



SUPPLEMENTARY FIGURE S1: Current model for the ribosome biogenesis pathway from *S. cerevisiae*. The different predicted particles along the synthesis of both SSUs and LSUs are depicted. The first detected particle is called 90S pre-ribosomal particle or SSU processome. This particle is nucleolar and contains either the nascent pre-rRNA, which has been cleaved at site A₂ in the co-transcriptional pre-rRNA processing branch, or 35S pre-rRNA in the post-transcriptional processing branch (not shown). This pre-rRNA is transcribed by the RNA polymerase I (RNAP I), while pre-5S is transcribed by RNAP III. 90S particles contain about three dozens of *trans*-acting factors and many r-proteins from the SSU. Maturation of the 90S particle involves the dissociation of the early pre-40S particle from the bulk of these factors, except few of them. Pre-40S particles are termed, according to their position in the pathway, early (E), late (L) and cytoplasmic (C). Cleavage D occurs in the cytoplasm within a 80S-like complex that contains not only the pre-40S particle C but also a mature LSU (not shown). Pre-60S particles assemble on the remaining part of the nascent pre-rRNA transcript. Pre-60S particles are termed early (E), middle (M), late (L) and cytoplasmic (C). The pre-rRNA processing reactions that occur inside the particles as they travel from the nucleolus to the cytoplasm are depicted. About 20 placeholder *trans*-acting factors have been described so far. In the figure, we have highlighted the dynamics of association and dissociation of ribosomal-like factors and their r-protein counterparts. Note that only two factors, Mrt4 and Rlp24, harbour placeholder activity. See text for further details.

A

RPP0 1 -----MG**GIREKKA**EY**FAKLR**EY---**L**EYKSL**FVGV**DNVSS**OOMHEV**RKEL**R**GRAVV
MRT4 11 -TLAQTDKK**GRENKERI**FDEV**REA**---LDTYRYV**VVWLHL**DDV**RT**PV**LQ**EIRTSWAGSKLI
MEX67 275 DALG**QS**STDFATN**FLNL**WDNN**REQL**LNLY**SP**Q**SQ**FSV**SVD**STIPPSTV**TD**SDQ**TPA**FGYY

RPP0 52 **LMGK**NTM**V**RAI-----**RG**FL**SD**LPDF**EK**LL**PF**VK**GN**V**G**F**V**FT**N**E**PL**TE**I**KN**V**I**V**S**N****RM**A
MRT4 67 -**MG**K**R**K**V**L**Q**K**AL**G**E**K**R**E**E**E**Y**K**EN**L**Y**Q**L**S**K**L---**C**S**G**V**T**G**L**L**F**T**D**E**D**V**N**T**V**K**E**Y**F**K**S****V****V****R**S
MEX67 335 -**M**S**S**S**R**N**I**S**K**V**S**S**E**K**S**I**Q**R**L**S-----**I**G**Q**E**S**I**N**S**I**F**K**T**L**P**K**T**K**H**H**

RPP0 107 APARAGAVAP-----**E**DIWVR**AV**NT**G**M**E**P**G**K**T**S**F**F**O**A**L**G**V**P**T**K
MRT4 123 D**Y**S**R**P**N**T**K**A**P**L**T**F**T**I**P**E--**G**I**V****Y**S**R**G**G****O**I**P**A**E**E**D**V---**P**M**I**H**S**L**E**P**T**M**R**N**K**F**E**---**I**P**T**K
MEX67 375 L**Q**E**O**P**N**E**Y**S**M**E**T**I**S****Y**P**Q**I**N**G**F**V**I**T**L**H**G**F**F**---**E**E**T**G--**K**P**E**L**S**N**K**K**T**G**K**N**Y**Q---**K**N**R**R

RPP0 145 I**A**R**G**T**I**E**I**V**S**D**V**K**V**D**A**G**N**K**V**G**Q**S**E**A**S**L**L**N**L**L**N**I**S**P**F**T**F****G**L**T**V**V**Q**V****Y**D**N**G**Q**V**F**P**S**S**I**L**D**I
MRT4 175 I**K**A**K**G**I**T**I**D**S**P**Y**L**V**C**T**E**G**E**K**L**D**V**R**Q**A**L**I**L**K**Q**F**G**I**A**A**S**E**F**K**V**K**V**S**A**Y****Y**D**N**---**D**S**S**T---
MEX67 428 **Y**N**H**C**Y**N**S**T**S**N**N**K**L**---**S**K**S**F**D**R**T**W**V**I**V**P**M**N**S****V**I**I**A**S**D**L**L**T**V**R**A--**Y**S**T**G**A**W**K**T**A**S**I**---

B

RPL24A 1 **M**K**V**E**I**D**S**F**S**G**A**K**I****Y**P**G**R**G**T**L**F**V**R**G**D**S**K**I**F**R**F**O**N**S**K**S**A**S**L**F**K**O**R**K**N**P**R**I**A**T**V**L**F**R**K**H**H**K**
RLP24 1 **M**R**I****Y**Q**C**H**F**C**S**S**P**C**Y**P**G**H**G**I**M**F**V**R**N**D**A**K**E**F**R**F**C**R**S**K**C**H**K**A**F**K**O**R**R**N**P**R**K**L**K**W**T**K**A**F**R**K**A**G

RPL24A 61 **K**G**I**T**E**E**V**A---**K**K**R**S**R**K**T**V**K**A**O**R**P**I**T**G**A**S**L**D**L**I**K**E**R**S**L**K**P**E**V**R**K**A**N**E**E**K**L**K**A**N**K**E**K**--
RLP24 61 **K**E**L**A**V**D**S**T**L**T**F**A**O**R**R**N**V**P**V**R**Y**N**R**E**L**V**A**T**T**L**K**A**M**A**R**I**E**E**I**R**Q**K**R**E**R**A**F**Y**K**N**R**M**R**G**N**E**K**E**D**F

RPL24A 116 -----**K**K**A**E**K**A**A**R**K**A**E**K**A**K**S**A**G**T**O**S**S**K**F**S**K**Q**O**-----**A**K**G**
RLP24 121 L**R**D**K**K**L**V**E**S**N**P**E**L**L**R**I**R**E**V**E**I**A**R**K**L**A**K**E**O**E**R**A**E**S**V**S**E**Q**E**E**S**E**E**E**E**E**D**M**E**I**D**S**D**E**E**E**E**E**Q**L**

RPL24A 146 **A**F**O**K**V**A**A**T**S**R-----
RLP24 181 **E**K**Q**K**I**L**L**K**N**R**R**R**N**T**K**K**I**A**F**

C

RPL7A 1 **M**A**A**E**K**-----**I**L-----**T**P**E**S**O**L**K**K**S**K**A**Q**O**-----**K**T**A**E
RLP7 1 **M**S**S**T**O**D**S**K**A**Q**T**L**N**S**N**P**E**I**L**L**R**K**R**R**N**A**D**R**T**R**I**E**R**Q**E**L**A**K**K**K**R**E**Q**I**K**K**R**S**N**K**N**K**F**V**R**A**E**S

RPL7A 25 **Q**V**A**A**E**R**A**A**R**K**A**A**N**K**E**K**R**A**I**L**L**E**R**N**A**A**Y**O**K**E**Y**E**T**A**E**R**N**I**I**O**A**K**R**D**A**K**A**G**S**-----
RLP7 61 I**V**A**K**T**L**A**T**S**R**E**K**E**R**I**K**R**V**S**I**L**E**D**K**K**A**K**N**E**T**Q**H**I**A**S**G**K**D**F**I**L**K**I**T**E**K**A**N**G**A**E**N**S**V**D**L**E**E**T

RPL7A 75 -----**Y**Y**V**E**A**Q**H**K**I**V**F**V**R**I**K**G--**I**N**K**I**P**P**K**P**R**K**V**L**O**L**L**R**I**T**R**I**N**S**G**T**F**V**K**V**T**
RLP7 121 **E**E**E**E**D**D**G**L**I**R**E**K**T**T**Y**D**G**K**P**A**L**L**F**I**V**R**V**R**G**P**L**A**V**N**I**P**N**K**A**F**K**I**L**S**L**L**R**L**V**E**T**N**T**G**V**F**V**K**L**T

RPL7A 121 **K**A**T**L**E**L**L**K**L**I**P**P**Y**V**A**Y**C**P**S****S**T**I**R**O**L**V**Y**K**R**G**F-----**G**K**I**N**K**O**R**V**P**L**S**D**N**A**I**I**E**A**N**L**G**
RLP7 181 **K**N**V**Y**P**L**L**K**V**I**A**P**Y**V**V**I**G**K**P**S**L**S**S**I**R**S**L**I**Q**K**R**G**R**I**I**Y**K**G**E**N**A**E**P**H**E**I**V**L**N**D**N**N**I**V**E**Q**L**G

RPL7A 175 **K**Y**G**I**L**S**I**D**D**I**I**H**E**L**I**T**V**C**P**H**F**K**O**A**N**N**F**L**W**P**F**K**L**S**N**P**S**G**W**G**V**P**R**K**F**K**H**F**I**O**G**G**S**F**G**N**R**E**E**
RLP7 241 **D**H**G**I**C**V**E**D**I**H**E**I**A**T**M**G**E**S**F**S**V**C**N**F**L**O**P**F**K**L**N**R**E**V**S**G**F**G**S**L**N**R**L**R**K**I**K**O**R**E**A**S**R**T**Q**

RPL7A 235 **F**I**N**-----**K**L**V**K**S**M**N**
RLP7 301 **F**S**N**A**A**T**A**P**V**I**E**V**D**I**D**S**L**L**A**K**L**N

D

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RPS9A 1 MPRAPRTYSKTYSTPKR----PYES SRLDAELKLAGEFGLKKNKKEIYRISFQLSKIRRAA
IMP3 1 MVRKCLKHHEQ--KLLKKVDFLEWKQDQGHRDTQVMRTYHIQNREYHKYNRICGDIRRLA

RPS9A 57 RDLLTRDEKDPKRLFEGNALTRRLVVRVGVLSDDKPKLDYVLALKVEDFLERRLQTQVYKL
IMP3 59 NKLSELLPPTDPFRRKHEQLLDKLYAMGVLTTKSKISDLENKVTVSAICRRRLPVMHRL

RPS9A 117 GLAKSVHARVLTORHIAVGRQIVNIPFSFVRLDSEKHIDFAPTSPFGGARPGRVARRN
IMP3 119 KMAETIQDAVKFIEQGHVVRVGPNLINDEAYLVTRNMEYVVTWVDNSKI---KKTLLRYRN

RPS9A 177 AARKAEASGEAADEADEADEE
IMP3 176 -----QIDDFDFS
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E

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RPS26A 2 --PKKRASNGRNKKGRG-----
NOB1 148 SVPKKKNKRGGKQKAKREAREAREAENANLELESKAEEHVVEEAGSKEQICNDENIKES

RPS26A 17 -----HVKEVRCVNCSSK
NOB1 208 SDLNEVFEDADDGDWITPENLTAIIKDSGEDTTGSLGVEASEEDRHVALNRPENQVAL

RPS26A 30 IPKDKATKRMAIR-----NIVEAAAVRDLSE-----ASVYPEYALPKTYNKLHYCVSCA
NOB1 268 ATGDFAVQNVVALQMNLMNMFMSGLKIKRIRNYMLRCHACFKIFPLPKDGKPKHFCASG

RPS26A 79 ITHARIVRVRSEDRK--NRAPPQRPFRF--NRENKVS PADAACK-----
NOB1 328 GQGTLLRCAVSVDSRTGNVTEHLKSNFQWNNRGNRYSVASPLSKNSQKRYGKKG
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SUPPLEMENTARY FIGURE S2: Alignment of distinct ribosomal proteins and their respective ribosomal-like protein counterpart from *S. cerevisiae*. Sequence alignments were performed using the slow and accurate version of MAFFT [1]. Alignments were visualised with Belvu [2]. Identical residues are marked by black boxes and similar amino acids are marked by grey boxes (BLOSUM62). Red boxes indicate residues of the ribosomal proteins situated at or closer than 5 Å from rRNA. Comparison of the amino acid sequences of yeast (A) P0 (uL10), Mrt4 and Mex67, (B) L24 (eL24) and Rlp24, (C) L7 (uL30) and Rlp7, (D) S9 (uS4) and Imp3, (E) S26 (eS26) and Nob1. All sequences were taken from the *Saccharomyces Genome Database* (<http://www.yeastgenome.org/>).

Supplementary references

1. Kazutaka, K, Standley, DM (2013). Multiple Sequence Alignment Software Version 7: improvements in performance and usability. *Mol Biol Evol* 30(4): 772-780. doi: 10.1093/molbev/mst010.
2. Sonnhammer, ELL, Hollich, V (2005). *Scoredist*: A simple and robust protein sequence distance estimator. *BMC Bioinformatics* 6: 108. doi: 10.1186/1471-2105-6-108.