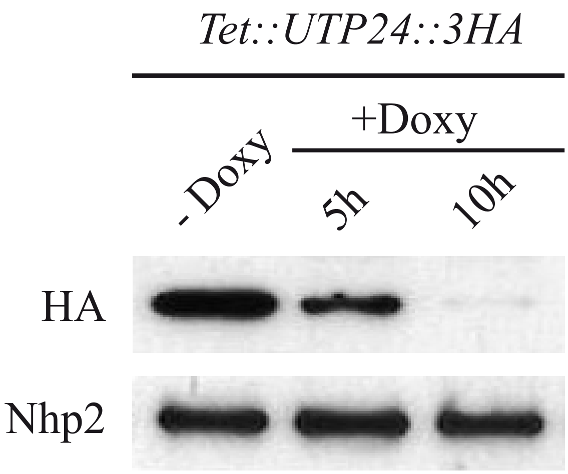
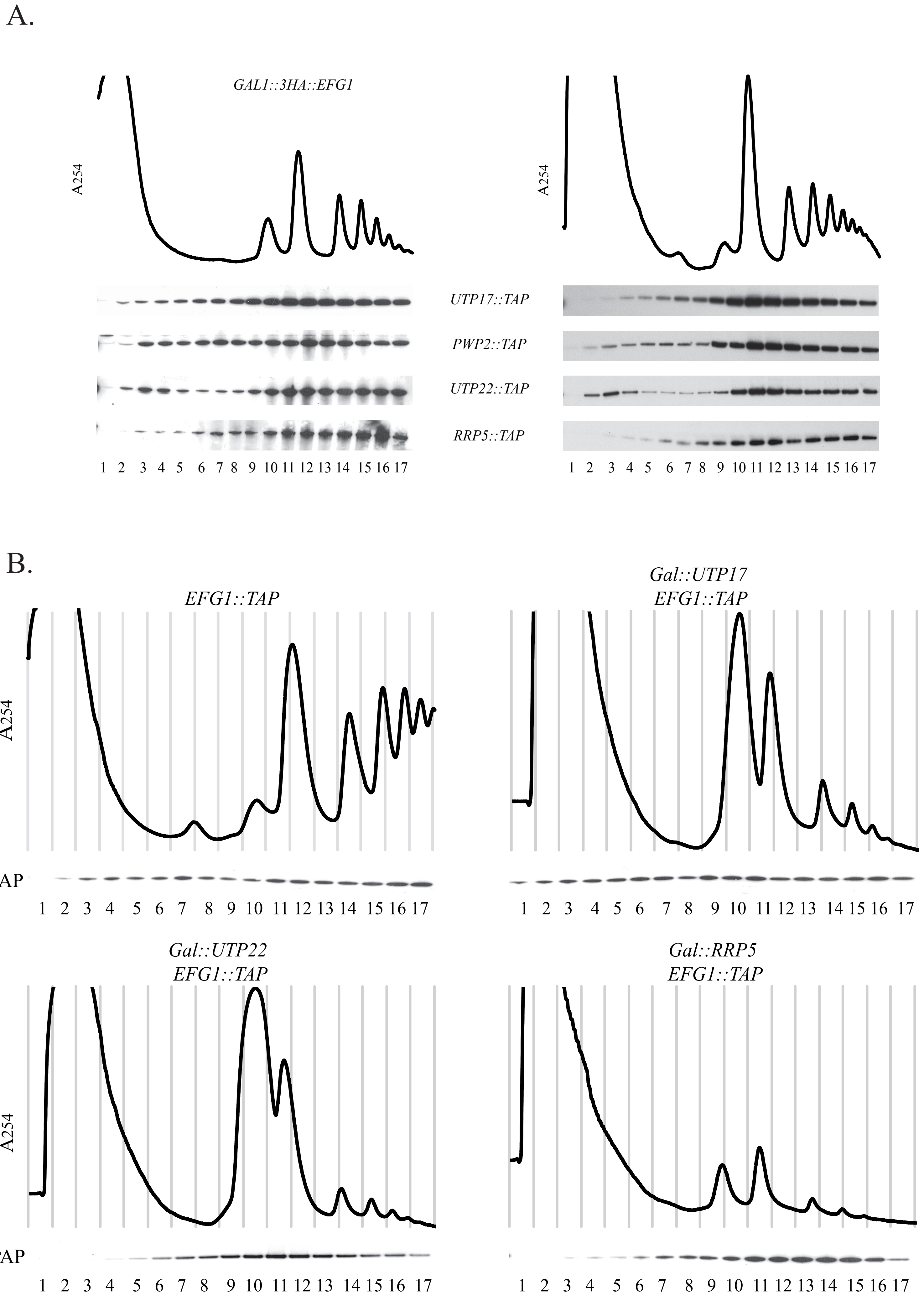
ORF	Gene	AC	ID	MW	Description	Bestscore	Peptides	Sequences	Coverage(%)	Total
YGR271CA	EFG1	A6ZUS8	EFG1P_YEAS7	27161,6	rRNA-processing protein EFG1	654,38	21	17	69,1	36
YLR197W	NOP56	Q12460	NOP56_YEAST	57057	Nucleolar protein 56	693,3	20	20	50,2	30
YLL045C	RPL8B	P29453	RL8B_YEAST	28151,4	60Sribosomalprotein L8-B	414,73	19	19	57,4	31
YDL014W	NOP1	P15646	FBRL_YEAST	34615	rRNA 2'-O-methyltransferasefibrillarin	575,98	19	16	50,8	33
YHL033C	RPL8A	B5VJP5	B5VJP5_YEAS6	28151,4	YHL033Cp-like protein	400,48	17	17	48,4	30
YPL090C	RPS6	P02365	RS6_YEAST	27036,9	40S ribosomal protein S6	292,12	16	16	55,5	20
YFR031CA	RPL22A	P05736	RL2_YEAST	27391,9	60S ribosomal protein L2	299,54	13	13	54,7	22
YOR310C	NOP58	A6ZPE5	NOP58_YEAS7	56978,3	Nucleolar protein 58	690,82	13	13	32,7	21
YIL133C	RPL16A	B3LM30	B3LM30_YEAS1	22493,5	60S ribosomal protein L13(Fragment)	305,72	12	12	55,3	17
YGR159C	NSR1	P27476	NSR1_YEAST	44565,9	Nuclear localization sequencebindingprotein	403,13	12	12	35	20
YPL131W	RPL5	B3LKU4	B3LKU4_YEAS1	33751,2	Ribosomal protein L5	357,03	11	11	44,1	20
YKL006W	RPL14A	P36105	RL14A_YEAST	15214,6	60S L14-A	314,82	10	10	55,8	14
YDL191W	RPL35A	P39741	RL35_YEAST	13958	60S L35	257,09	10	10	52,5	13
YGR123W	RPS2	P25443	RS2_YEAST	27490	40Sribosomalprotein S2	259,84	10	10	42,9	19
YOR204W	DED1	A6ZP47	DED1_YEAS7	65740,5	ATP-dependent RNA helicase DED1	385,65	10	10	24	16
YJL177W	RPL17B	P46990	RL17B_YEAST	20539	60Sribosomalprotein L17-B	370,75	9	9	54,3	19
YNL299W	TRF5	P48561	TRF5_YEAST	74179	Poly(A) RNA polymerase protein 1	217,65	9	9	15,9	12
YGR118W	RPS23	P32827	RS23_YEAST	16141,9	40S S23	126,68	8	8	56,6	9
YIL069C	RPS24	P26782	RS24_YEAST	15319,5	40S S24	146,01	8	8	48,1	9
YBL087C	RPL23A	P04451	RL23_YEAST	14577,7	60S L23	280,77	8	5	42,3	14
YHR010W	RPL27A	P0C2H6	RL27A_YEAST	15521,7	60S L27-A	245,2	7	7	47,1	14
YGR148C	RPL24B	A6ZUG0	A6ZUG0_YEAS7	17566,9	Ribosomal protein L24B	135,85	7	7	32,3	11
YHR064C	SSZ1	P38788	SSZ1_YEAST	58316,2	Ribosome-associated complexsubunit SSZ1	301,46	7	7	21,7	12
YER131W	RPS26B	P39939	RS26B_YEAST	13666,4	40S S26-B	176,45	6	6	48,7	13
YLR061W	RPL22A	P05749	RL22A_YEAST	13685	60S L22-A	476,13	5	5	67,8	11
YJR094W	RPL43A	B3LLA2	B3LLA2_YEAS1	10394,5	Ribosomal L43A	235,78	5	5	51,1	7
YPL249CA	RPL36B	O14455	RL36B_YEAST	11128,3	60S L36-B	85,72	5	5	43	6
YCL037C	SRO9	B3LU45	B3LU45_YEAS1	48090,8	Protein SRO9	133,3	3	3	11,3	5
YGR128C	UTP8	B3LIA0	B3LIA0_YEAS1	80692,3	U3 small nucleolar RNA-associated protein 8	136,93	3	3	5,5	4
YOR369C	RPS12	P48589	RS12_YEAST	15462,2	40S S12	62,53	2	2	18,9	3
YLR167W	RPS31	B3RH62	B3RH62_YEAS1	17433,4	Also encodes a ubiquitin protein	51,43	2	2	17,1	3
YOR293W	RPS10A	B5VSH1	B5VSH1_YEAS6	18041,3	YOR293Wp-like protein	44,32	2	2	16	2
YEL026W	SNU13	P39990	SNU13_YEAST	13731,4	13 kDa ribonucleoprotein-associatedprotein	45,8	2	2	14,3	3
YHR089C	GAR1	P28007	GAR1_YEAST	21638,1	H/ACA ribonucleoprotein complexsubunit 1	109,75	2	2	14,1	4
YPL093W	NOG1	Q02892	NOG1_YEAST	74762,5	Nucleolar GTP-binding protein 1	112,61	1	1	2,8	3
YGR185C	TYS1	P36421	SYYC_YEAST	44220,2	Tyrosyl-tRNA synthetase,cytoplasmic	49,1	1	1	2,8	1
YGR121W	ATP2	P00830	ATPB_YEAST	54817	ATP synthase subunit beta,mitochondrial	58,46	1	1	2,7	1

Choque et al., Figure S1



Choque et al., Figure S2



Choque et al., Figure S3

Figure S1:

Efg1-TAP was affinity purified under native conditions as described in (32). As a control, the parental WT strain, devoid of TAP-tagged protein, was handled similarly. Purified samples were separated by SDS-polyacrylamide gel electrophoresis and stained with coomassie protein staining solution. Bands were excised and polypeptides contained in these bands were subjected to in-gel trypsin digestion. The resulting peptides were analyzed by Mass Spectrometry as described in Materials and Methods. A non-exhaustive list of peptides found in the analysis is presented in this table.

Figure S2: Western-blot analysis of Utp24-3HA depletion

TET::UTP24-3HA strains were grown in YPD media and YPD media containing doxycycline (40µg/ml). Total proteins were extracted at the times indicated and analyzed by Western blot. Utp24-3HA and Nhp2 were detected using anti-HA and Nhp2-specific antibodies respectively.

Figure S3: Efg1 and U3 processome assembly.

(A) Depletion of Efg1 in yeast does not affect the incorporation of components of the UTP-A, UTP-B, or UTP-C modules within preribosomes. Strains expressing TAP-tagged versions of Utp17p, Pwp2p, Utp22p or Rrp5p that were otherwise WT (right panel) or expressing 3HA-Efg1 under the control of the *GAL1* promoter (left panel) were transferred from galactose- to glucose-based medium and grown for 3 h. Total extracts prepared from these cells were sedimented through sucrose gradients. Western blot experiments were carried out using rabbit PAP to detect TAP-tagged proteins in the different fractions. **(B)** Sedimentation profile of Efg1-TAP in WT cells (upper left panel) or in cells lacking Utp17p, Pwp2p, or Rrp5p. The *GAL1*::*UTP17*, *GAL1*::*UTP22*, and *GAL1*::*RRP5* strains expressing Efg1-TAP were shifted from galactose- to glucose-containing medium and grown for 3 h, to deplete the corresponding proteins. As a control, the *EFG1::TAP* strain grown in the presence of glucose was used. Total extracts prepared from these cell samples were sedimented through sucrose gradients. The proteins contained in each fraction were analyzed by Western blotting using PAP antibodies to detect Efg1-TAP.