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Supplementary Information

The different footprints of the Zika and Dengue surface proteins on the viral membrane

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Figure SI1: The root mean squared fluctuation (RMSF) of the M protein amino acids around their mean positions. Left: DENV and Right: ZV simulations. The ZV M protein N-terminus is significantly more disordered.



Figure SI2: The radial distribution functions of different lipid species around the protein for all three copies of the simulation. Left: DENV and Right: ZV simulations. Thee three panels are for the three different copies of the simulations.



Figure SI3: Sequence alignment of the DENV and ZV M protein sequences from the structures used in the current work. Residues 10, 11, 15 and 23 of ZV are cationic, while those on DENV are not.



Figure SI4: GM1 (left) and NAG (right) shown with their Martini mapping. NAG Martini mapping based on already parametrized GM1 Martini beads. GM7 represents a P4 beads, GM8 a SP1 bead, GM9 a SP1 bead, GM11 by a P1 bead and GM12 by a P4 bead.



Figure SI5: Radial distribution functions between POPE and specific residues on M proteins for the each copy of the DENV simulations. .