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## Supporting Information

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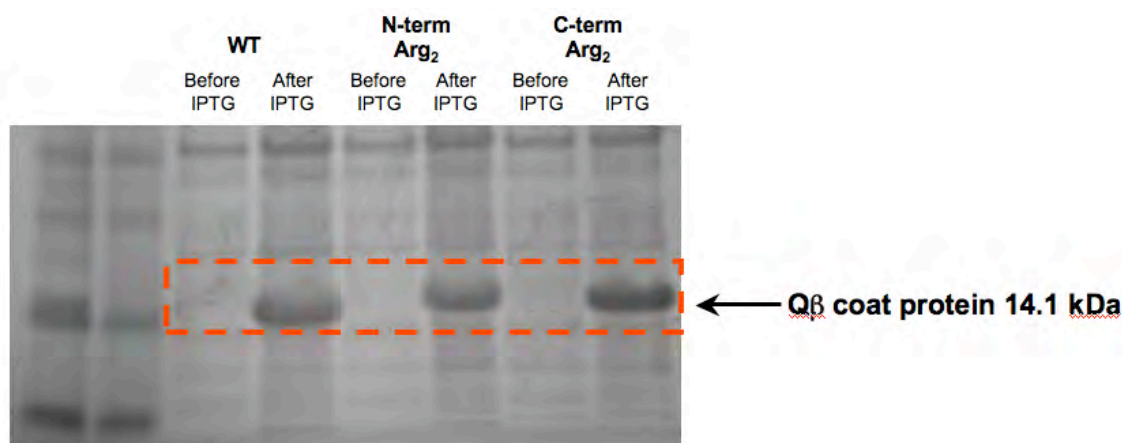
## Heparin Antagonism by Polyvalent Display of Cationic Motifs on Virus-Like Particles

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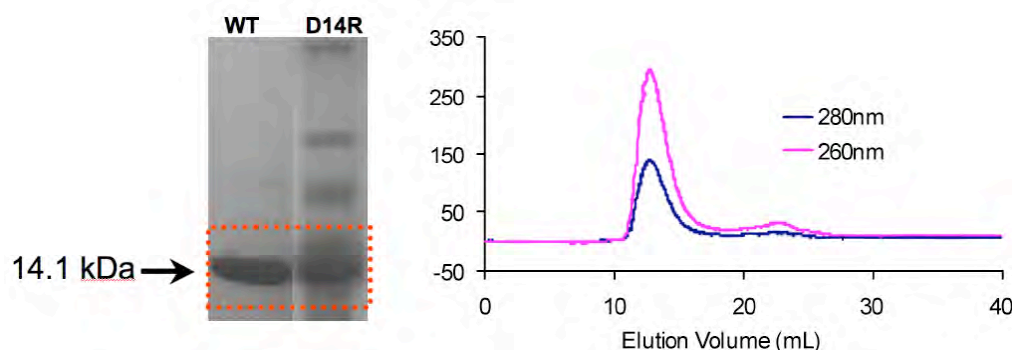
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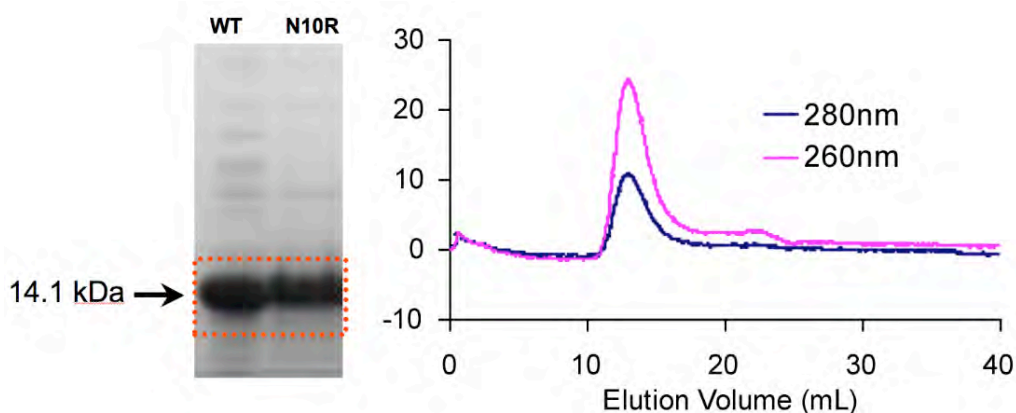
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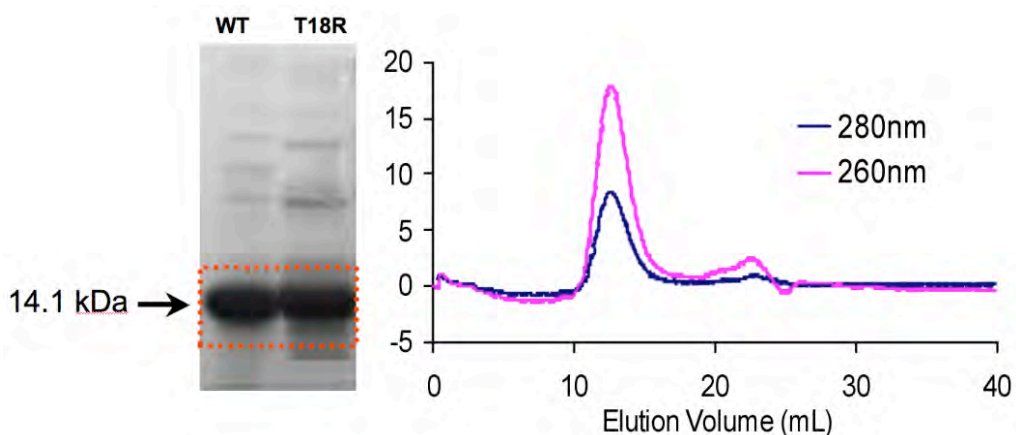
**Figure S1.** Exemplary Coomassie-stained protein gel of cell lysates after expression of wild-type and poly-Arg mutant bacteriophage Q $\beta$  coat proteins. After IPTG induction, significant quantities of coat protein are produced. However, in addition to the two mutants shown above, the following mutants also did not yield isolable intact virus particles, despite detecting synthesized coat proteins: N-terminal Arg<sub>2</sub>, Arg<sub>5</sub>, Arg<sub>8</sub>; C-terminal Arg<sub>2</sub>, Arg<sub>5</sub>, Arg<sub>8</sub> with and without Gly<sub>2</sub> or Gly<sub>5</sub> spacers; replacing D<sup>14</sup>GKQT<sup>18</sup> with Arg<sub>5</sub>.



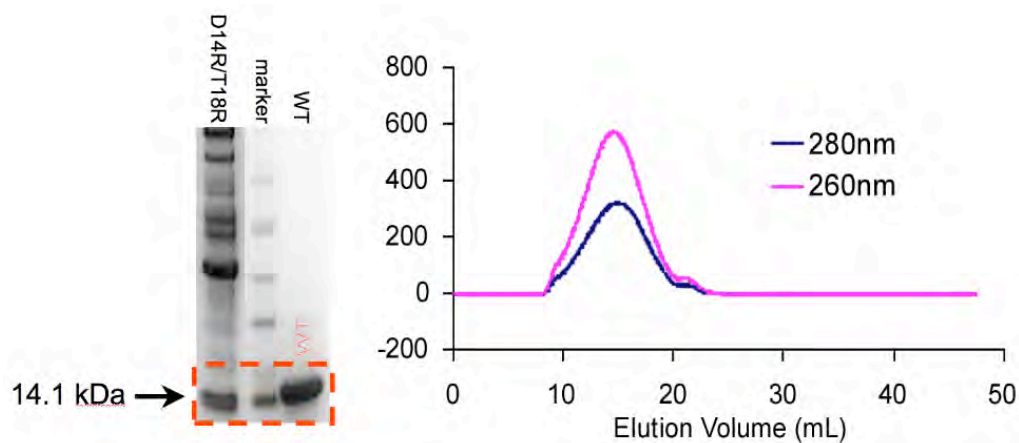
**Figure S2.** Coomassie-stained protein gel (*left*) and size-exclusion FPLC chromatogram (*right*) of mutant D14R particles obtained after a single sucrose gradient, confirming the presence of virus-like particles eluting at 12 mL. The particles were subjected to a second gradient purification before use.



**Figure S3.** Coomassie-stained protein gel (*left*) and size-exclusion FPLC chromatogram (*right*) of mutant N10R particles obtained after a single sucrose gradient, confirming the presence of virus-like particles eluting at 12 mL.



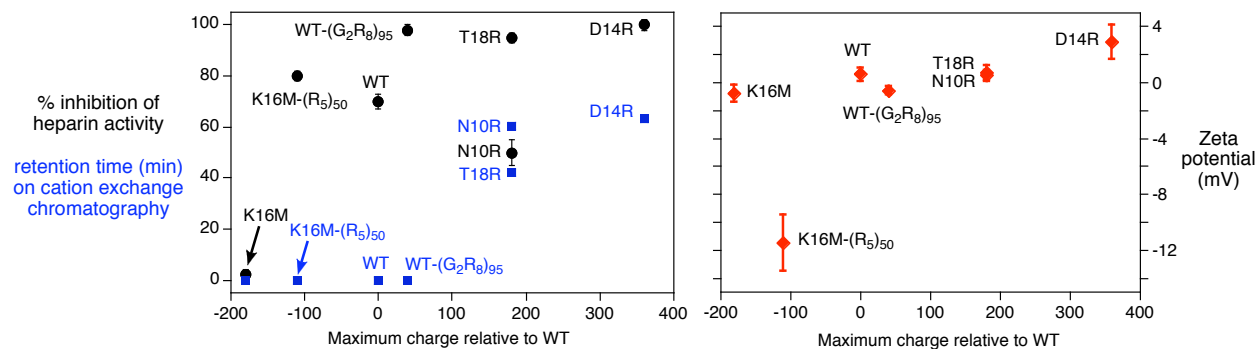
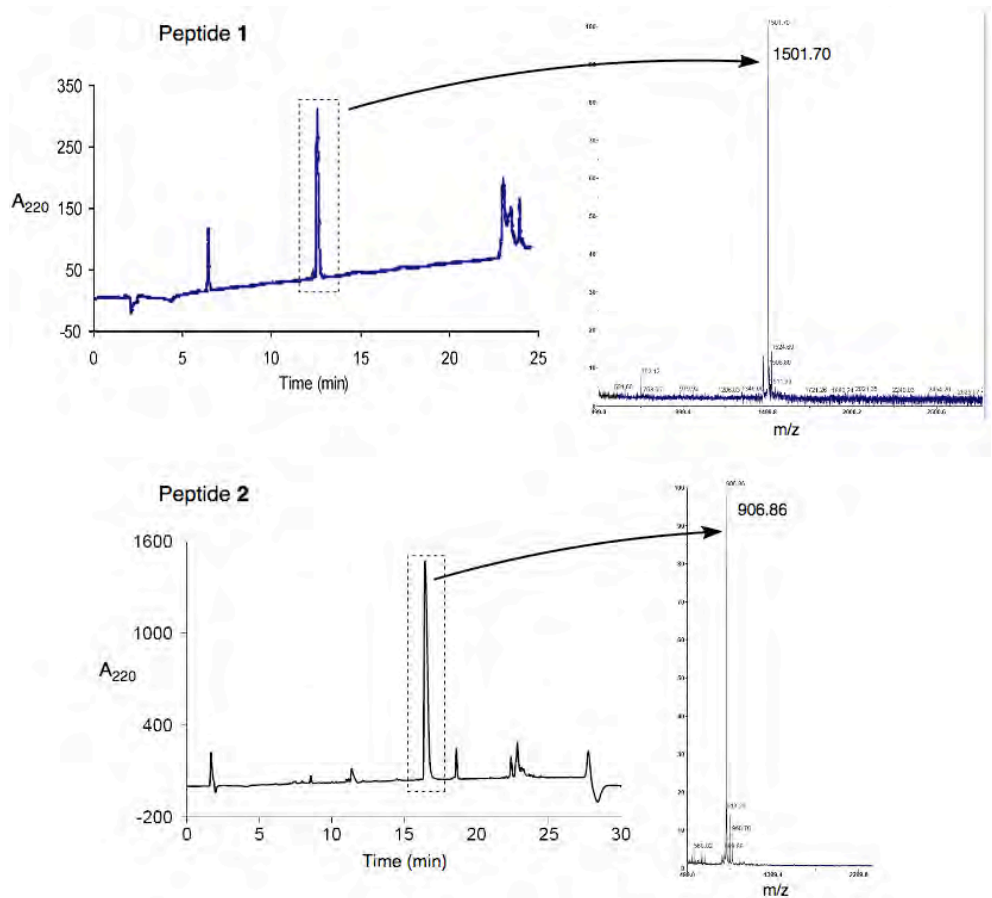
**Figure S4.** Coomassie-stained protein gel (*left*) and size-exclusion FPLC chromatogram (*right*) of mutant T18R particles obtained after a single sucrose gradient, confirming the presence of virus-like particles eluting at 12 mL.



**Figure S5.** Coomassie-stained protein gel (*left*) and size-exclusion FPLC chromatogram (*right*) of mutant D14R/T18R particles obtained after a single sucrose gradient, confirming the presence of

virus-like particles eluting at 12 mL. However, these particles proved to be too unstable for use; the relatively broad elution profile shown above is likely to be a consequence of this instability.

**Figure S6.** HPLC (left) and MALDI-MS analysis (right) of peptides 1 and 2. The mass spectra were obtained on the collected indicated fraction eluted from preparative HPLC



**Figure S7.** Plots of values in Table 1, correlating maximum charge relative to wild type with observed parameters of cation exchange chromatography, inhibition of heparin activity, and zeta potential.