SUPPLEMENTARY DATA

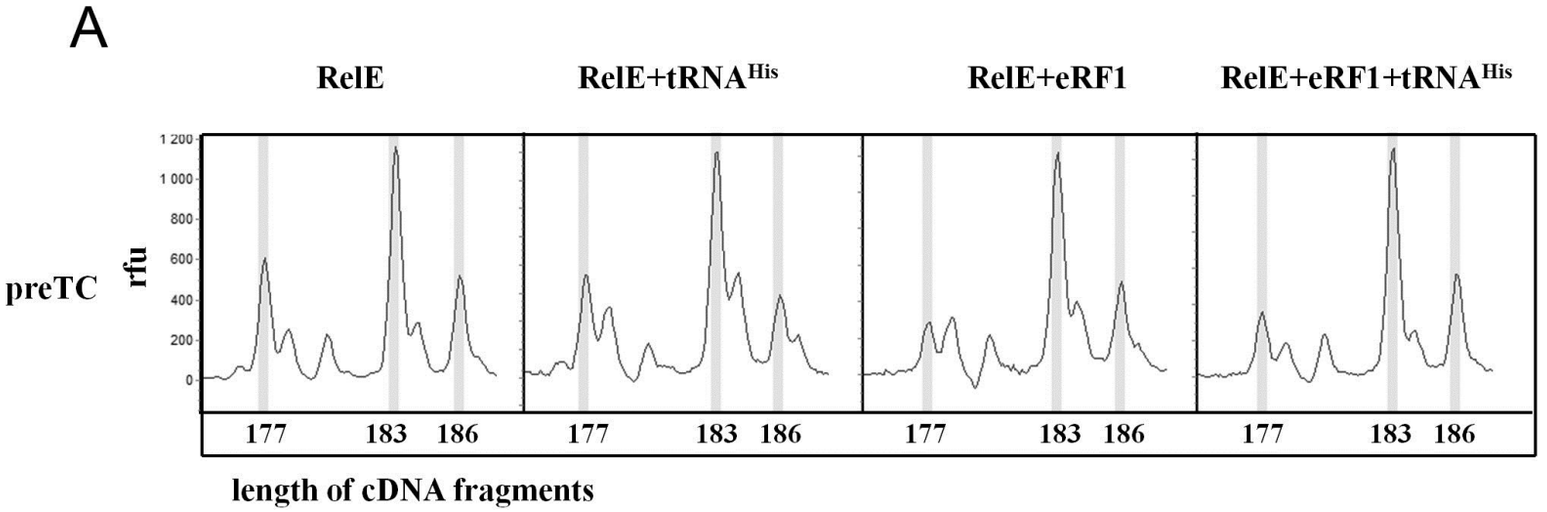
Table S1. Sequences of primers used in $tRNA^{Val2}$ mutagenesis and obtaining of mini-helix structures.

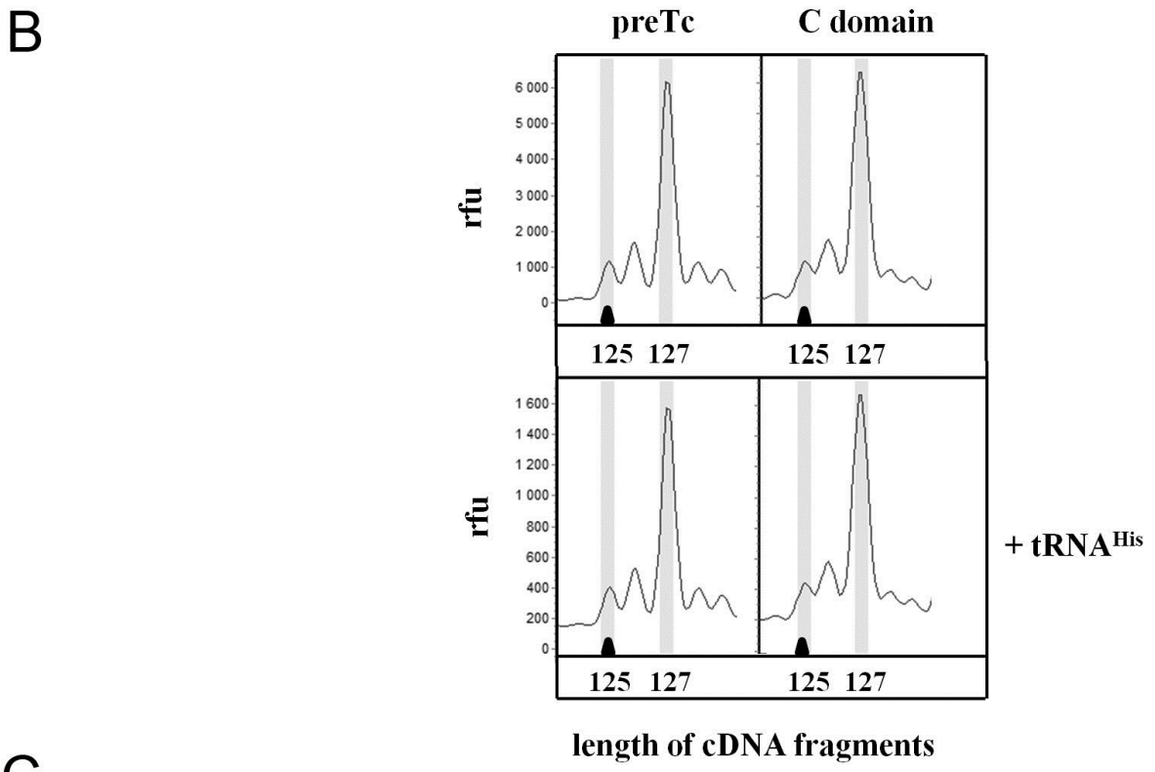
primer	5'-3' sequence
V3_for	AAA AAA AAG CTT CTC CAC ACA TTA CAC CAC CAC CAT
DV9994_for	AAG CTT TAA TAC GAC TCA CTA TAG CTT CTG TAG
DV9994_rev	TCT AGA CCT GGT GCT TCT GCC C
DV9994(GC)_for	AAG CTT TAA TAC GAC TCA CTA TAG GTT CTG TAG
DV9994(GC)_rev	TCT AGA CCT GGT GGT TCT GCC C
DV9994_5'(mini)	AAA AAG CTT TAA TAC GAC TCA CTA TAG CTT CTG CCC GGT TCG AGA CC
DV9994_3'(mini)	AAA TCT AGA CCT GGT GCT TCT GCC CGG TCT CGA ACC GGG CAG AAG C

Figure S1. Additional results, obtained by testing of TC in the presence of $tRNA^{His}$ (**A**) RelE analysis of termination complex stabilized by $tRNA^{His}$. (**B**) Toe-prints with the C domain of eRF1 at UAA stop codon. cDNAs corresponding to preTC and TC have the 127 and 125 nt length, respectively. RFU, relative fluorescence unit. (**C**) The efficiency of hydrolysis of the peptidyl-tRNA in the presence of eRF1, eRF3, GTP and $tRNA^{His}$. All the experiments have been replicated at least three times.

Figure S2. Functional characteristics of tRNA mutants. Toe-prints of preTC obtained during elongation of translation with $tRNA^{Val2}$, $tRNA^{Val(CG)}$, $tRNA^{Val(GC)}$. cDNAs corresponding to preTC, TC and RelE-print have the 127, 125 and 184 nt length, respectively. RFU, relative fluorescence unit.

Figure S3. Structure of H68 and H69 helixes from the yeast 25S rRNA. Grey selections show nucleotides participating in interaction of the ribosome with acceptor stem of E site tRNA and N domain of eRF1.


A
RelE
RelE+tRNA^His
RelE+eRF1
RelE+eRF1+tRNA^His
preTC
rfu
1 200
1 000
800
600
400
200
0
177
183
186
length of cDNA fragments


B
preTc
C domain
rfu
6 000
5 000
4 000
3 000
2 000
1 000
0
125
127
1 600
1 400
1 200
1 000
800
600
400
200
+ tRNA^His
length of cDNA fragments

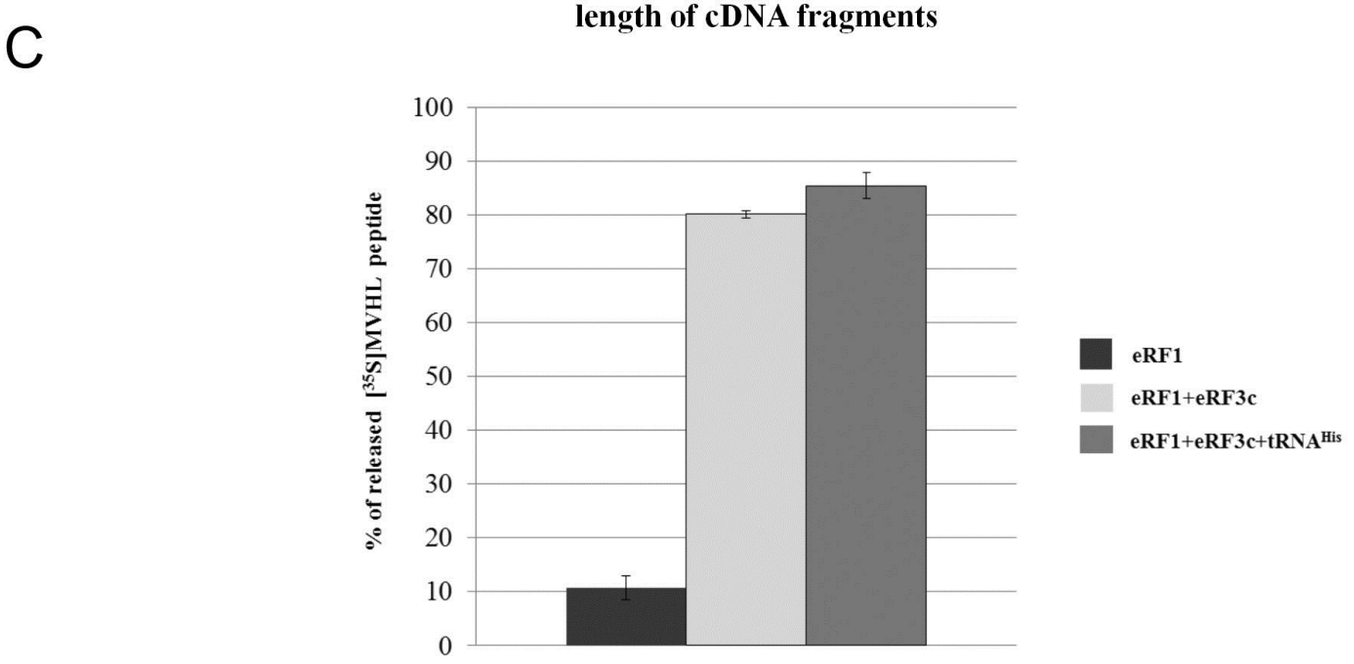

C
% of released [35S]MVHL peptide
100
90
80
70
60
50
40
30
20
10
0
eRF1
eRF1+eRF3c
eRF1+eRF3c+tRNA^His

Figure S1.

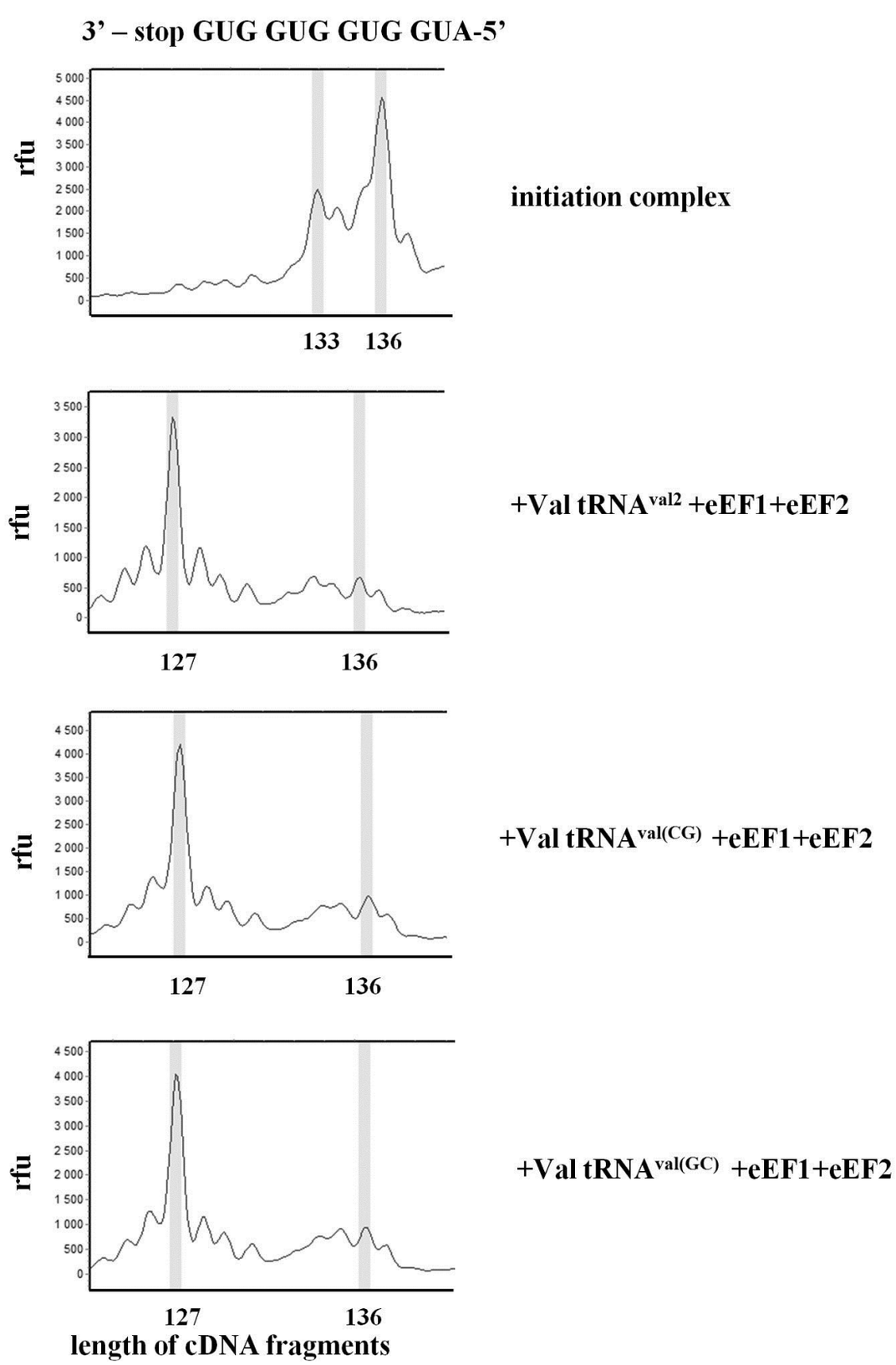

3' – stop GUG GUG GUG GUA-5'
rfu
initiation complex
133
136
+Val tRNA^val2 +eEF1+eEF2
127
136
+Val tRNA^val(CG) +eEF1+eEF2
127
136
+Val tRNA^val(GC) +eEF1+eEF2
127
136
length of cDNA fragments

Figure S2.

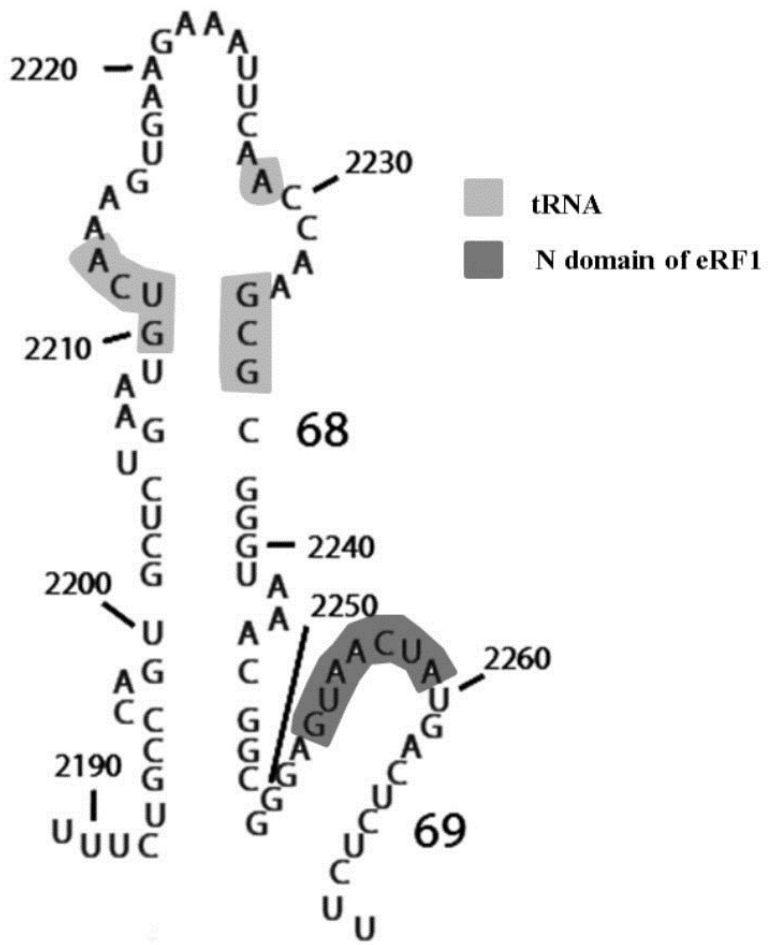

2220
2230
2210
2200
2190
2240
2250
2260
68
69
tRNA
N domain of eRF1

Figure S3.