Supplemental Information

FIG. S1. Heparan sulfate and heparin. Top) Cartoon representation of the NS and NA domains of a heparan sulfate glycosaminoglycan chain. The NS domain is composed of 3-8 repeating disaccharides, and the NA domain is composed of 2-12 repeating disaccharides. Bottom) Chemical structure of the heparan sulfate and heparin repeating disaccharides. The repeating disaccharide of the heparan sulfate NS domain is similar to the repeating disaccharide of heparin.

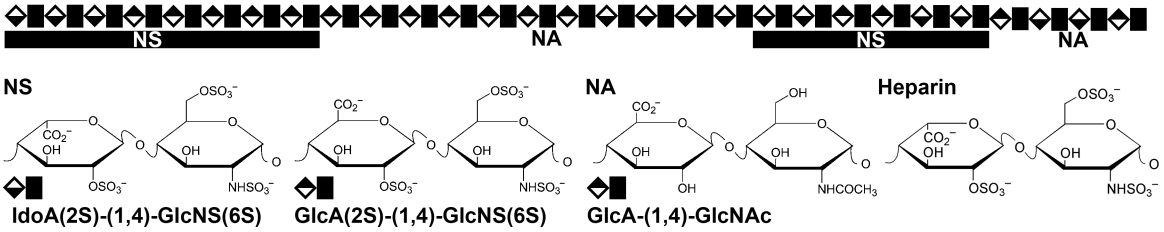

FIG. S2. SDS-PAGE densitometry of PCV2 VLP heparin binding interaction. Images represent the interaction between PCV2 VLP and HyperD™ chromatography sorbent. The contrast of each digitized SDS-PAGE was scaled to enhance the signal for visualization. This modification does not affect the intensity reported by the Image Studio™ software used for the analysis. The numbers above each band represent the intensity corrected by background subtraction within each box. A) Binding kinetics of 370nM and 97nM VLP demonstrating that the signal from 370nM produces a robust readout (Fig. 2A). B) Elution of VLP from the sorbent with increasing heparin concentration (Fig. 2B). GAG competition assay representatives of: C) 6-hexose, D) 10-hexose, E) 20-hexose, F) 36-hexose heparin, G) dextran sulfate 8kDa, H) dextran 6kDa, I) hyaluronic acid, J) chondroitin sulfate B. K) Linear response curve of the LI-CORR Odyssey CLX to increasing amount of PCV2 capsid protein, indicating that intensity is directly correlated to protein content. L) Binding efficiency of *in vitro* assembled WT, K58A, R59A, K63A, R73A, R89A, N128A, R186A, and Q188A capsids (Fig. 5). Inset is: WT K58A, R59A, K63A, R73A, R89A, WT, N128A, R186A, and Q188A capsids. Figures made with Image Studio™ (LI-CORR Biosciences) and Origin 2016 (OriginLab).

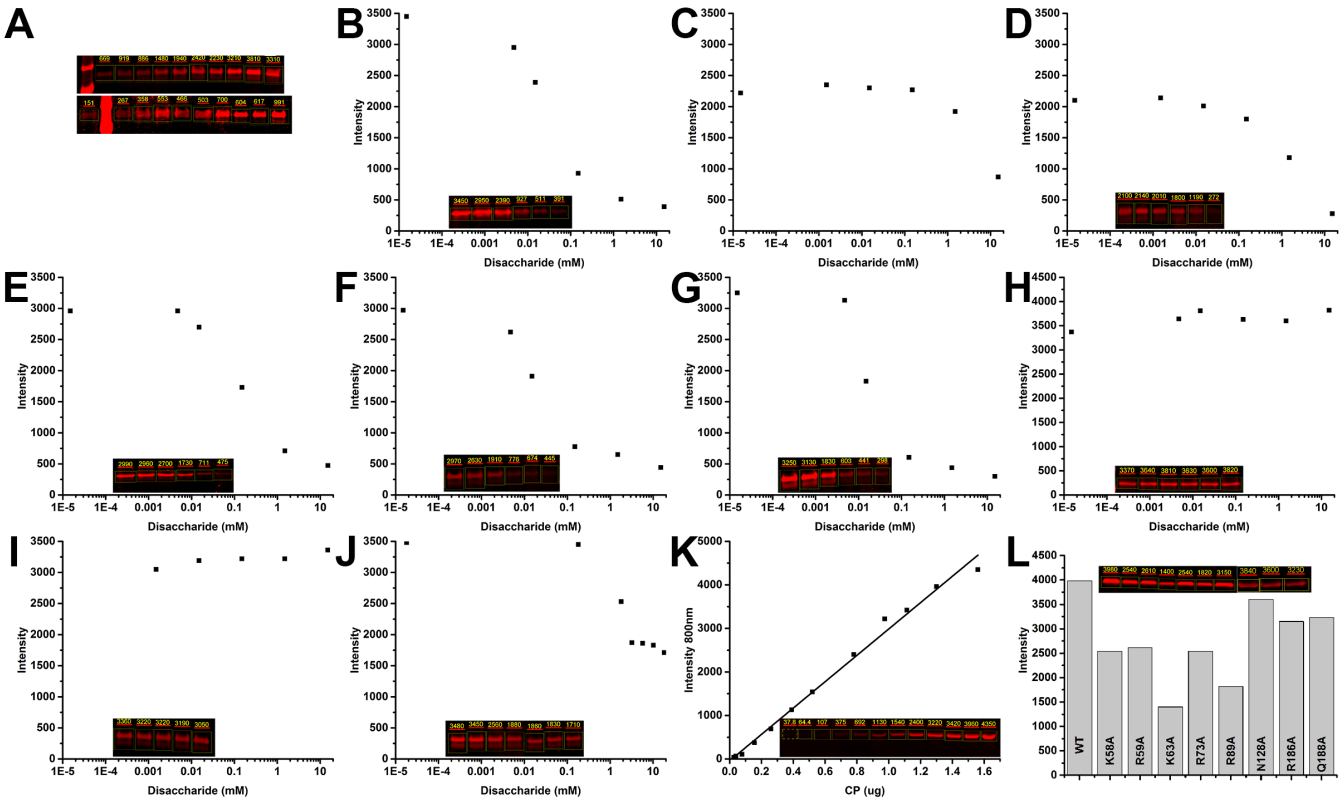

FIG. S3. Local resolution. The local resolution for each of the 10 classes was determined using the program MonoRes. Two plots are shown for each class due to the large range in resolution. The color bar on the left of each row depicts the resolution for the indicated color. A) The top plot was calculated using a resolution range of 2.8Å to 6Å and the bottom plot was calculated using a resolution range of 2.8Å to 30Å for classes 1 to 5. B) Similar to A but for classes 6 to 10 (48). Image generated using UCSF Chimera (64).

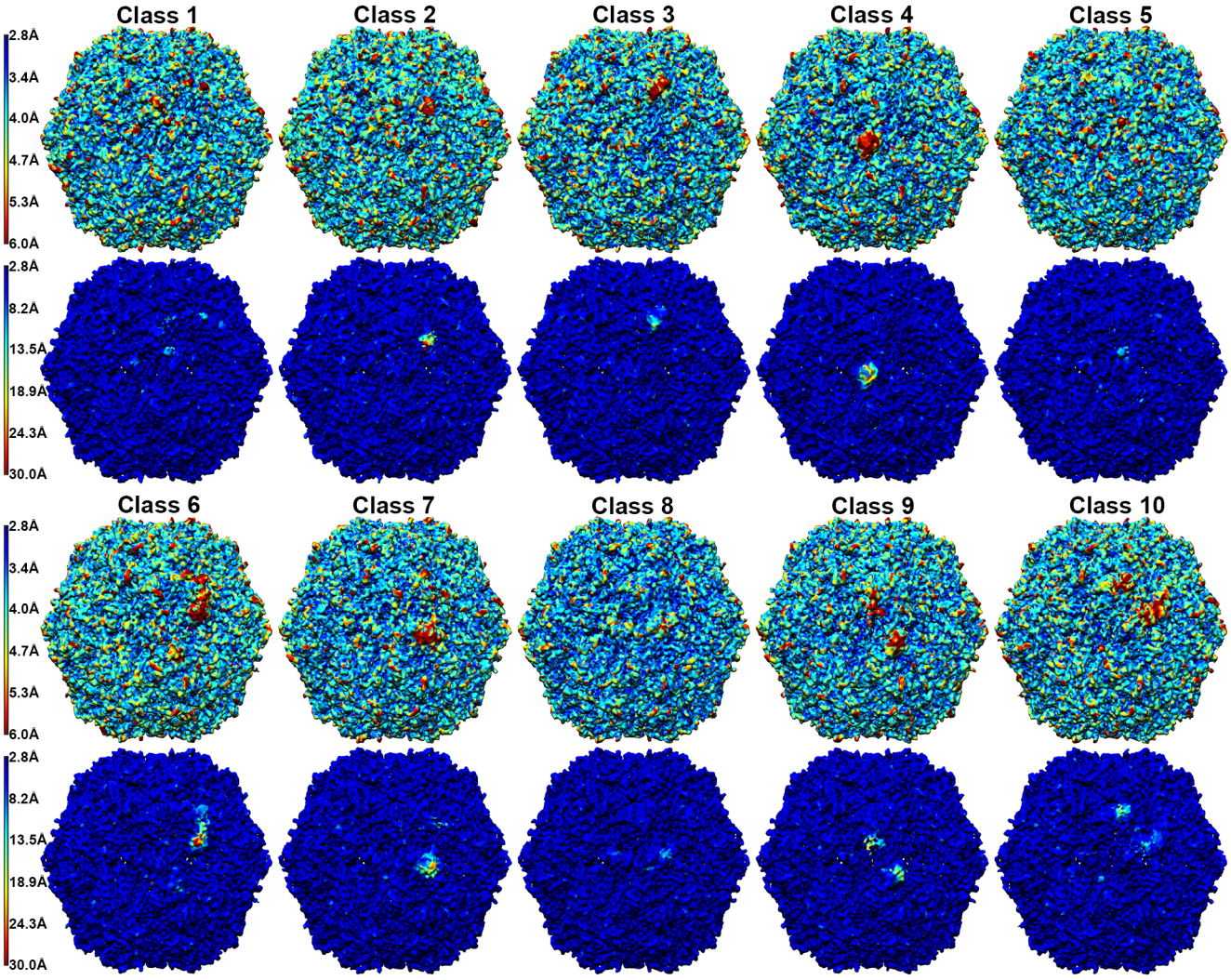

FIG. S4. Assembly of mutant VLP. Size exclusion chromatography profile of an *in vitro* assembled PCV2 VLP. Image made with Unicorn 6.1 (GE Health Care Life Sciences) and a corresponding electron microscope micrograph of the negative stained wild-type VLP.

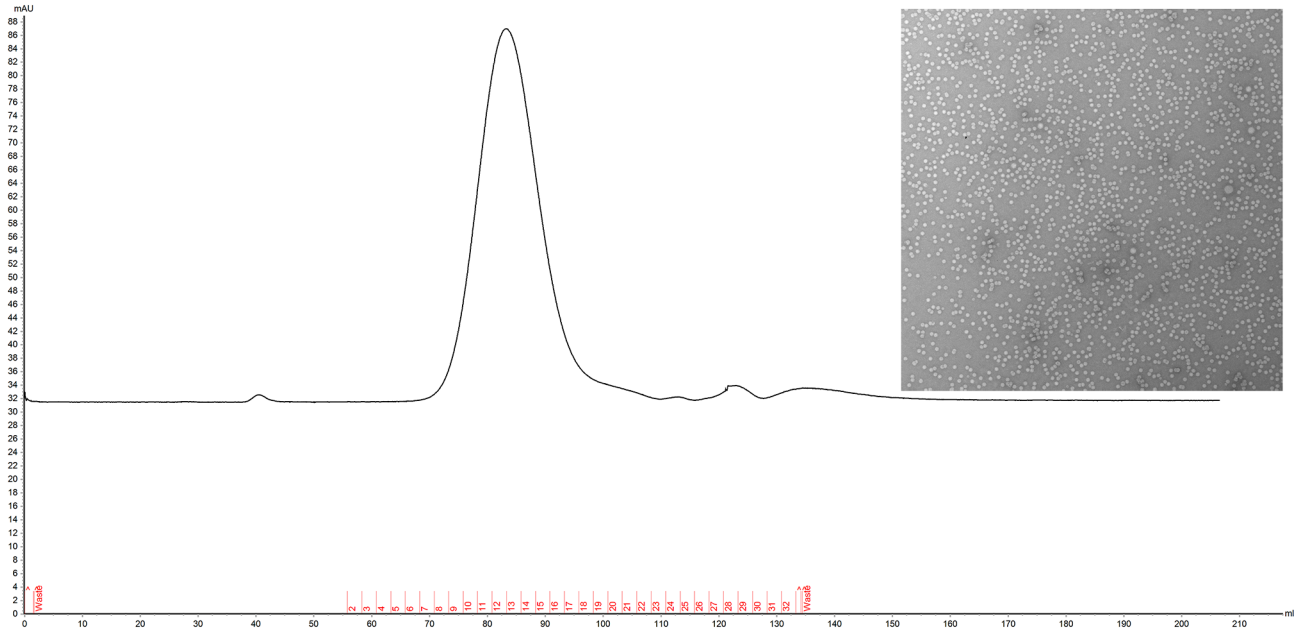

FIG. S5. Occupied heparin binding sites on PCV2 VLPs. The distribution follows a Gaussian profile with a minimum of 17, a mode of 31, and a maximum of 44 binding sites occupied on individual VLPs. Image made with Origin 2016 (OriginLab).