Interaction of Zika Virus Envelope Protein with Glycosaminoglycans

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Supporting Information for Publication

Figure S1. Multiple sequence alignment (MSA) of flavivirus envelope proteins generated using MSAviewer and a BLOSUM62 scoring matrix.[90]. Putative GAG binding sites are boxed in red (GAG binding site I) and green (GAG binding site II). The sequence alignment of the full-length envelope proteins from ZIKV, DENV 1-4, WNV, and YFV are presented with residues aligned and color coded based on their percent identity. The greatest percent identity is represented in the darkest shade of blue, which transits to lighter shades of blue, gray, and finally white to represent the lowest percent identity amongst flavivirus envelope proteins.

Figure S2. Polyacrylamide gel electrophoresis (PAGE) analysis for the HS decasaccharide library used in the 'fishing' experiment. Lane 1: heparin oligosaccharide standards; Lane 2: HS dp10**.**

Figure S3. Instrumental error in analysis of HS and CS standards. Seventeen disaccharide standards were mixed and AMAC-labeled into 12.5 ng/μL. Three injections were used to calculate the standard derivations. Extracted ion chromatograms (EICs) were used to perform peak integration. The calibration constants were calculated as: $\frac{Injection\ amount\ (ng)}{Peak\ Area} \times 10^5$.

Figure S1

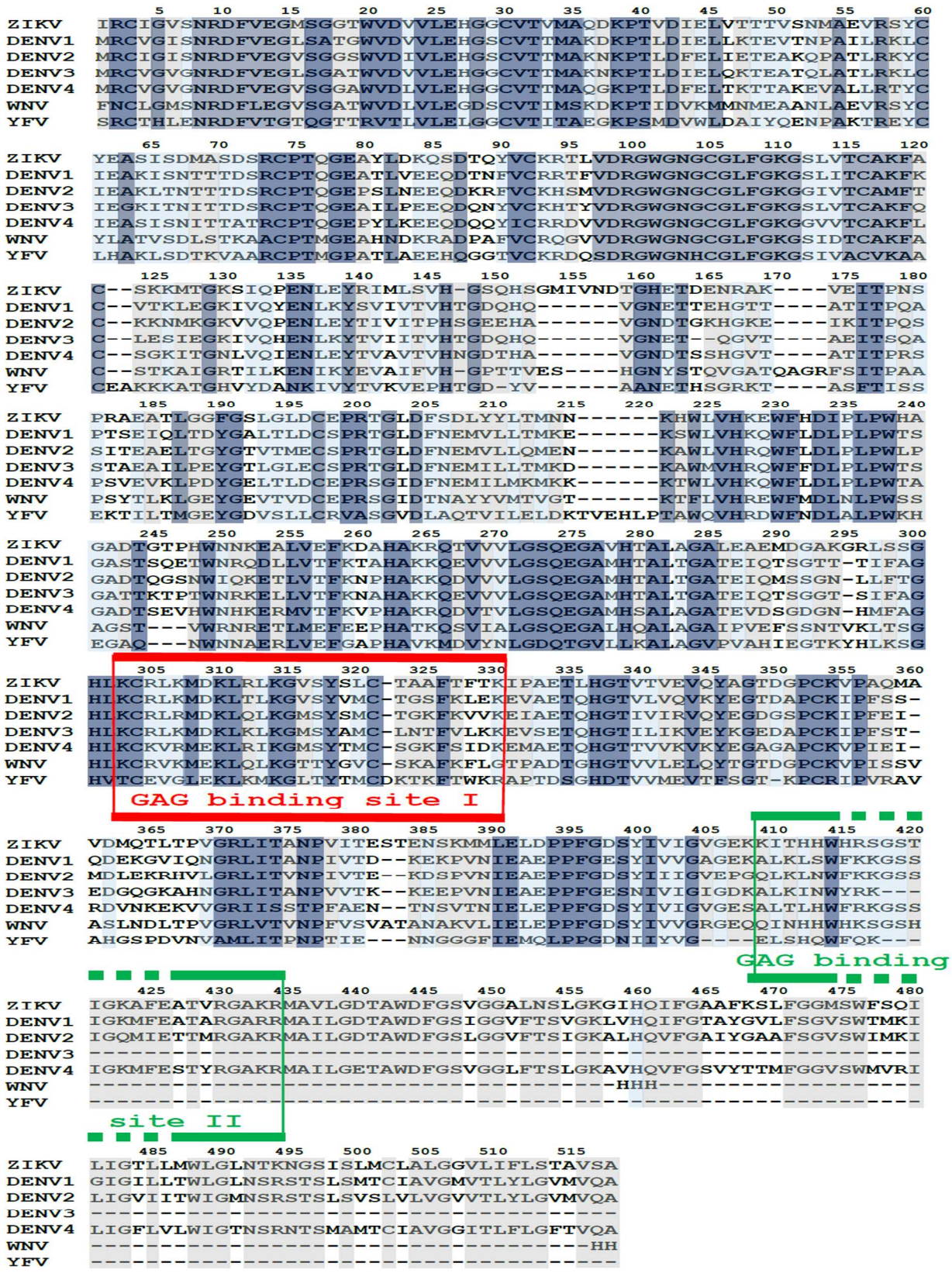

ZIKV
DENV1
DENV2
DENV3
DENV4
WNV
YFV
GAG binding site I
GAG binding
site II

Figure S2

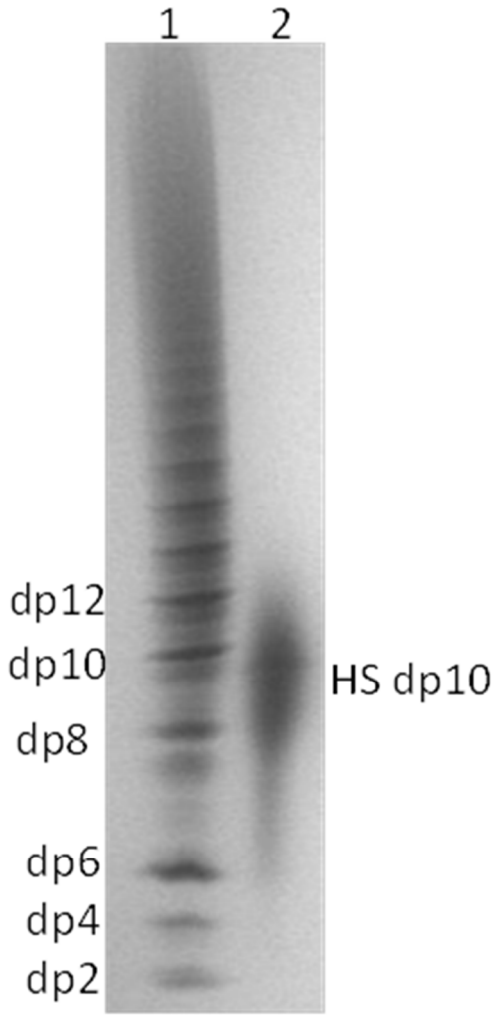
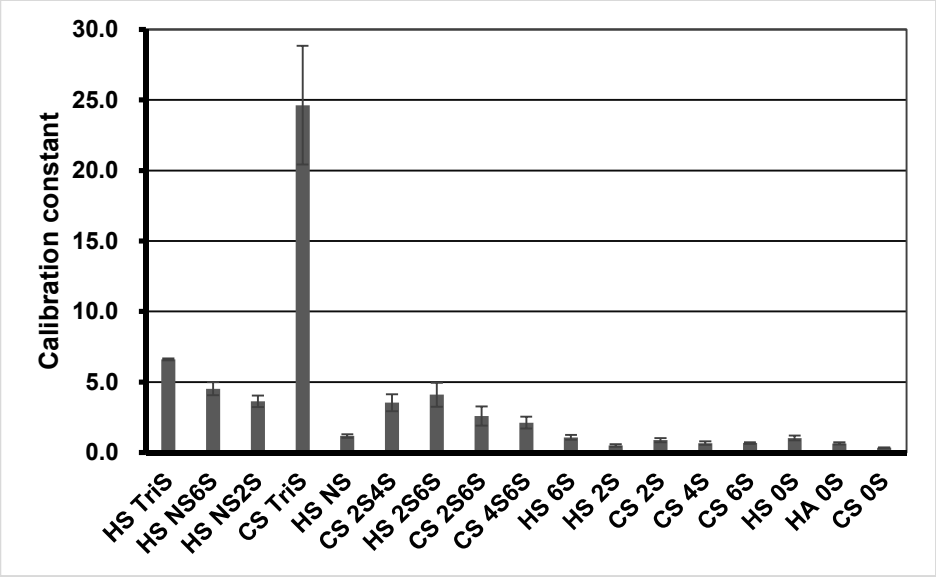


Figure S3


Calibration constant
30.0
25.0
20.0
15.0
10.0
5.0
0.0
HS TriS
HS NS6S
HS NS2S
CS TriS
HS NS
CS 2S4S
HS 2S6S
CS 2S6S
CS 4S6S
HS 6S
HS 2S
CS 2S
CS 4S
CS 6S
HS 0S
HA 0S
CS 0S