

Supporting tables

5'UTR variant*	GenBank Acc. No.:	Length [nt]	uAUGs [no.]	GC-content [%]	ΔG [kcal/mol]	Translation** efficiency [%]
control	-	29	0	55.17	-6.3	100
A	AY286465.1	211	4	54.98	-69.0	24.09
B	AY286466.1	229	5	54.15	-82.0	12.08
C	AY286467.1	195	4	56.41	-77.5	14.99
D	AY286468.1	314	5	48.09	-95.0	7.01
E	AY286469.1	305	5	47.54	-92.5	7.99
F	AY286470.1	339	7	58.41	-128.9	4.02
G	AY286471.1	388	6	52.84	-127.0	3.00

Table S1. Basic characteristics of selected TR β 1 5'UTR variants A-G.

Prediction of secondary structures of 5'UTRs was performed as described in bioinformatic analysis. The least and most folded TR β 1 variants are shown in bold. uAUGs represent start codons located upstream of the main start codon and Kozak consensus sequence. *TR β 1 5'UTR splice variants termed according to Frankton et al 2004. ** Translation efficiency measured with RTS 100 Wheat Germ CECF system.