Supporting Information

Cao and Zhang 10.1073/pnas.1301911110

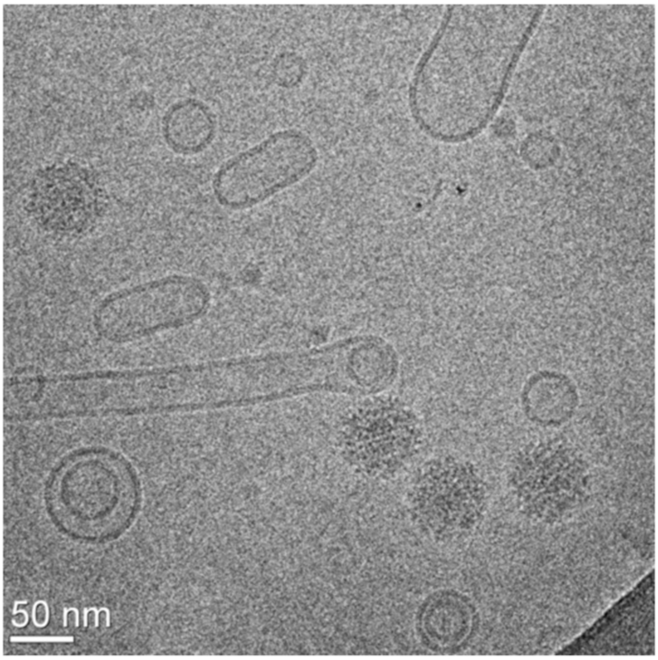

Fig. S1. Cryo-EM image of SINV and liposome mixture at pH 7.4 after being incubated at 37 °C for 30 min.

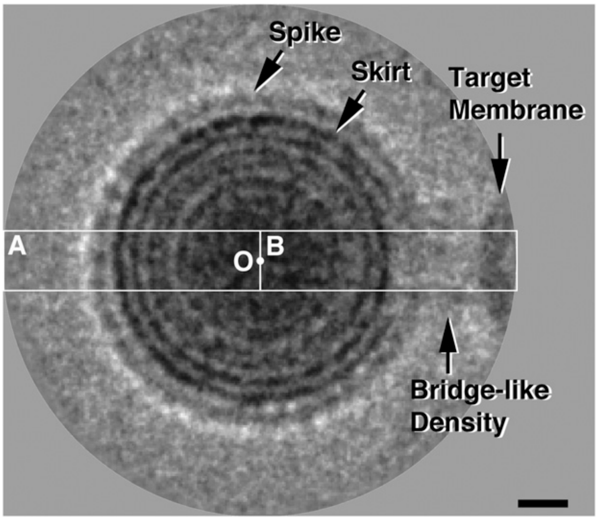

Fig. S2. Sampling areas in the 2D average image used for calculation of the radial density profiles. O is the center of the virus. A and B represent subareas extending in the 9 o'clock and 3 o'clock directions, respectively.

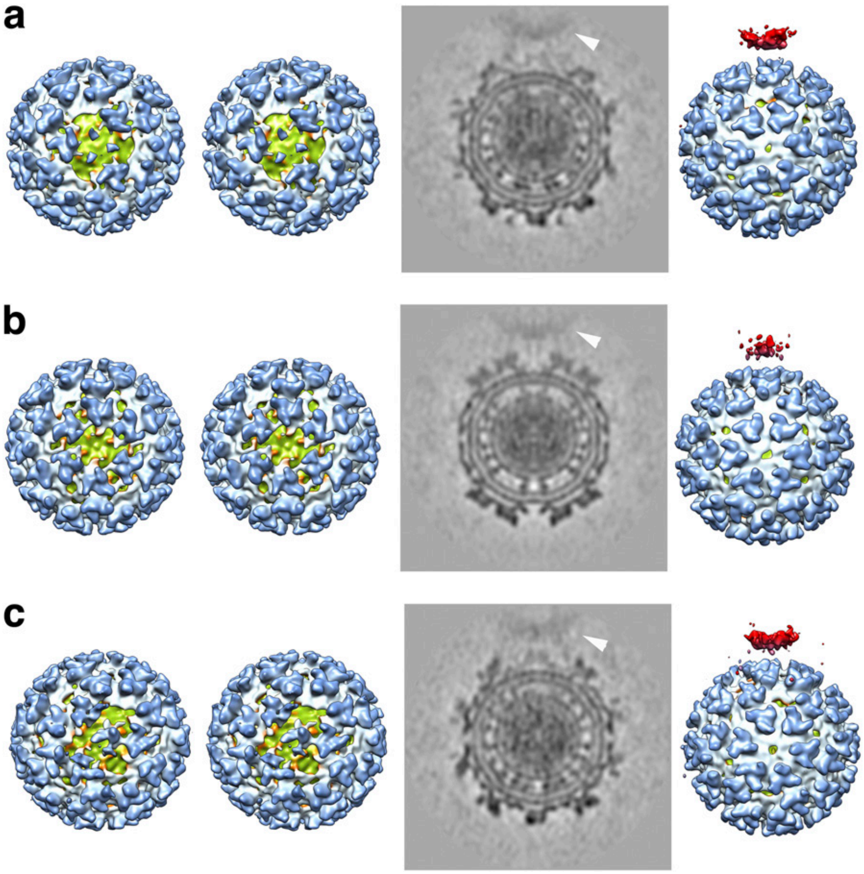

Fig. S3. Three-dimensional reconstruction maps of the virus–liposome complex when the liposome is bound near the icosahedral 3- (*A*), 2- (*B*), or q3-fold (*C*) axis. (*Left*) Stereoview of the reconstruction map contoured at the 1.5σ level and showing virus spikes (blue) and the viral membrane (green) exposed due to loss of the skirt densities (white). (*Center*) The central cross-section of the reconstruction map showing the target membrane at the top (white arrowheads). (*Right*) The shaded surface contoured at the 1.0σ level and showing the virus surface and the target membrane (red).

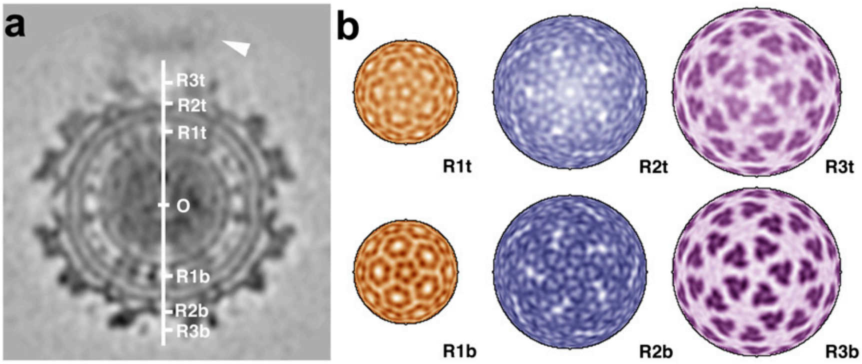

Fig. S4. Central cross-section (*A*) and radial projections (*B*) of the virus–liposome complex reconstruction maps, assuming that the liposome is bound near the icosahedral fivefold axis. The arrowhead indicates the target membrane. O is the center of the virus particle. R1t and R1b represent positions on the viral capsid at a radius of 192 Å. R2t and R2b represent positions on the skirt at a radius of 284 Å. R3t and R3b represent positions on the spikes at a radius of 312 Å.

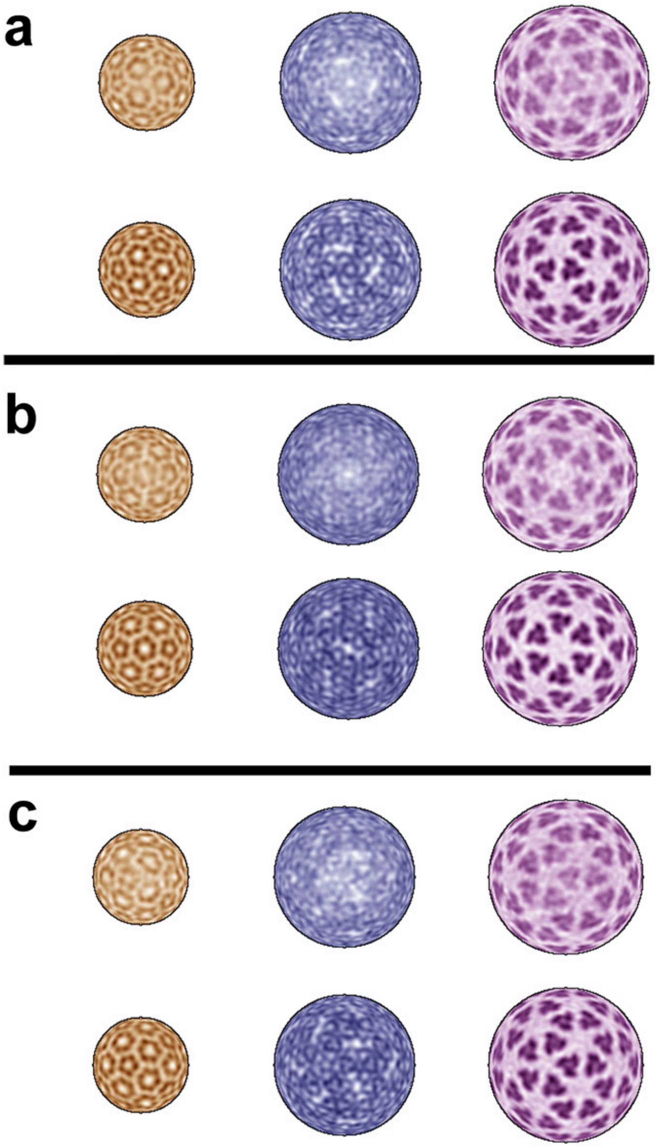

Fig. S5. Radial projections of the virus–liposome complex reconstruction maps, assuming that the liposome is bound near the icosahedral 3- (*A*), 2- (*B*), or q3-fold (*C*) axis. The radial positions and color code are the same as in Fig. S4*B*. (*Left*) Density distribution maps of the viral capsid at a radius of 192 Å. (*Center*) Density distribution maps of the skirt region at a radius of 284 Å. (*Right*) The densities in the spike region at a radius of 312 Å.

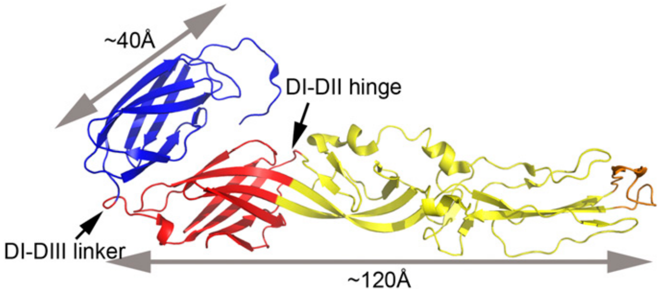

Fig. S6. Dimension of Chikungunya virus E1 protein ectodomain (PDB: 3N42) at neutral pH. The three domains of E1 are colored in red (DI), yellow (DII), and blue (DIII). The fusion loop is colored in orange.