Table S1: Evolutionary divergence over ZIKV sequence pairs between groups

	I	II	III	IV	V	VI
I		0.000	0.000	0.000	0.001	0.001
II	0.004		0.000	0.000	0.000	0.000
III	0.004	0.004		0.000	0.000	0.000
IV	0.004	0.004	0.004		0.000	0.001
V	0.004	0.004	0.003	0.003		0.000
VI	0.004	0.004	0.004	0.004	0.003	

The number of base substitutions per site from averaging over all sequence pairs between groups are shown below the diagonal.
Standard error estimate are shown above the diagonal.
Roman algorisms indicate ZIKV variants inferred by this study.

Table S2: Average of evolutionary divergence over ZIKV sequence pairs within groups

	d	S.E.
I	0.003	0.000
II	0.003	0.000
III	0.003	0.000
IV	0.002	0.000
V	0.000	0.000
VI	0.002	0.000

d = Number of base substitutions per site from averaging over all sequence pairs within each group.
S.E. = Standard error.
Roman algorisms indicate ZIKV variants inferred by this study.