

Supplementary Information:

Evolutionary development of redundant nuclear localization signals in the mRNA export factor NXF1

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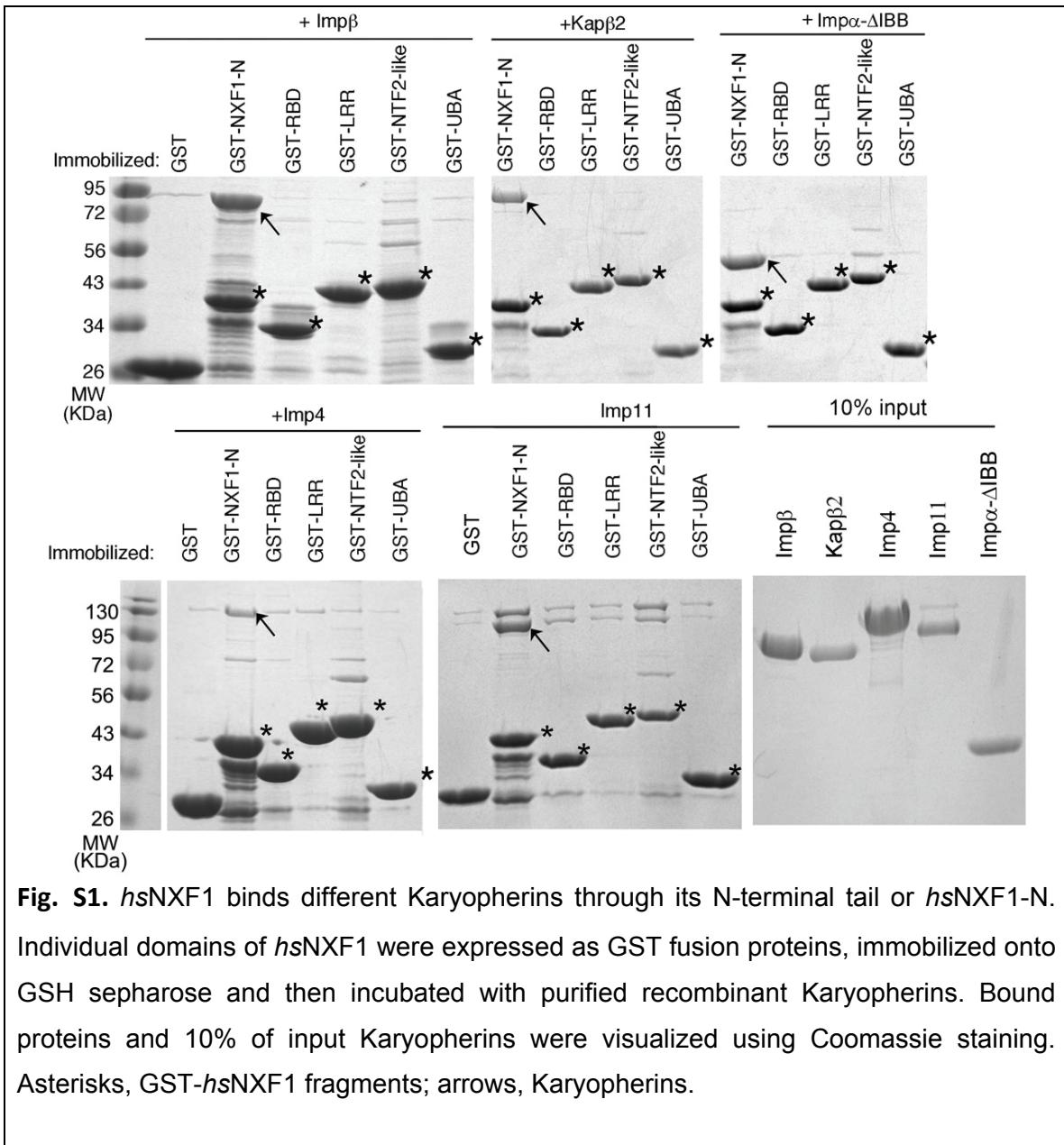
Table S1. Binding affinity of *hsNXF1-N* fragments for Kap β 2

Karyopherin	<i>hsNXF1-N</i> fragments	K_D^a (nM)	ΔH (kcal/mol)	$T\Delta S^b$ (kcal/mol/K)
Kap β 2	1-109	40±13	-17.21±1.25	-7.31±1.42
	30-109	91±13	-18.51±1.13	-9.16±1.12
	1-92	54±4	-19.57±0.05	-9.82±0.03
	1-80	109±33	-17.74±0.89	-8.40±0.88
	30-80	204±29	-19.16±1.31	-10.17±1.40

^a Stoichiometry = 0.9-1.1.

^b $T\Delta S = \Delta H - \Delta G$.

All experiments were performed 3-5 times (\pm standard deviation)



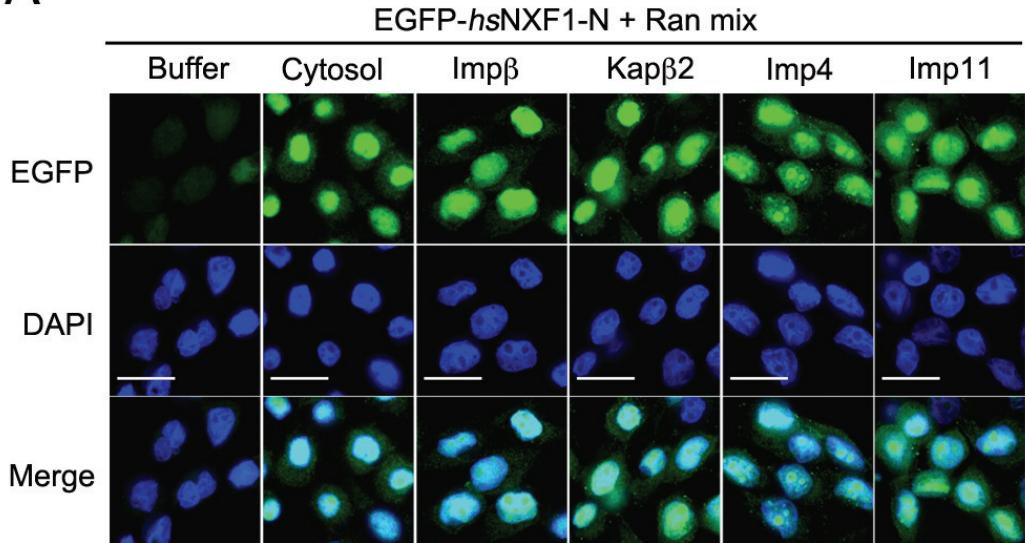
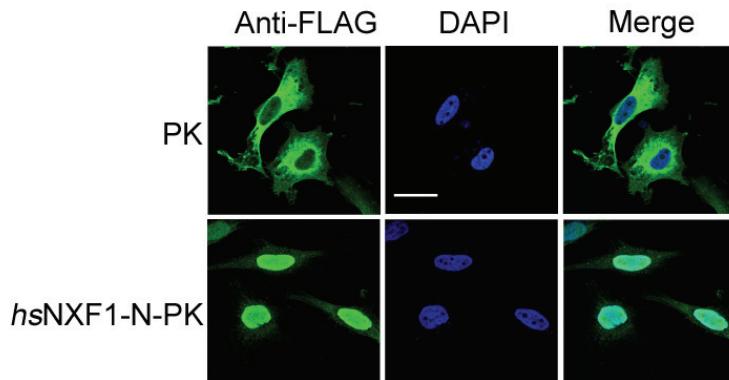
A**B**

Fig. S2. *hsNXF1-N* is sufficient for nuclear import. (A) Nuclear import assays were performed in digitonin-permeabilized HeLa cells with MBP-EGFP-*hsNXF1-N* in the presence of purified Kap β s or buffer. Samples were fixed and stained with DAPI, then subjected to immunofluorescence analysis (B) *hsNXF1-N* was fused to the N-terminus of pyruvate kinase (PK) gene and cloned into pFLAG-CMV vector and transfected into HeLa cells. *hsNXF1-N*-PK was detected by immunofluorescence using anti-Flag antibodies. Scale bar, 10 μ m.

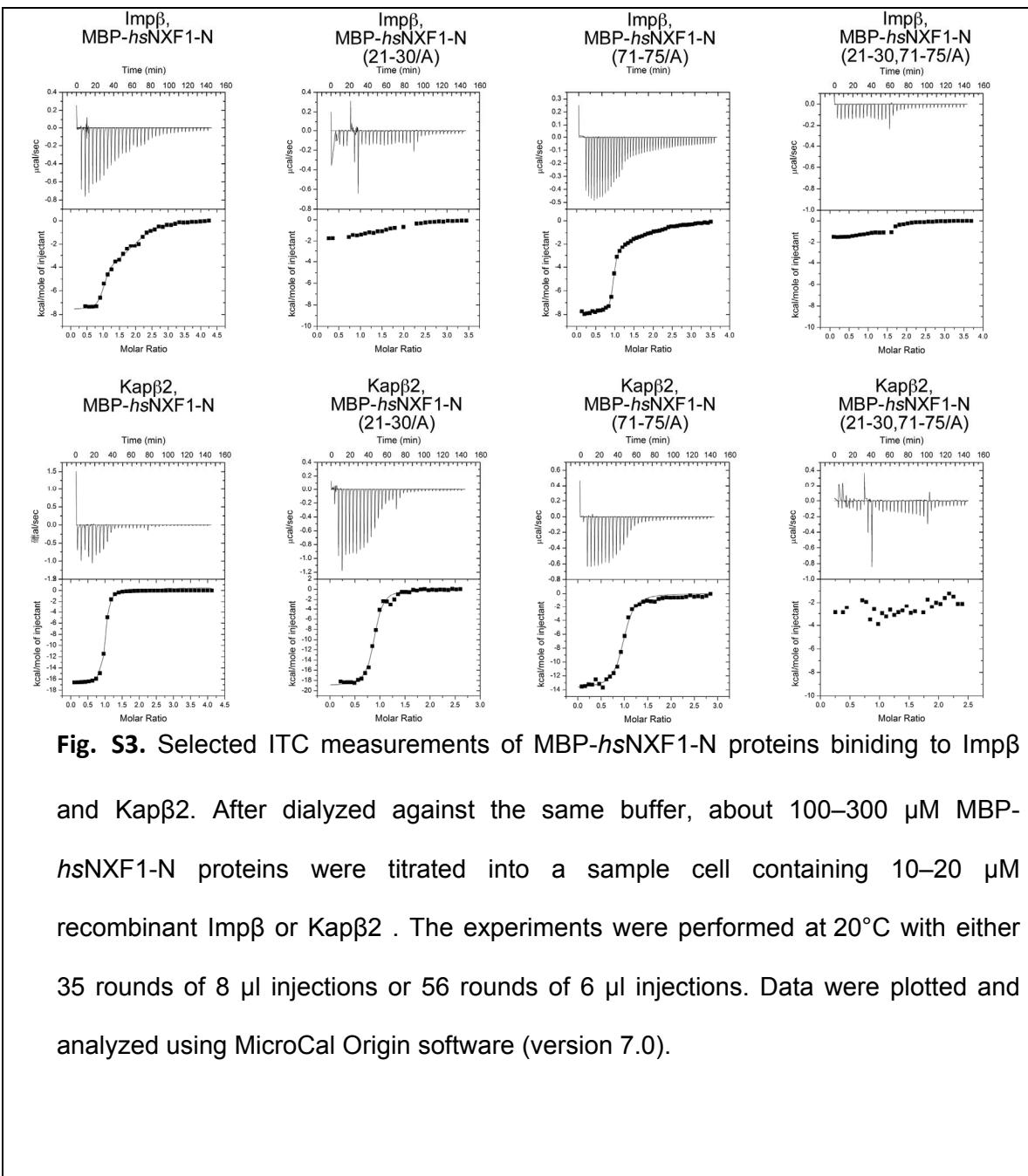
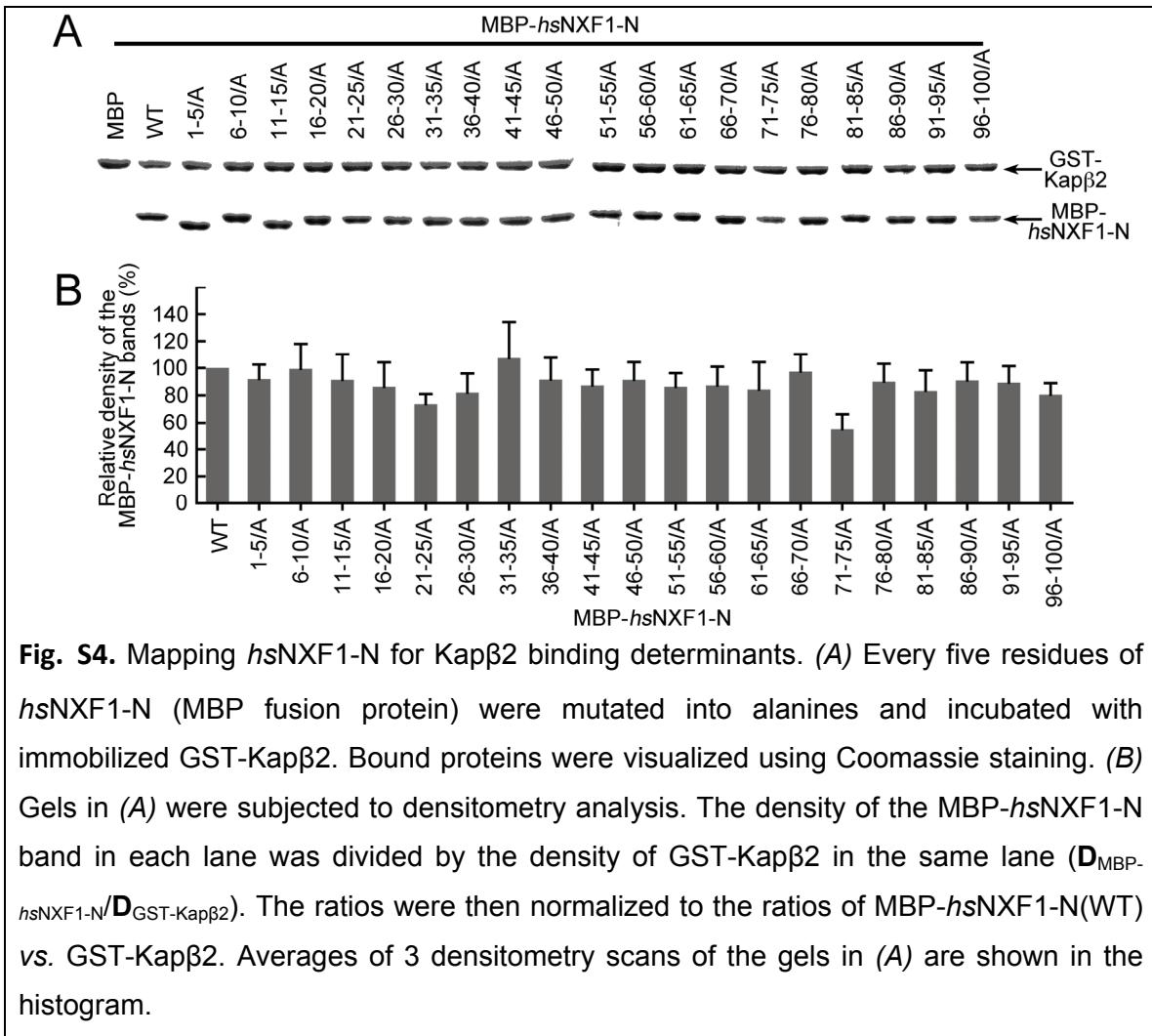


Fig. S3. Selected ITC measurements of MBP-hsNFX1-N proteins biniding to Imp β and Kap β 2. After dialyzed against the same buffer, about 100–300 μM MBP-hsNFX1-N proteins were titrated into a sample cell containing 10–20 μM recombinant Imp β or Kap β 2 . The experiments were performed at 20°C with either 35 rounds of 8 μl injections or 56 rounds of 6 μl injections. Data were plotted and analyzed using MicroCal Origin software (version 7.0).



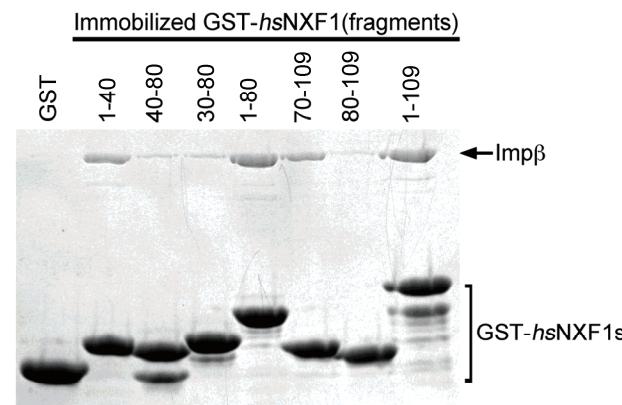
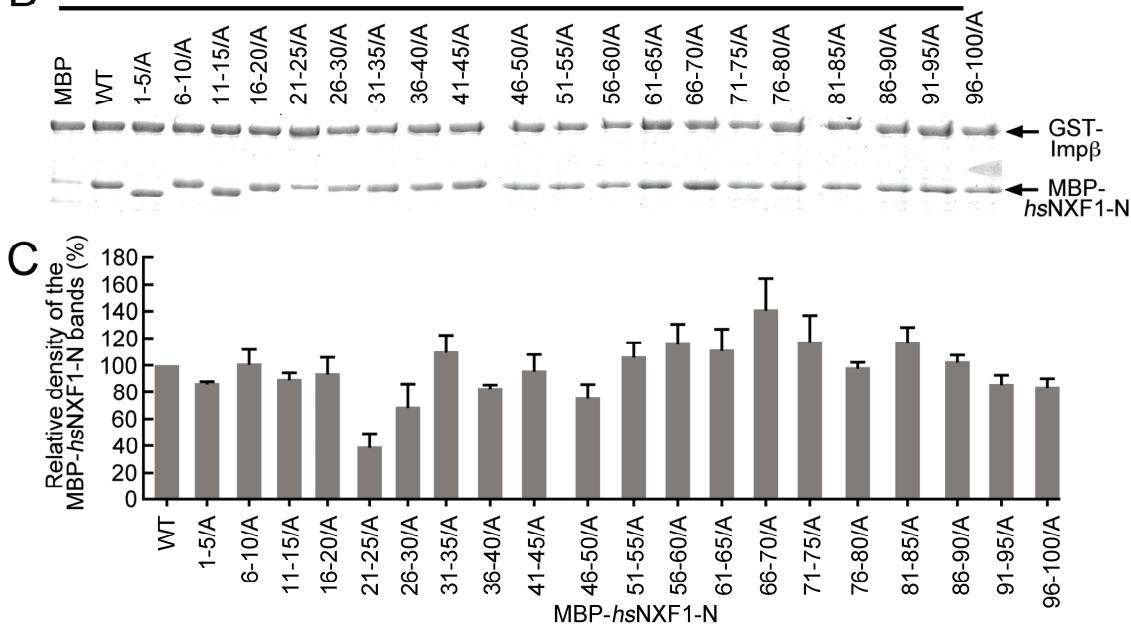
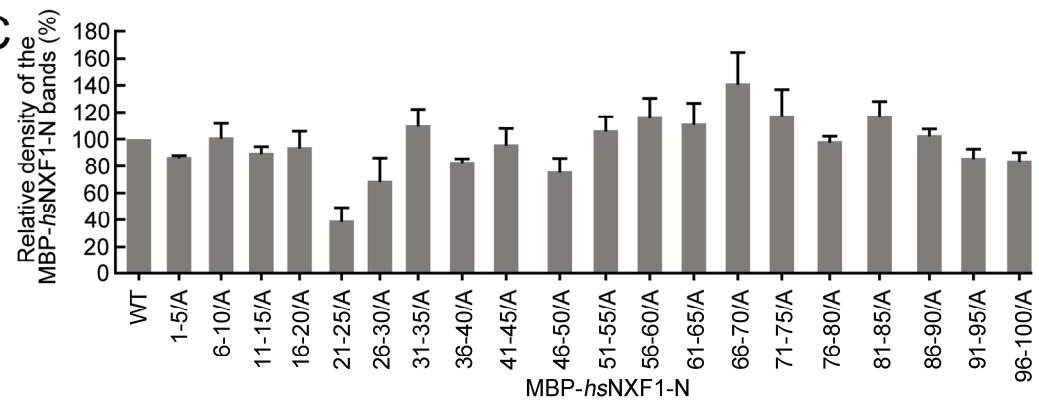
A**B****C**

Fig. S5. Mapping *hsNFX1-N* for Impβ binding determinants. (A) Immobilized GST fusion proteins of *hsNFX1-N* fragments were incubated with purified recombinant Impβ. (B) Every five residues of *hsNFX1-N* (MBP fusion protein) were mutated into alanines and incubated with immobilized GST-Impβ. Bound proteins in (A) and (B) were visualized using Coomassie staining. (C) Gels in (B) were subjected to densitometry analysis. The density of the MBP-*hsNFX1-N* band in each lane was divided by the density of GST-Impβ in the same lane ($D_{MBP-hsNFX1-N}/D_{GST-Imp\beta}$). The ratios were then normalized to the ratios of MBP-*hsNFX1-N*(WT) vs. GST-Impβ. Averages of 3 densitometry scans of the gels in (B) are shown in the histogram.

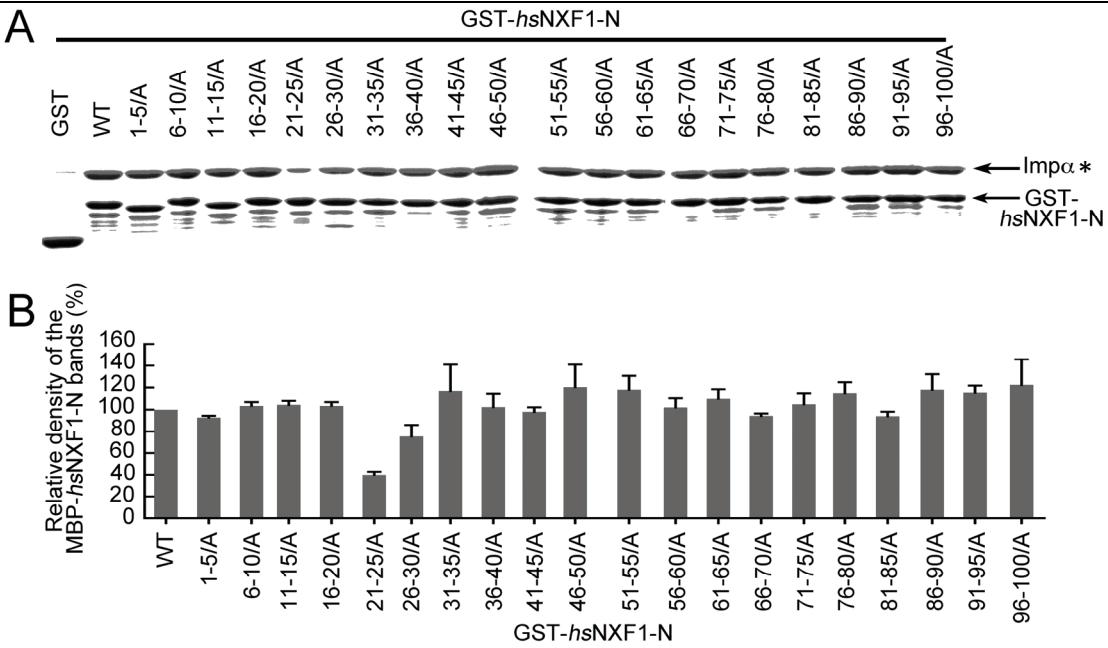


Fig. S6. Mapping hsNFX1-N for Impα binding determinants. (A) Every five residues of hsNFX1-N (GST fusion protein) were mutated into alanines, immobilized and incubated with purified Impα* (the Impα construct used is missing its N-terminal IBB domain). Bound proteins were visualized using Coomassie staining. (B) Gels in (A) were subjected to densitometry analysis. The density of the GST-hsNFX1-N band in each lane was divided by the density of Impα in the same lane ($D_{MBP\text{-}hsNFX1\text{-}N}/D_{GST\text{-}Imp\alpha}$). The ratios were then normalized to the ratios of GST-hsNFX1-N(WT) vs. Impα. Averages of 3 densitometry scans of the gels in (A) are shown in the histogram.

