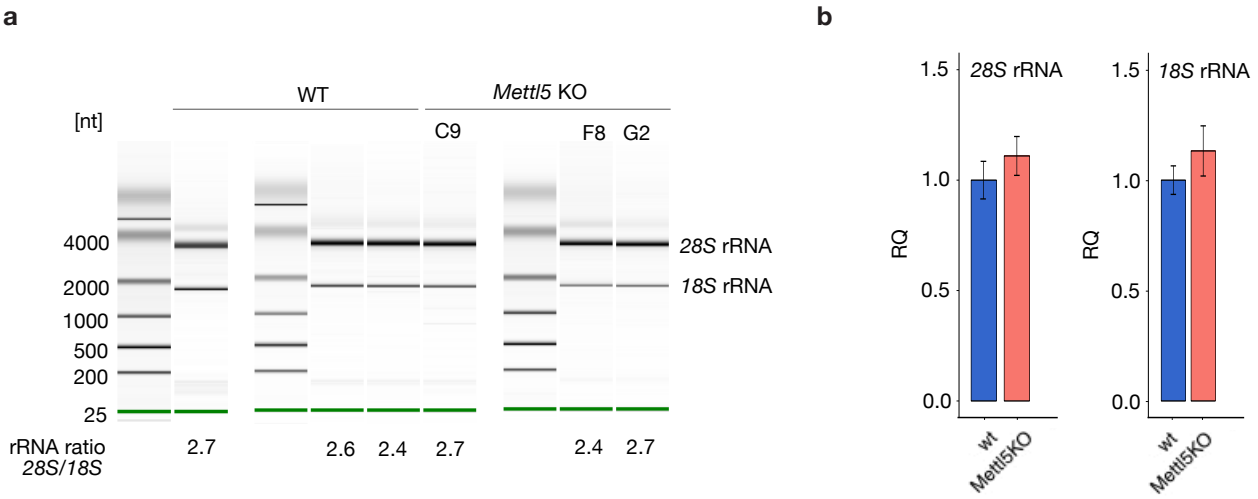
Figure S5


a
WT
Mettl5 KO
[nt]
C9
F8
G2
4000
2000
1000
500
200
25
28S rRNA
18S rRNA
rRNA ratio
28S/18S
2.7
2.6
2.4
2.7
2.4
2.7
b
1.5
28S rRNA
1.0
0.5
0.0
RQ
wt
Mettl5KO
1.5
18S rRNA
1.0
0.5
0.0
RQ
wt
Mettl5KO

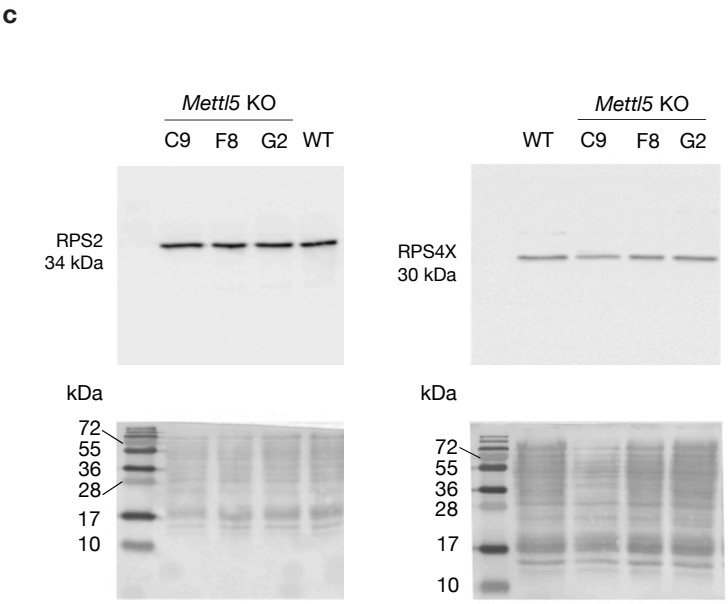

c
Mettl5 KO
C9
F8
G2
WT
RPS2
34 kDa
kDa
72
55
36
28
17
10
Mettl5 KO
WT
C9
F8
G2
RPS4X
30 kDa
kDa
72
55
36
28
17
10

Figure S5. Levels of ribosome components are largely unaltered in *Mettl5* KO mESCs

a. Quantification of *28S* rRNA vs *18S* rRNA ratios by bioanalyzer profiling on total RNA from wt and *Mettl5* KO mESCs (clones C9, F8, G2). The ratio of *28S* RNA to *18S* RNA for three wt controls and three *Mettl5* KO clones is indicated at the bottom.

b. qRT-PCR analysis of the expression levels of *28S* (left) and *18S* rRNA (right) in *Mettl5* KO mESCs compared to wt mESCs after 6 days in Serum-LIF media. Plotted is the relative quantification (RQ) compared to wt displayed as fold change compared to wt. Error bars indicate the standard error on the average of RQ values of three independent KOclones (C9, F8, G2).

c. Immuno blot analysis of RPS2 (left) and RPS4X (right) proteins levels in total cell lysates from wt and *Mettl5* KO (clones C9, F8, G2) mESCs. Ponceau staining (bottom panel) is shown as a loading control.