S1 Table. Summary of Illumina HighSeq 2000 RNA-sequencing using Partek Genomic Suite v6.6

Sample ID	Number of Alignments	Total Number of Reads	Percentage of reads which fully overlap exon	Percentage of transcripts with reads	Total reads with junctions	Reads with junctions that are compatible with a transcript
DENV2ST	32567237	15880324	67.3503	81.8814	2202876	1716335
Uninfected	11994298	4676021	55.1425	67.906	346293	245503