

Supplementary Figure S3. The maximum likelihood consensus tree of the flavivirus polyprotein (A: 118 amino acids, B: 454 amino acids) sequences. The trees are constructed using 1,000 replicates. Branches achieving $\geq 95\%$ bootstrap support are annotated with red dots. Viruses are indicated by GenBank accession, name and isolate identifier where available. Haseki Tick Virus and related viruses are marked. Sequences detected in the study are indicated by sample IDs.

