

Figure S1

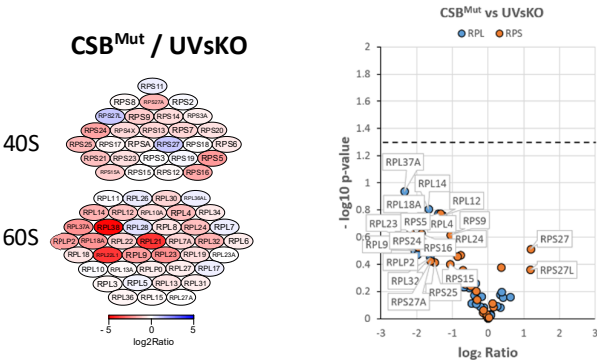


Primer	Forward	Reverse
47S	<i>TGTCAGGCGTTCTCGTCTC</i>	<i>AGCACGACGTCACCACATC</i>
18S	<i>CGATGCGGCGGCGTTATTCC</i>	<i>GAACGGCCATGCACCACCAC</i>
28S	<i>AGTCGGGTTGCTTGGAATGC</i>	<i>CCCTTACGGTACTTGTGTGACT</i>
28S/ETS	<i>ACCTGGCGCTAAACCATTCGT</i>	<i>GGACAAACCCTTGTGTGAGG</i>
5.8S/ITS2	<i>TCGTGCGTCGACGCAG</i>	<i>ATTGATCGGCAAGCGACGCTCAG</i>

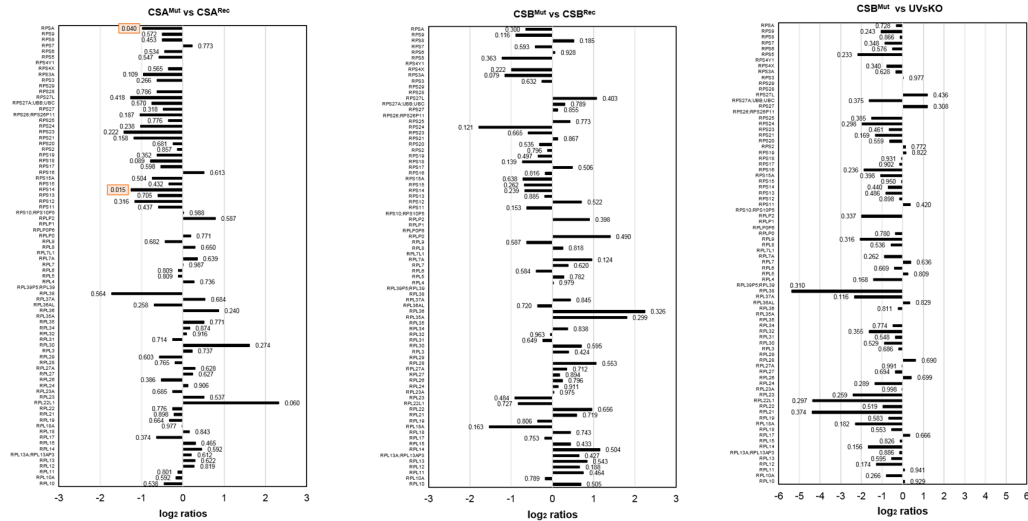
Figure S1. (A) Full image of a northern blot analysis in all cell lines. Membranes were hybridized with ITS1 probe, further stripped and re-probed with ITS2. (B) Quantification of different intermediates of pre-rRNA species normalized to the 47S level. (C) Relative quantification of the mature 28S rRNA abundance in CS cells. Values are represented as mean \pm SD of at least three independent experiments (*= p <0.05, **= p <0.01, ***= p <0.001). (D) QPCR was run with the different annealing temperatures **60°C (28S/ETS)**, **64°C (5.8/ITS2, 18S)** and **68°C (47S)**. (E) Primer list used in this study

Figure S2

A



B



C

Protein names	Peptide counts (unique)	Protein names	Peptide counts (unique)
RPL1	12	RPS10-RPS20S	5-3
RPL10A	13	RPS11	13
RPL11	10	RPS12	13
RPL12	7	RPS13	8
RPL13	8	RPS14	11
RPL13A-RPL13AP3	0.5	RPS15	6
RPL14	5	RPS15A	7
RPL15	11	RPS16	10
RPL17	7	RPS17	8
RPL18	10	RPS18	10
RPL18A	6	RPS19	8
RPL19	6	RPS21	10
RPL21	7	RPS22	6
RPL22	5	RPS23	7
RPL22L1	3	RPS24	7
RPL23	8	RPS25	6
RPL23A	12	RPS25S	6
RPL24	7	RPS26-RPS26P11	5-4
RPL26	2	RPS27	3
RPL27	8	RPS27A-UBB-UBC	6-0-0
RPL27A	6	RPS27L	2
RPL28	9	RPS28	2
RPL29	2	RPS29	1
RPL3	21	RPS3	71
RPL30	6	RPS3A	10
RPL31	8	RPS4X	7
RPL32	6	RPS4P1	6
RPL34	6	RPS5	24
RPL35	5	RPS6	11
RPL35A	2	RPS7	12
RPL36	5	RPS8	10
RPL36A	5	RPS9	12
RPL37A	4	RPSA	15
RPL38	6		
RPL38P5-RPL38	1-1		
RPL4	12		
RPL5	15		
RPL6	18		
RPL7	10		
RPL7A	21		
RPL7L1	4		
RPL8	11		
RPL9	13		
RPL9P	7		
RPL9P9	1		
RPL9P2	11		

Figure S2. (A) Mass spectrometric analysis shows protein intensity of isolated ribosomes of CSB-deficient cells compared to UVsKO cells, and quantification by volcano plot of the small 40S ribosome subunit and the large 60S ribosome subunit. (B) A bar plot of MS data with p-values (C) List of unique peptides/RP for label-free MS quantification.

Figure S3

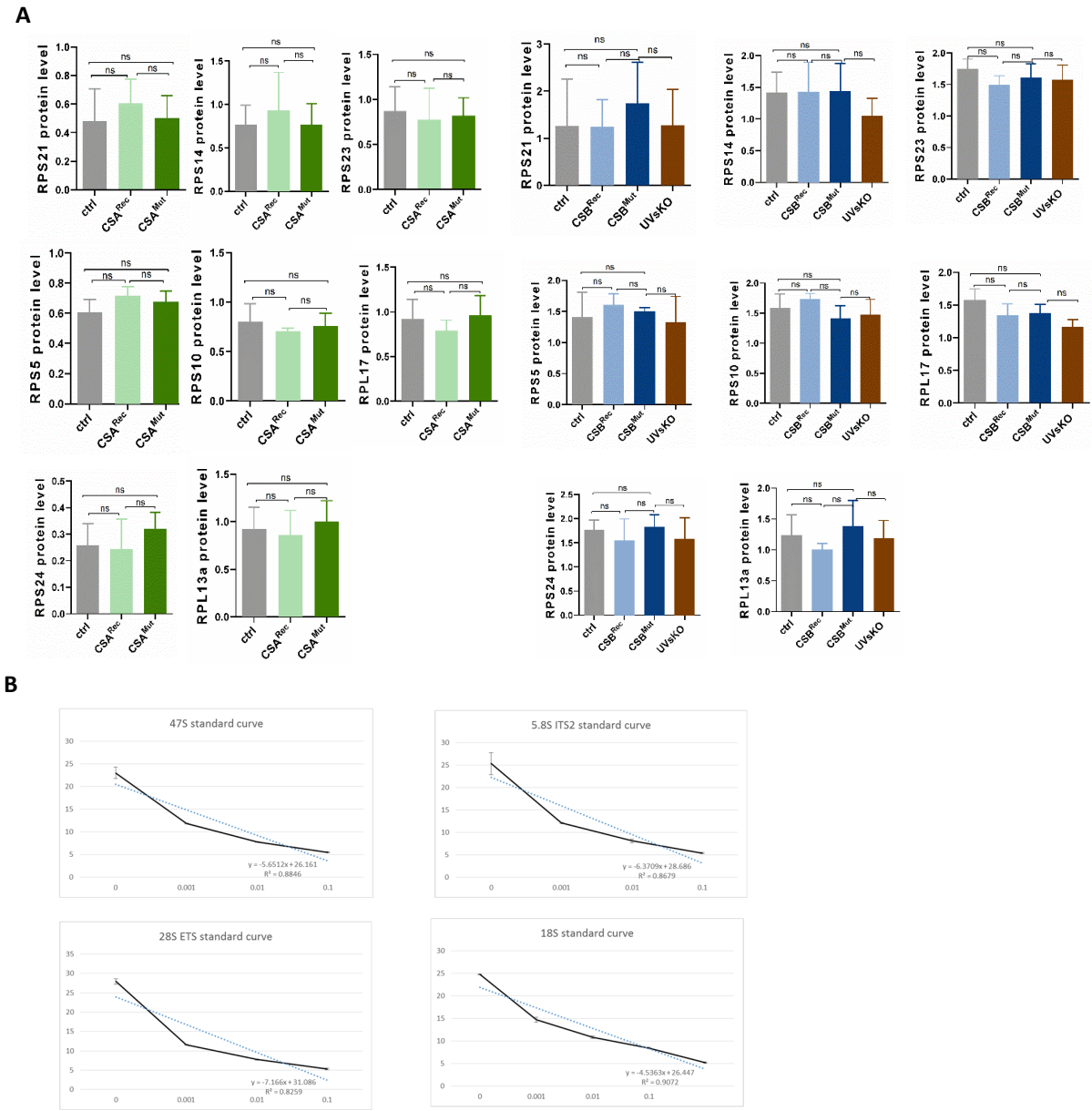


Figure S3 A.Quantification of Western Blots of ribosomal proteins in lysates. Values are represented as mean \pm SD of at least three independent experiments (*= $p < 0.05$, **= $p < 0.01$, ***= $p < 0.001$) **B.** Standard curves for qPCR