

Supplementary Fig. 1. Molecular mass estimates for CIV minor capsid proteins. (a)

Plot of the estimated molecular mass for each of nine finger proteins as a function of density contour level (numbering scheme same as in Fig. 4). The CIV map was scaled to give a density range from 0 to 100, but only the range from 0 to 65 is shown. The mass of the minor capsid proteins at each data point is based on the known mass and segmented volume of the averaged P50 capsomer. At a contour level less than about 35, the ratio of the volumes of the minor and major capsid proteins becomes constant allowing for a reasonable estimate of the mass of the protein. (b) Same as (a) for each of the eight zip monomers within the icosahedral asymmetric unit (c) Same as (a) for a monomer of the 5-fold pentamer complex. At a contour level greater than 35, the mass is over estimated because the maximum density in the complex is greater than that of P50. (d) Same as (a) for the anchor protein. .