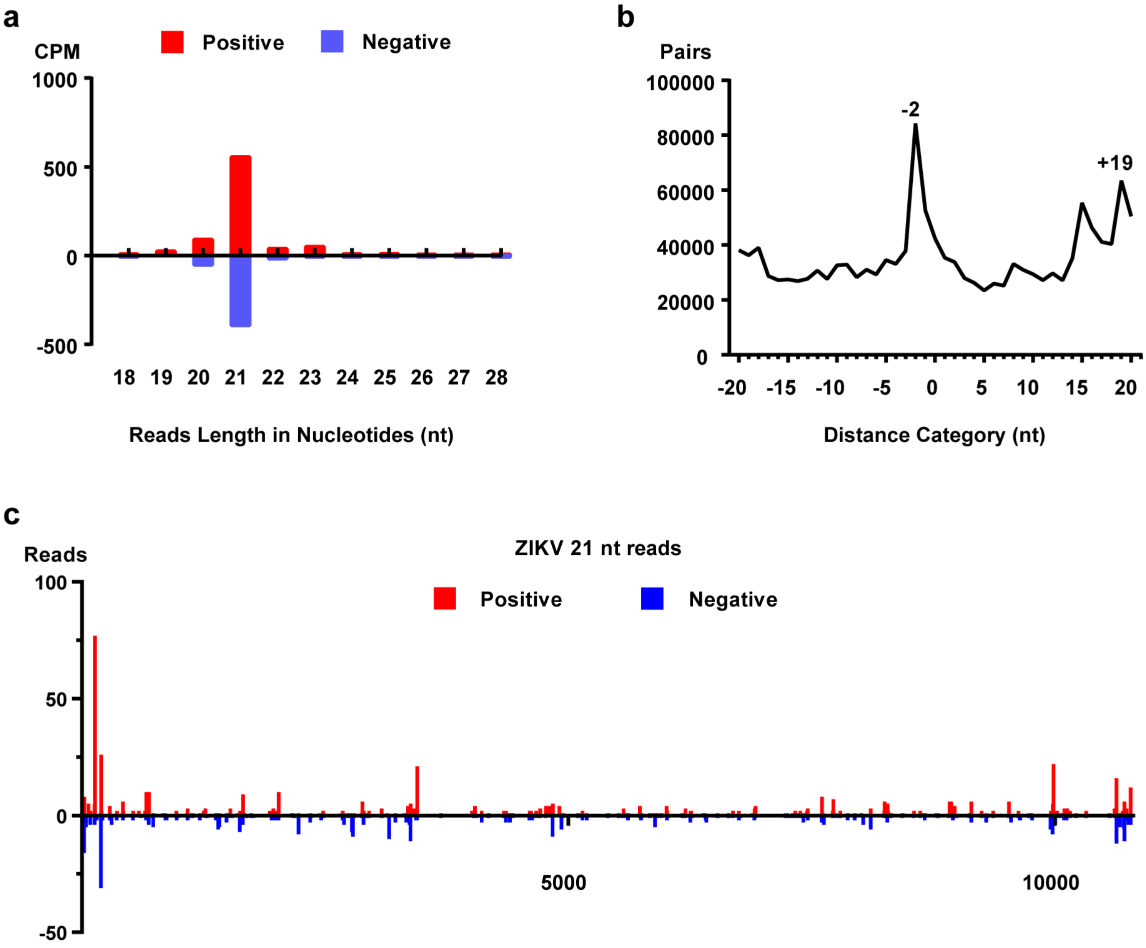

Fig. S1. The production of vsiRNAs in ZIKV-infected mosquito Aag2 cells.

Aag2 cells were infected with ZIKV (strain GZ01) at an MOI of 2, and total RNAs were extracted and subjected to deep sequencing at 96 hours post infection (h.p.i.). **a,** The size distribution and abundance (counts per million of total reads, CPM) of total vsRNAs. Red, positive-stranded vsRNAs; blue, negative-stranded vsRNAs. **b,** Total pairs of complementary 21-nt vsRNAs derived from ZIKV in each distance category between the 5′ and 3′ ends of a complementary vsRNA pair, showed as -2 for pairs with 2-nt overhang at the 3′ end of each strand defined as the canonical viral siRNAs (vsiRNAs). **c,** Distribution of vsRNA reads (21 nt size) in the positive-stranded genome and negative-stranded anti-genome of ZIKV and the relative abundances of positive- and negative stranded vsiRNAs are indicated.