

Figure S1, Related to Figure 1. Sedimentation Equilibrium of human NatA.

- (A) Log plot of sedimentation equilibrium experiments a sedimentation experiment showing theoretical monomer (blue) and theoretical dimer (red) slopes of hNatA ($\text{OD}_{\text{A}280}=0.8$) at 12,000 rpm (black).
- (B) The corresponding residuals for all three speeds associated with A.

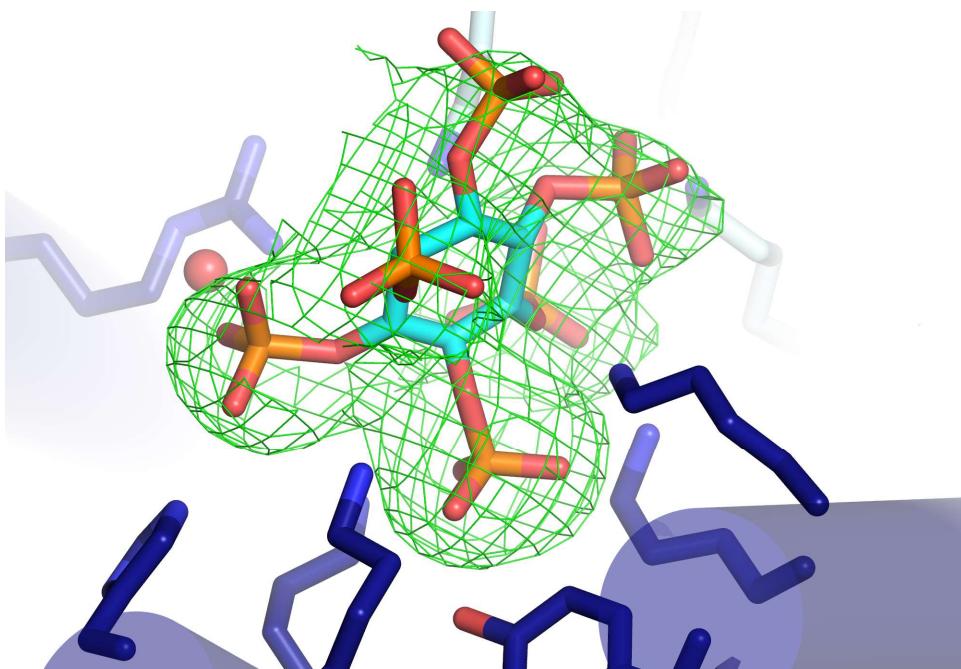


Figure S2, Related to Figure 1. IP_6 F_o - F_c Map.

Human NatA-bound IP_6 density contoured to 3.5σ (shown in green).

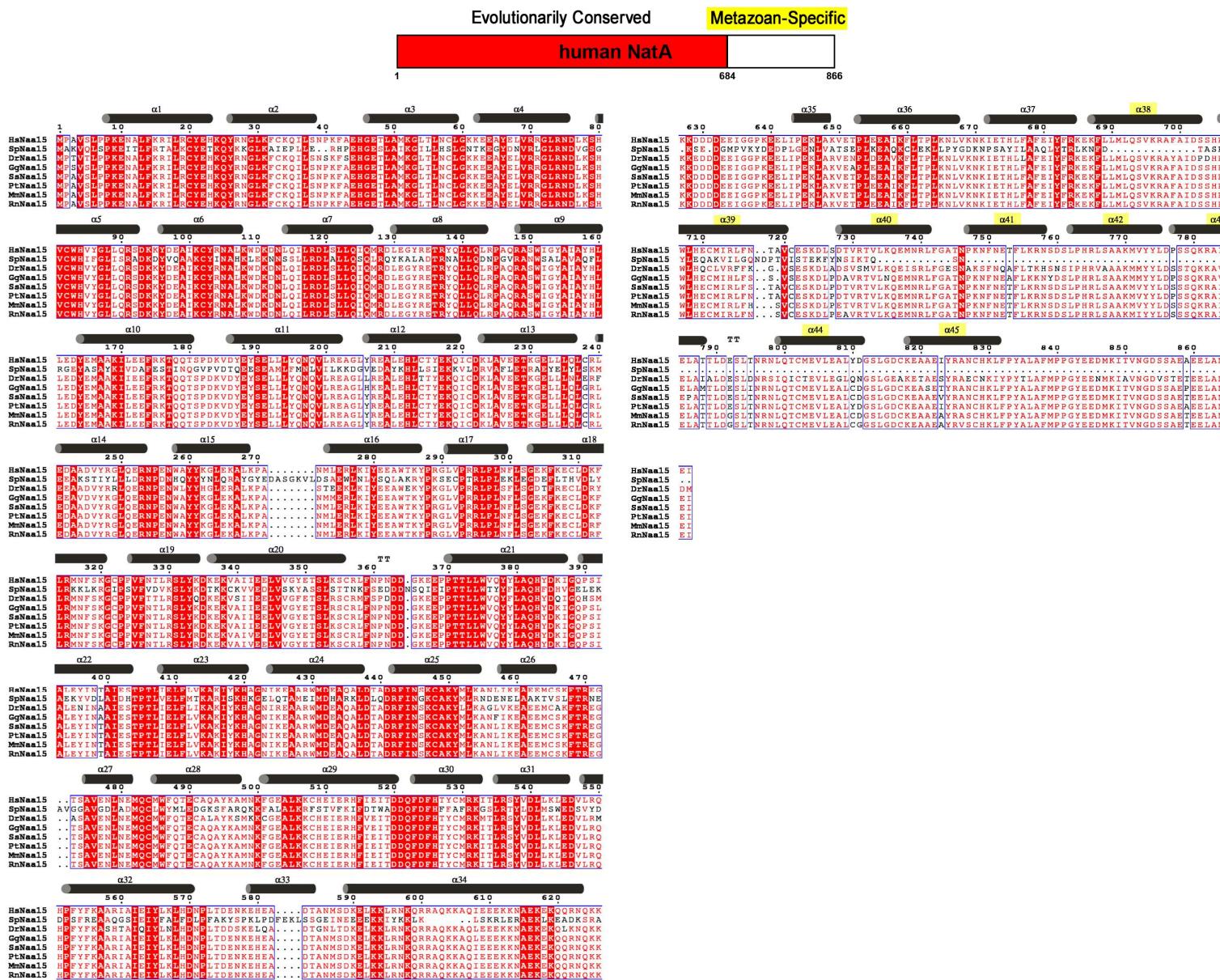


Figure S3, Related to Figure 1. Alignment of Naa15 Homologues. Sequence alignment of Naa15 homologues from *H. sapiens* (Hs); *S. pombe* (Sp); *S. cerevisiae* (Sc); *D. rerio* subunit b (Dr); *G. gallus* (Gg); *S. scrofa* (Ss); *P. troglodytes* Isoform XI (Pt); *M. musculus* (Mm); and *R. norvegicus* (Rn) demonstrating the divergence of the metazoan Naa15 C-termini (highlighted in yellow) from SpNaa15.

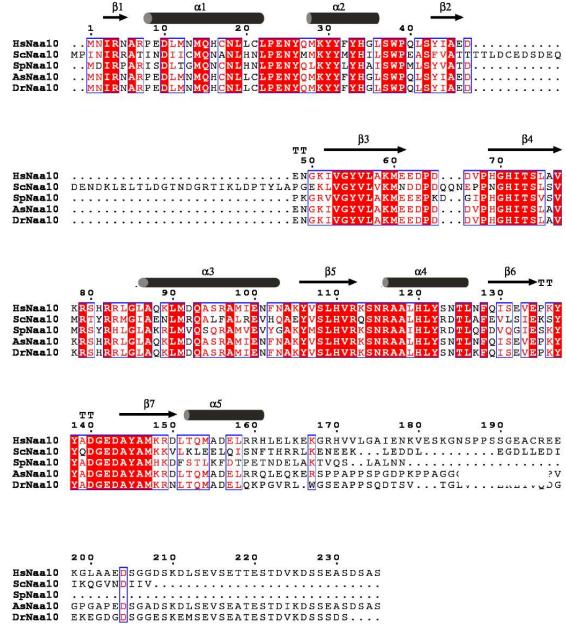


Figure S4, Related to Figure 1. Alignment of Naa10 Homologues. Sequence alignment of Naa10 homologues from *H. sapiens* (Hs); *S. cerevisiae* (Sc); *S. pombe* (Sp); *A. sinensis* (As); and *D. rerio* subunit b (Dr). The dashed line indicates the truncation construct used for all experimental studies.

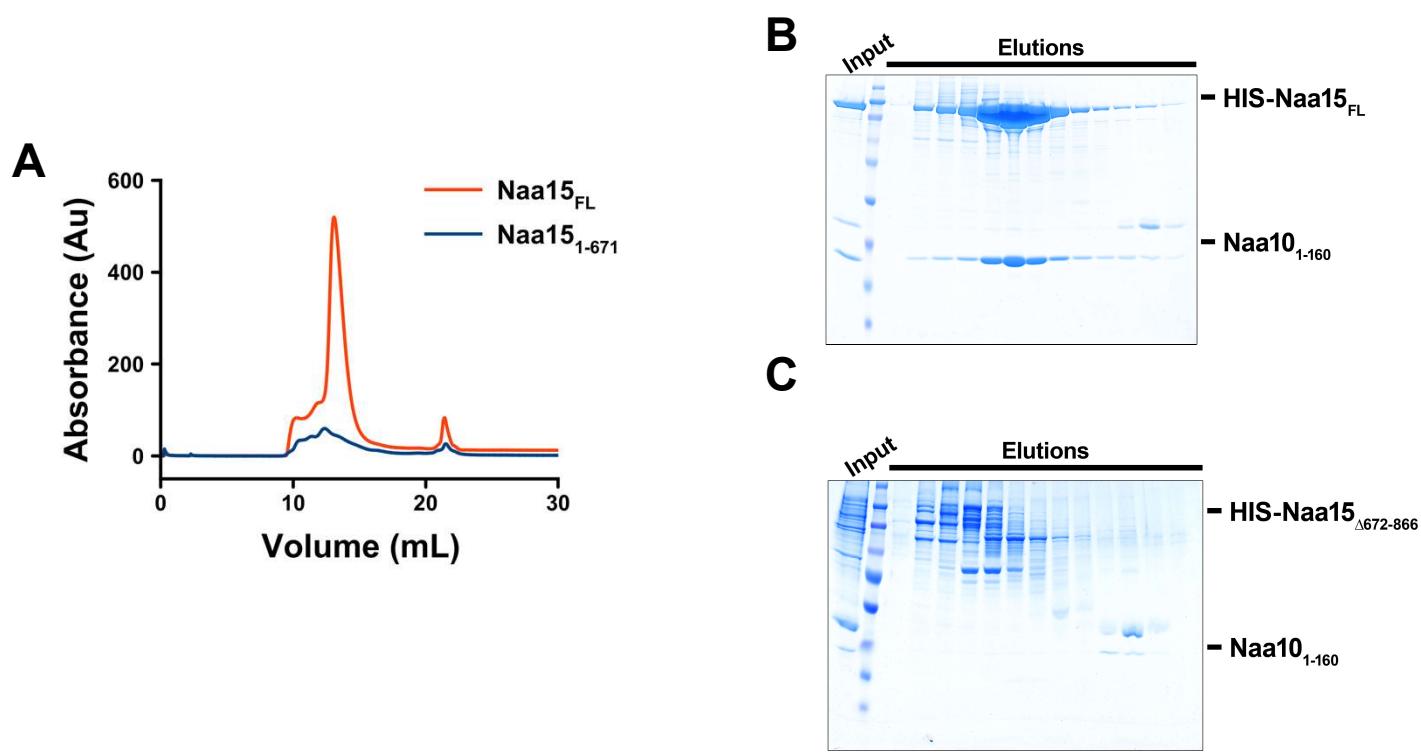


Figure S5, Related to Figure 1. C-terminal Truncation of Naa15 Abrogates NatA Binary Complex Formation.

(A) S200 gel filtration chromatogram.

(B) Corresponding SDS-PAGE gel to the trace of HIS-Naa15_{FL}/Naa10₁₋₁₆₀ complex (red) for A.

(C) Corresponding SDS-PAGE gel to the trace of HIS-Naa15_{Δ672-866}/Naa10₁₋₁₆₀ complex (blue) for A.