) Alignment of Sanger sequenced fragment and assembled contig derived from Ion torrent sequencing.