

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Characterisation of snR85 and snR80. **(A)** and **(C)** Potential secondary structure of yeast snR85 and snR80 predicted by using the *Mfold* program (Walter et al., 1994). The H and ACA motifs are indicated. **(B)** and **(D)** The 5' end sequences of snR85 and snR80 were mapped by reverse transcription using 5' end-labelled oligonucleotides CT41 and CT124 respectively (see supplemental Table S3) as primer and total RNAs extracted from wild-type BMA64 strain as template. DNA sequencing reactions performed with the same 5' end-labelled primers on DNA sequences of snR85 and snR80 were run in parallel (lanes G; A, T, C). An arrow indicates the 5' end of the snoRNAs.

Figure S2. Characterisation of RUF9. **(A)** 5' end sequences of RUF9 were mapped by reverse transcription using 5' end-labelled oligonucleotides CT35 (see supplemental Table S3) as primer and total RNAs extracted from wild-type BMA64 strain as template. DNA sequencing reactions performed with the same 5' end-labelled primers on DNA sequences of RUF9 were run in parallel (lanes G; A, T, C). Arrows indicate the 5' end of each RUF9 RNA species. The sequence shown corresponds to the coding strand. **(B)** Potential secondary structure of the yeast smallest RUF9 RNA species, predicted by using the *Mfold* program (Walter et al., 1994). Putative H and ACA motifs are indicated.

Figure S3. Primer extension analyses of small and large subunit rRNAs pseudouridylations. Formation of Ψ s was monitored by the CMC-primer extension method (see Material and Methods). Results are shown for 11 strains, each depleted of a different snoRNA with two independent clones 1 and 2 except for Δ snR80 with one clone and for the WT strain, BY4742. Only the rRNA regions affected are shown. When appropriate, CMC treatment is indicated by – (untreated) and + (treated) for WT RNAs. Positions of pseudouridine residues

are indicated. Lanes M represents size markers. **(A)** Ψ s within SSU rRNA. **(B)** Ψ s within LSU rRNA. The oligonucleotides used are listed in supplemental Table S3.

Figure S4. Potential secondary structure of yeast RPS28A mRNA predicted by using the *Mfold* program (Walter et al., 1994). Putative H and ACA motifs are indicated. The AUG start and UAG stop codons of the RPS28A ORF are boxed and the ORF shown with upper case letters.