Table S1. Phi and psi angles from TALOS+ [1] for the residues surrounding the $N40_{\Delta 62-71}$ deletion confirm alpha-helical secondary structure

N40 Residue	Phi (φ) Angle	Psi (ψ) Angle
Helix One		
A56	-64° ± 5°	-41° ± 8°
A57	-62° ± 5°	-40° ± 6°
D58	-63° ± 8°	-40° ± 7°
N59	-66° ± 7°	-35° ± 12°
N60	-101° ± 19°	3° ± 21°
Linker		
V61	-75° ± 55°	129° ± 14°
G72	89° ± 8°	2° ± 15°
S73	-62° ± 71°	115° ± 54°
K74	n.a.	n.a.
V75	-96° ± 22°	-6° ± 22°
S76	-90° ± 62°	145° ± 24°
E77	-77° ± 60°	124° ± 26°
N78	n.a.	n.a.
Helix Two		
S79	n.a.	n.a.
F80	-63° ± 6°	-42° ± 7°
I81	-63° ± 5°	-63° ± 9°
L82	-63° ± 6°	-36° ± 8°
E83	-63° ± 5°	-42° ± 6°
A84	-63° ± 5°	-43° ± 5°
K85	-64° ± 5°	-33° ± 10°

n.a. - no assignment for HN, N, CA, and/or CB

[1] Shen, Y., Delaglio, F., Cornilescu, G., and Bax, A. (2009) TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts, *J Biomol Nmr 44*, 213-223.

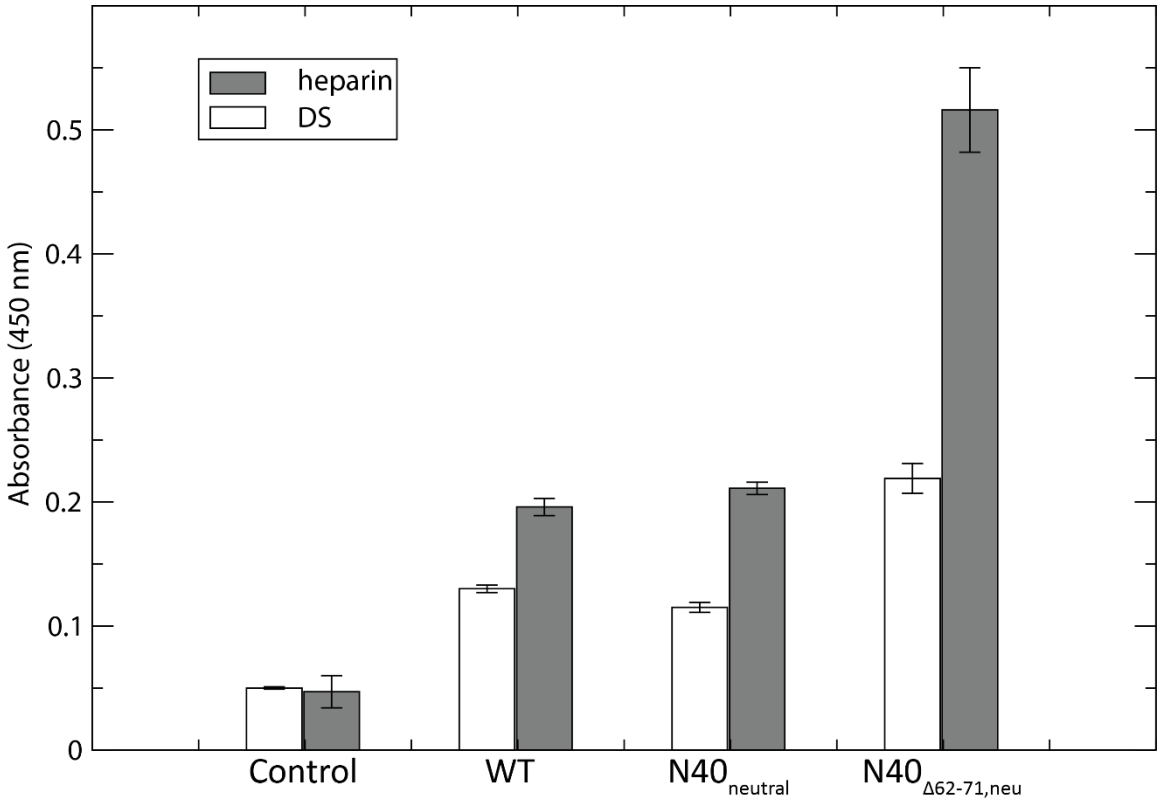

Figure S1. Effect of linker neutralization mutations in WT N40 DBPA and $N40_{\Delta 62\text{-}71}$ on GAG-binding as determined by ELISA. Mutating the charged residues in the linker to Ser had a negligible effect on GAG-binding for N40 DBPA. The increased GAG affinity for $N40_{\Delta 62\text{-}71,neu}$ is due to GAG interaction with the exposed basic pocket, not with the linker. Student's *t* tests comparing WT N40 DBPA and $N40_{neutral}$ with $N40_{\Delta 62\text{-}71,neu}$ indicate the changes in GAG affinities due to linker shortening are statistically significant ($p < 0.0001$ for both heparin and DS).