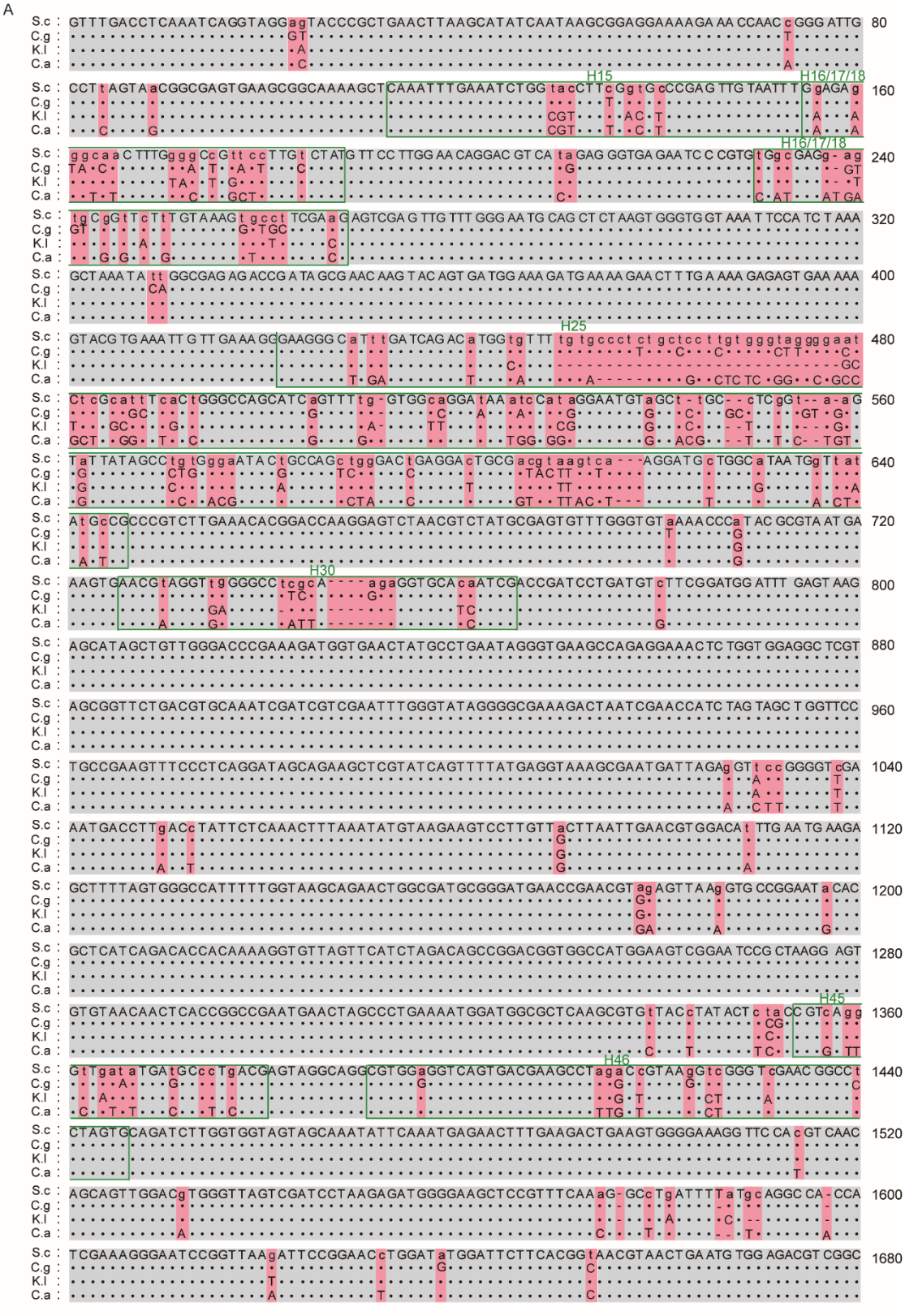
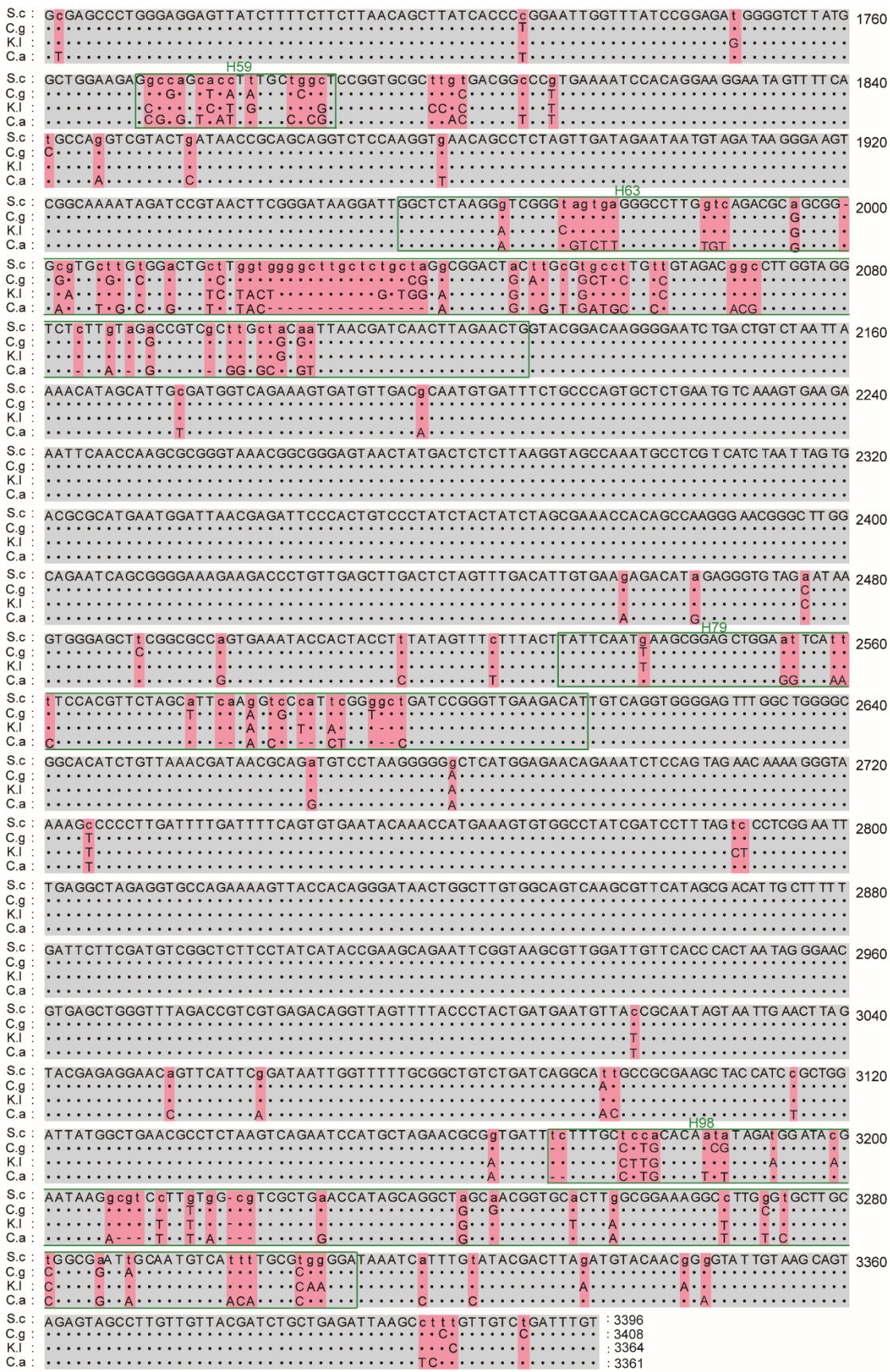
SUPPLEMENTARY DATA

Supplementary Figure S1



(To be continued)


S.c
C.g
K.l
C.a
H59
H63
H79
H98

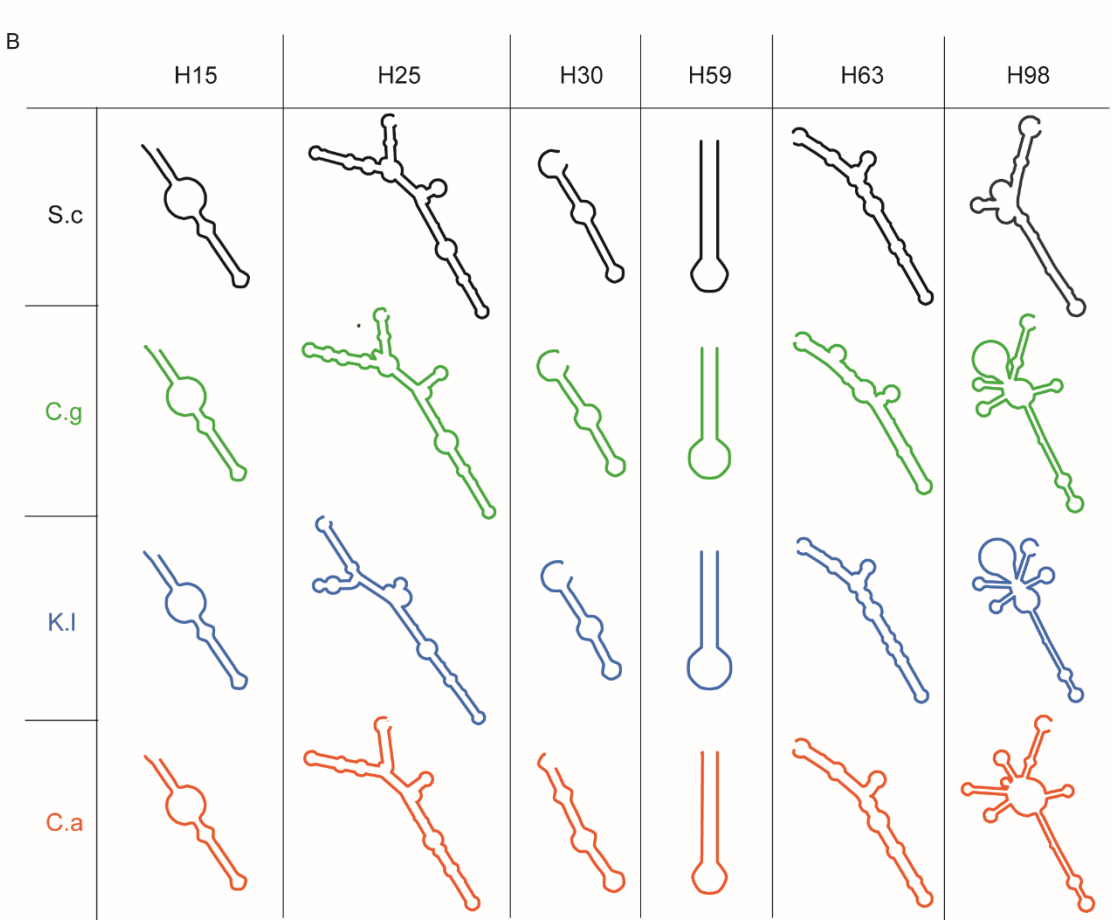


Figure S1. Sequence alignments and secondary structure analysis of 25S rRNAs of S.c, C.g, K.l and C.a.

(A) Sequence alignments of 25S rDNA sequences. '·' denoted consensus sequence; Pink color marked the variable sequence; the most variable regions were labeled by green rectangle.

(B) Secondary structures of the most variable six helices among the 25S rRNAs of S.c, C.g, K.l and C.a. The secondary structures were predicated by RNAfold.

Supplementary Figure S2

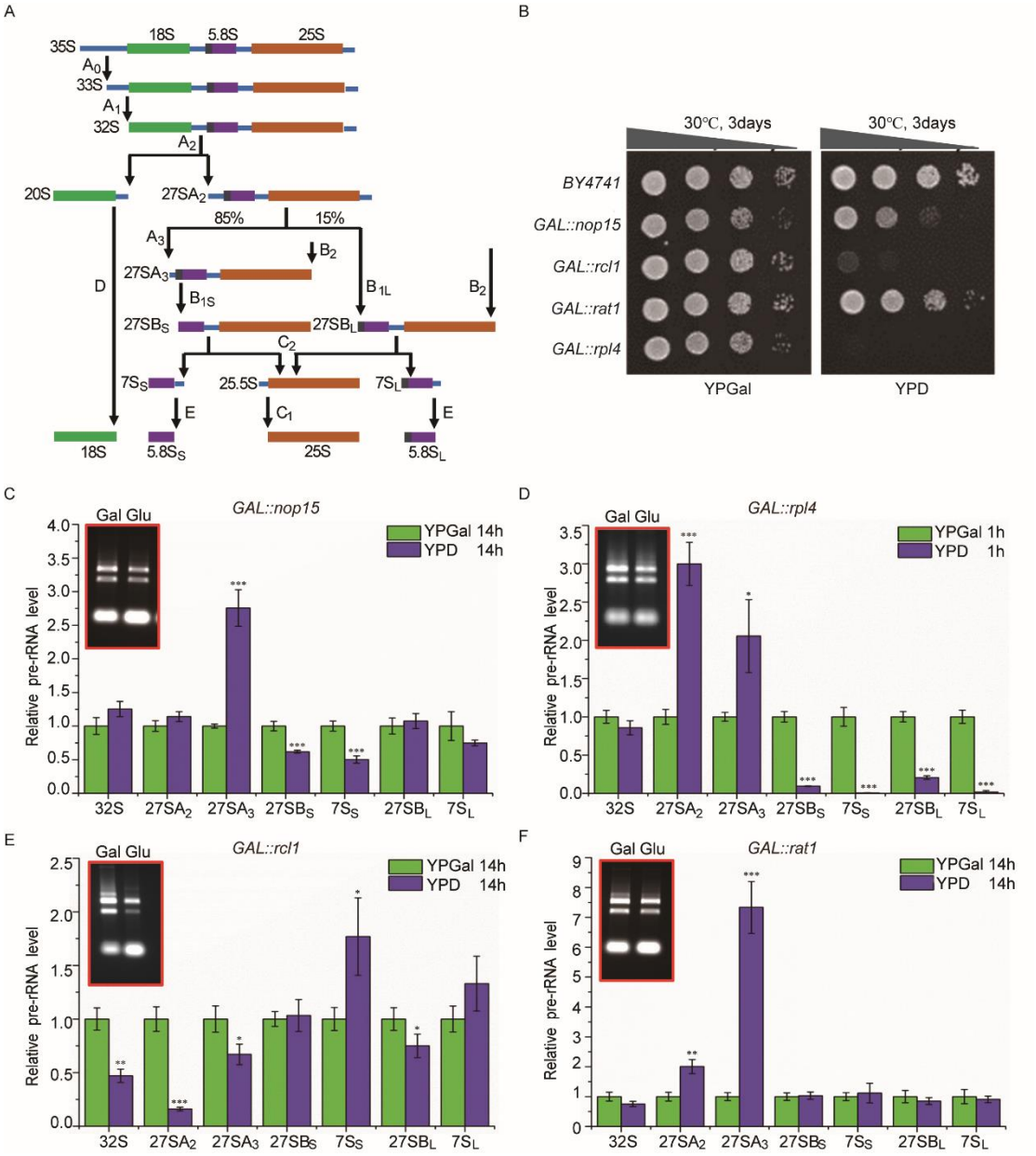


Figure S2. Quantitative analysis of the pre-rRNA processing defects.

(A) Diagram of the pre-rRNA processing pathway in *S. cerevisiae*.

(B) Growth analysis of the wild-type (BY4741) and conditional null mutants grown either on YPGal or YPD solid medium.

(C-F) Relative levels of the pre-rRNA intermediates in *Gal::nop15*(C), *Gal::rpl4* (D), *Gal::rcl1* (E) and *Gal::rat1* (F) cultured either in YPGal (left) or YPD (right). Levels of the pre-rRNA intermediates of each strain cultured in YPGal were set as 1.0. Error bars represent the standard deviation of three replicate reactions (t- test, *p < 0.05, **p<0.01, ***p<0.001). Electrophoresis patterns of the total RNAs of each strain were shown in the up left of each panel.

Supplementary Figure S3

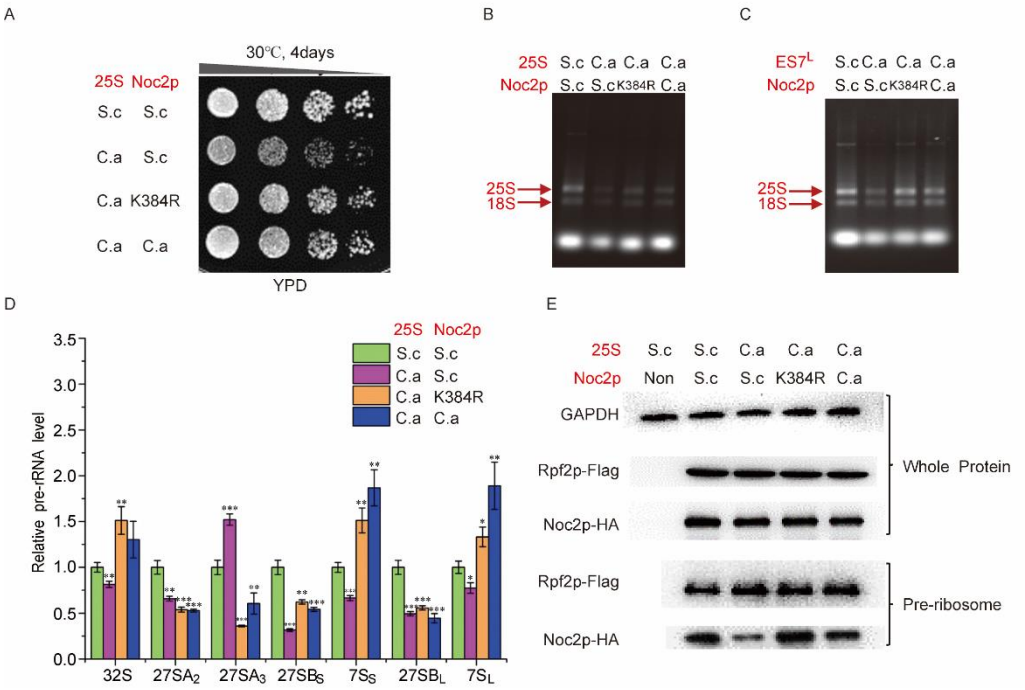


Figure S3. Defects in C.a-25S could be suppressed by *noc2* mutation.

(A) Both *noc2* mutant and C.a *NOC2* rescue the growth defect in C.a-25S. 'S.c' denoted the corresponding component was derived from *S. cerevisiae*; 'C.a' denoted the corresponding component was derived from *C. albicans*; 'K384R' denoted the Noc2 K384R mutant.

(B)(C) Electrophoresis patterns of total RNA. Mature 25S and 18S rRNAs were labeled by arrows, respectively.

(D) Relative levels of key pre-rRNA intermediates in the 25S rRNA biogenesis pathway between S.c-25S strain carrying S.c Noc2p and C.a-25S strains carrying S.c Noc2p, S.c Nop2p K384R or C.a Noc2p. Levels of the pre-rRNA intermediates in S.c-25S were set as 1.0. Error bars represent the standard deviation of three replicate reactions (t test, *p < 0.05, **p<0.01, ***p<0.001).

(E) Western blot analysis of HA-tagged Noc2p in the whole cell extracts or in the pre-ribosomes purified by Flag-tagged Rpf2p. 'Non' denoted extracts from the strains without Rpf2p and Noc2p labeled, which was used to verify the specificity of antibodies. 'GAPDH' was used as a loading control.

Supplementary Figure S4

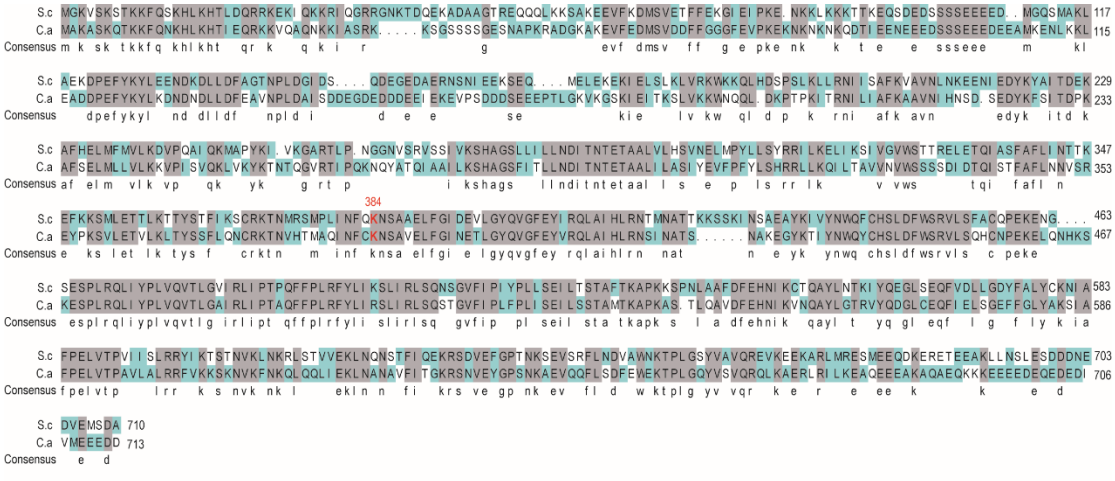


Figure S4. Amino acid sequence alignments of between S.c Noc2p and C.a Noc2p. Gray color denoted the consensus sequence; Blue color denoted the variable sequence; "." denoted the absent sequence; Amino acid K384 was labeled by red color.

Supplementary Figure S5

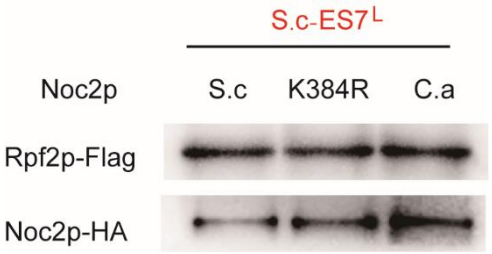


Figure S5. Western blot analysis of the levels of C.a Noc2p and S.c Noc2p K384R in Sc-ES7^{L} rRNA-containing pre-ribosomes.

Sc-ES7^{L} rRNA-containing pre-ribosomes were purified by Flag-tagged Rpf2p. 'S.c' denoted the corresponding component was derived from *S. cerevisiae*; 'C.a' denoted the corresponding component was derived from *C. albicans*; 'K384R' denoted the Noc2 K384R mutant.

Supplementary Figure S6

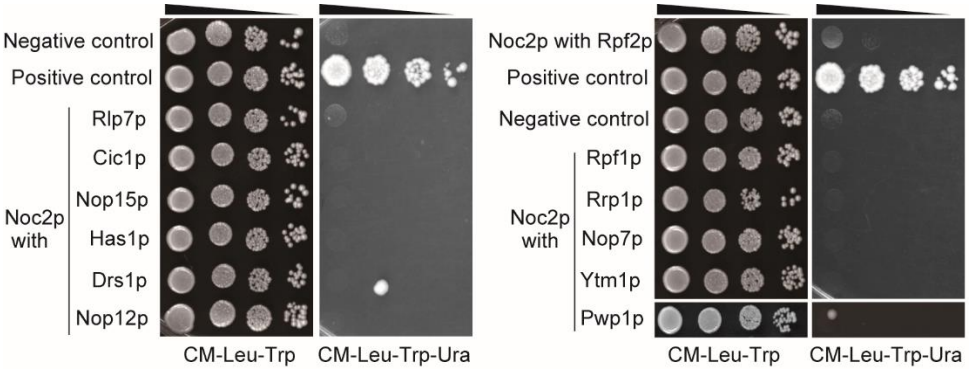


Figure S6. The yeast two-hybrid assay for interaction of Noc2p with A_3 factors or Rpf2p.

Ten-fold serial dilutions of yeast were spotted on CM-Leu-Trp or CM-Leu-Trp-Ura media. Growth of yeast cells in the absence of uracil was observed from positive control.

Supplementary Figure S7

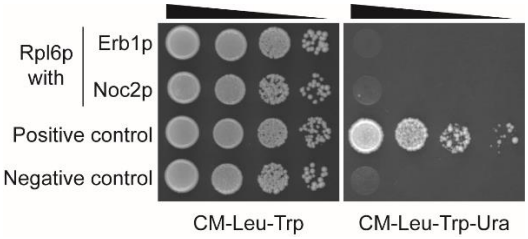


Figure S7. The yeast two-hybrid assay for interaction of Rpl6p with Erb1p or Noc2p. Ten-fold serial dilutions of yeast were spotted on CM-Leu-Trp or CM-Leu-Trp-Ura media. Growth of yeast cells in the absence of uracil is indicative of a positive Y2H interaction.