



Supplementary information

Flow-seq evaluation of translation driven by a set of natural *Escherichia coli* 5'-UTR of variable length

Ekaterina S. Komarova¹, Anna N. Slesarchuk², Maria P. Rubtsova², Ilya A. Osterman³, Alexey E. Tupikin⁴, Dmitry V. Pyshnyi⁴, Olga A. Dontsova^{2,3,5,6}, Marsel R. Kabilov^{4*} and Petr V. Sergiev^{1,2,3,6*}

¹ Institute of Functional Genomics, Lomonosov Moscow State University, 119992, Moscow, Russia

² Department of Chemistry, Lomonosov Moscow State University, Moscow, 119991, Russia

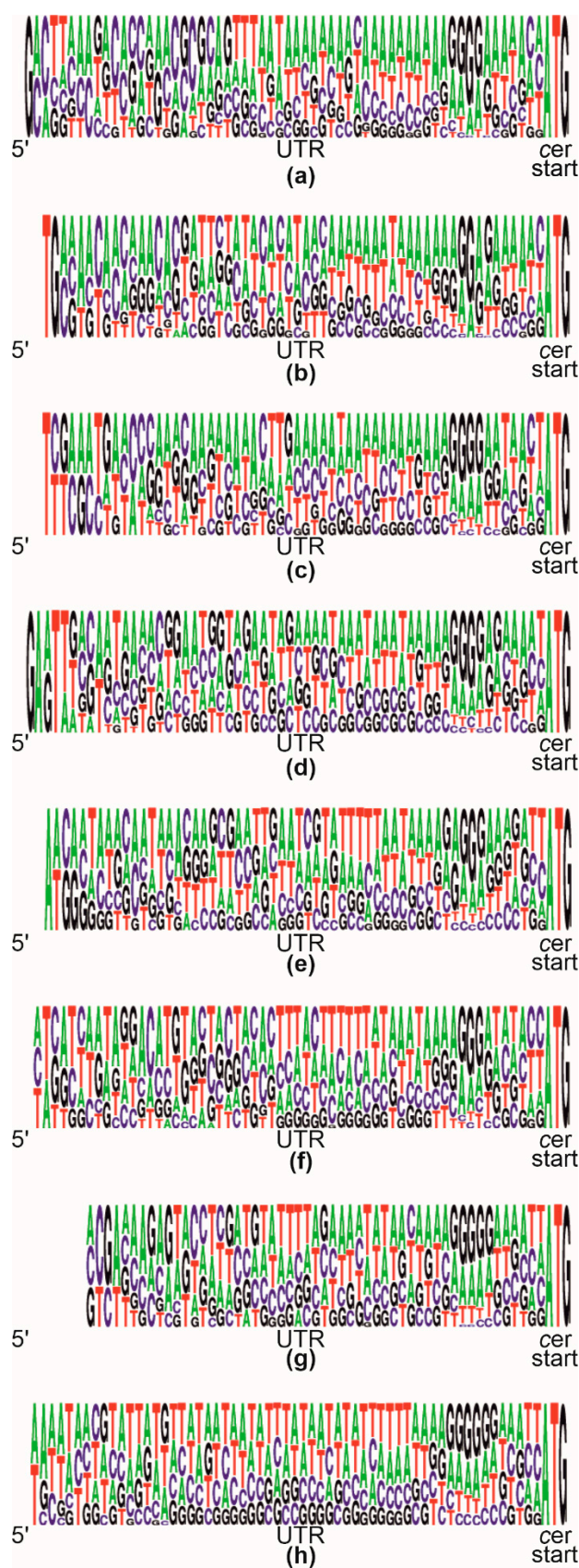
³ Center for Life Sciences, Skolkovo Institute of Science and Technology, Skolkovo, Moscow region 143025, Russia

⁴ Institute of Chemical Biology and Fundamental Medicine, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, 630090, Russia

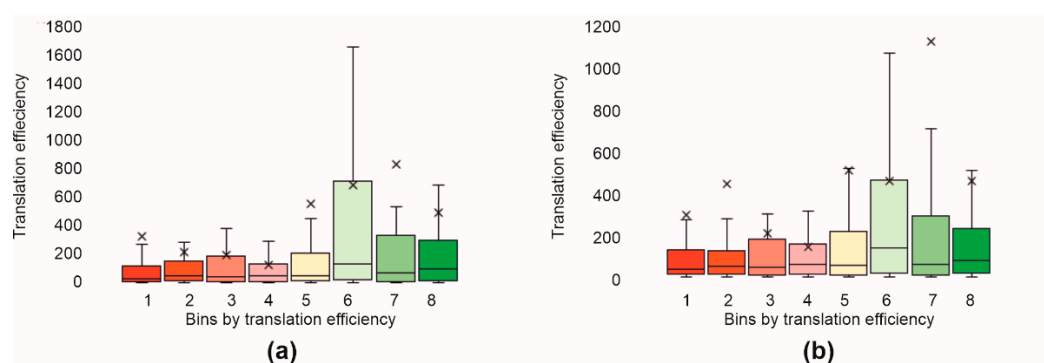
⁵ Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, Russian Academy of Sciences, Moscow 119992, Russia

⁶ Belozersky Institute of Physico-Chemical Biology, Lomonosov Moscow State University, Moscow 119992, Russia

* Correspondence: petya@genebee.msu.ru (P.V.S.) and kabilov@niboch.nsc.ru (M.R.K.)



Supplementary Figure S1. Nucleotide composition of the 5'-UTR sequences sorted by translation efficiency shown as sequence logo [1]. (a-h) Bins from 1 to 8, ordered by increase in translation efficiency. The sequences are aligned by their 3'-edge (ATG start codon). Height of a letter represents an occurrence of particular nucleotide at particular position of the 5'-UTR.



Supplementary Figure S2. Comparison of translation efficiencies observed by Flow-seq and those obtained by ribosome profiling. **(a)** Bins sorted by translation efficiency are marked below the bars. Y-axis corresponds to the translation efficiency determined by ribosome profiling in [2]. **(b)** The same as (a) for the ribosome profiling described in [3]. Quartile ranges are shown as solid bars (25% to 50%)

Supplementary references

1. Crooks, G.E.; Hon, G.; Chandonia, J.-M.; Brenner, S.E. WebLogo: A Sequence Logo Generator: Figure 1. *Genome Res.* **2004**, *14*, 1188–1190, doi:10.1101/gr.849004.
2. Elgamal, S.; Katz, A.; Hersch, S.J.; Newsom, D.; White, P.; Navarre, W.W.; Ibba, M. EF-P Dependent Pauses Integrate Proximal and Distal Signals during Translation. *PLoS Genet* **2014**, *10*, e1004553, doi:10.1371/journal.pgen.1004553.
3. Kannan, K.; Kanabar, P.; Schryer, D.; Florin, T.; Oh, E.; Bahroos, N.; Tenson, T.; Weissman, J.S.; Mankin, A.S. The General Mode of Translation Inhibition by Macrolide Antibiotics. *Proc Natl Acad Sci USA* **2014**, *111*, 15958–15963, doi:10.1073/pnas.1417334111.