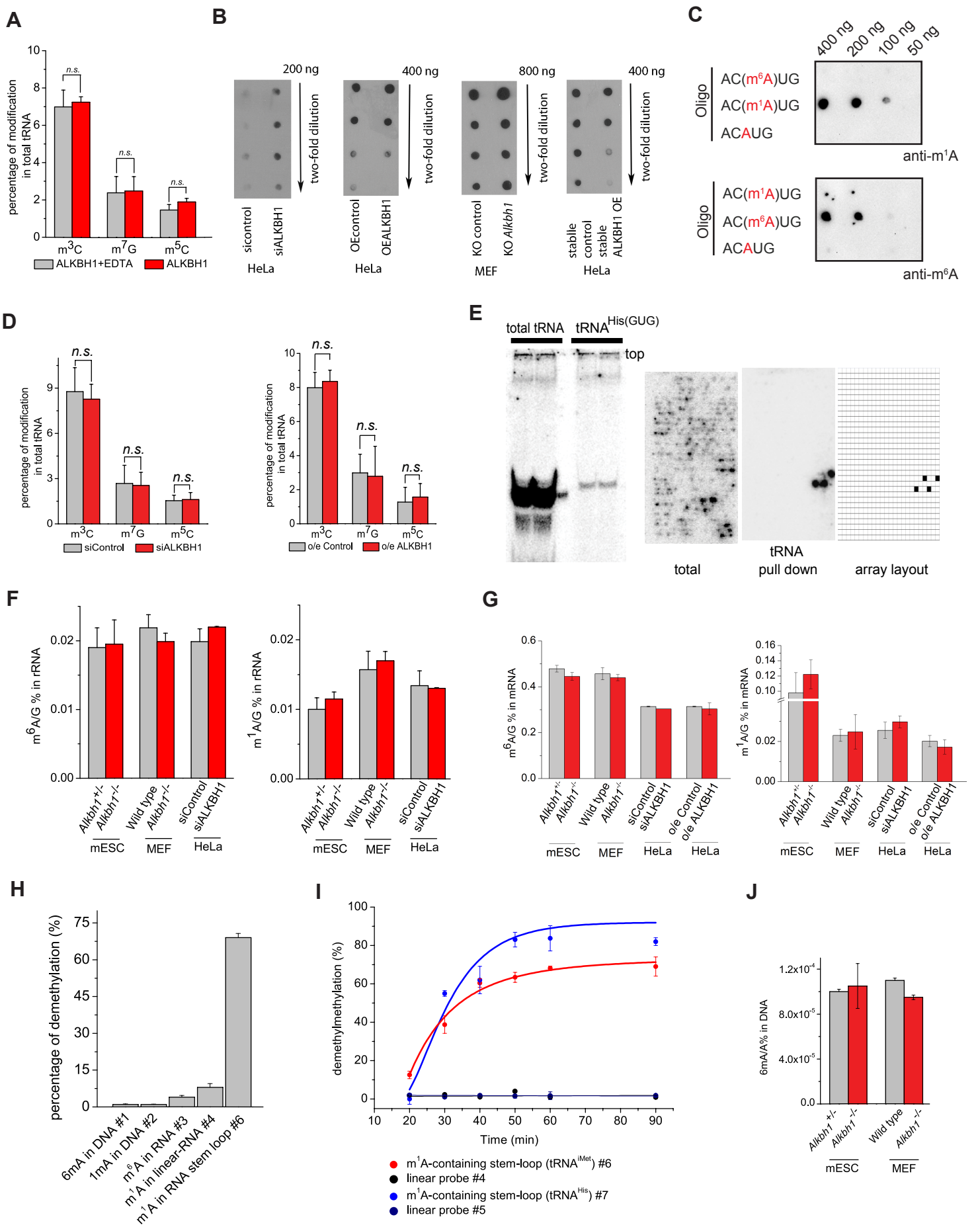
Figure S2


A
percentage of modification in total tRNA
n.s.
m3C
m7G
m5C
ALKBH1+EDTA
ALKBH1
B
200 ng
400 ng
800 ng
400 ng
two-fold dilution
sicontrol
siALKBH1
HeLa
OEcontrol
OEALKBH1
HeLa
KO control
KO Alkbh1
MEF
stablle control
stable ALKBH1 OE
HeLa
C
400 ng
200 ng
100 ng
50 ng
Oligo
AC(m6A)UG
AC(m1A)UG
ACAUG
anti-m1A
AC(m1A)UG
AC(m6A)UG
ACAUG
anti-m6A
D
siControl
siALKBH1
o/e Control
o/e ALKBH1
E
total tRNA
tRNAHis(GUG)
top
total
tRNA pull down
array layout
F
m6A/G % in rRNA
m1A/G % in rRNA
Alkbh1+/- Alkbh1-/-
Wild type Alkbh1-/-
siControl
siALKBH1
mESC
MEF
HeLa
G
m6A/G % in mRNA
m1A/G % in mRNA
o/e Control
o/e ALKBH1
H
percentage of demethylation (%)
6mA in DNA #1
1mA in DNA #2
m6A in RNA #3
m1A in linear-RNA #4
m1A in RNA stem loop #6
I
demethylmethylation (%)
Time (min)
m1A-containing stem-loop (tRNAiMet) #6
linear probe #4
m1A-containing stem-loop (tRNAHis) #7
linear probe #5
J
6mA/A% in DNA