

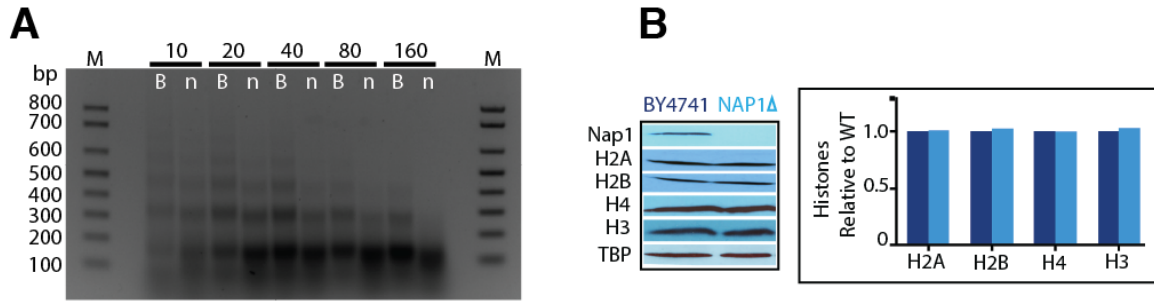
Appendix

Structure of the Nap1–H2A–H2B complex and implications for nucleosome assembly

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Table of contents:

1. Appendix Figure S1
2. Appendix Table S1-2



Appendix Figure S1. Controls. Related to Figure 1 (A) MNase titration on yeast chromatin in wild type (B) BY4742 and *nap1Δ* (n) strains. Total MNase units per 50 ml of culture are indicated on the top of the lanes. M: DNA Marker. **(B)** Nap1, H2A, H2B, H3 and H4 levels in the BY4741 (WT) and *nap1Δ* strain. TBP (TATA Binding Protein) is used as a loading control.

Appendix Table S1. Yeast strains used in this study.

Name	Genotype	Plasmid	Reference
BY4741	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0</i>	none	Open Biosystems
<i>nap1Δ</i>	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 nap1::KanMX</i>	none	Open Biosystems
pNAP1	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 nap1::KanMX</i>	pRS316-Flag- <i>NAP1</i> (Miyaji-Yamaguchi et al., 2003)	This study
HBR1	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 nap1::KanMX</i>	pRS316-Flag- <i>NAP1</i> HBR1	This study
HBR2	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 nap1::KanMX</i>	pRS316-Flag- <i>NAP1</i> HBR2	This study
HBR1+2	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 nap1::KanMX</i>	pRS316-Flag- <i>NAP1</i> HBR1+2	This study
IF1	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 nap1::KanMX</i>	pRS316-Flag- <i>NAP1</i> IF1	This study

Appendix Table S2. Summary of mutagenesis data

Mutation	Structural alteration	Histone binding*
yNap1		
D201R	Histone binding region 1	+++
D205R	Histone binding region 1	+++
E310R	Histone binding region 1	+++
D201R, D205R	Histone binding region 1	+++
HBR1 (D201R, D205R, E310R)	Histone binding region 1	+++
E332R	Histone binding region 2	+++
D333R	Histone binding region 2	+++
E336R	Histone binding region 2	+++
HBR2Δ	Deletion 314–337	+++
HBR2 (E332R, D333R, E336R)	Histone binding region 2	+++
HBR1+2 (D201R, D205R, E310R, E332R, D333R, E336R)	Charge reversal mutation	–
HBR1+2A (D201A, D205A, E310A, E332A, D333A, E336A)	Histone binding region 1+2 Alanine mutations	–
IF1 (G225D, S237D, T244D, D246R)	Oligomerization	+++
HBR1+2 + IF1 (D201R, D205R, E310R, E332R, D333R, E336R, G225D, S237D, T244D, D246R)	Histone binding region 1+2 and Oligomerization	–
xH2A		yNap1 binding*
R30E	Nap1 binding region 1	+++
R33E	Nap1 binding region 1	+++
R78E	Nap1 binding region 2	+++
R82E	Nap1 binding region 2	+++
K75E	Nap1 binding region 2	+++
R36E, K75E	Nap1 binding region 1+2	–
R36E, K37E, R82E	Nap1 binding region 1+2	–
R36E, K37E, R78E	Nap1 binding region 1+2	–
NBR1 (R30E, R33E, R36E, K37E)	Nap1 binding region 1	–
NBR2 (K75E, R78E, R82E)	Nap1 binding region 2	+/-
NBR1+2 (R30E, R33E, R36E, K37E, K75E, R78E, R82E)	Nap1 binding region 1+2	–
IF2 (N94E, G98D, R99D, T101D)	Oligomerization	+/-

* +++ not significantly reduced; +/- residual binding; – no binding