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Length-dependent translation initiation benefits the functional proteome of human cells

Jieming Guo, Xinlei Lian, Jiayong Zhong, Tong Wang, Gong Zhang

Supplementary Materials

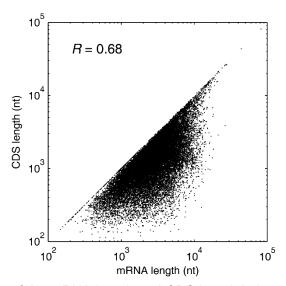


Figure S1: Correlation of the mRNA length and CDS length in human hg19 RefSeq-RNA database (downloaded from UCSC Genome Browser on 1.21.2013). Spearman R=0.68, P<10⁻¹⁶.

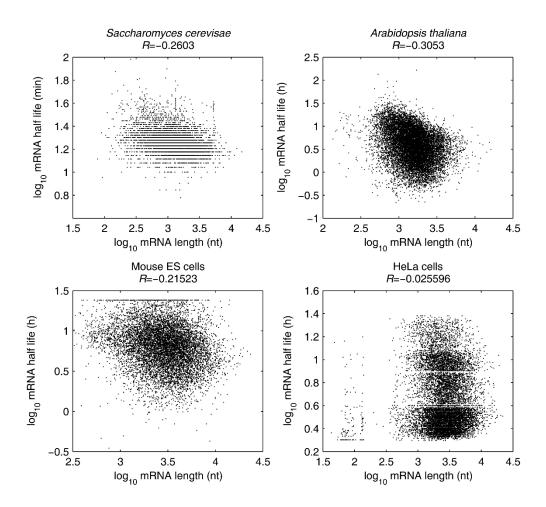


Figure S2: mRNA half life is minimally correlated with mRNA length in *Saccharomyces cerevisiae*, *Arabidopsis thaliana*, mouse embryonic stem cells and human HeLa cells. Data were obtained from literatures (Munchel et al., 2011; Narsai et al., 2007; Sharova et al., 2009; Tani et al., 2012).

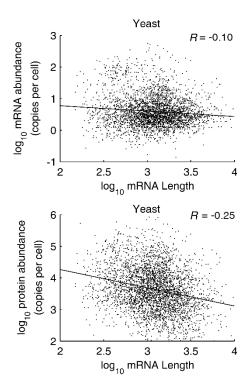


Figure S3: The mRNA abundance and protein abundance versus mRNA length in fission yeast. Data were obtained from literature (Marguerat et al., 2012).

References

Marguerat, S., Schmidt, A., Codlin, S., Chen, W., Aebersold, R., and Bahler, J., 2012. Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. Cell 151, 671-683.

Munchel, S.E., Shultzaberger, R.K., Takizawa, N., and Weis, K., 2011. Dynamic profiling of mRNA turnover reveals gene-specific and system-wide regulation of mRNA decay. Mol Biol Cell 22, 2787-95.

Narsai, R., Howell, K.A., Millar, A.H., O'Toole, N., Small, I., and Whelan, J., 2007. Genome-wide analysis of mRNA decay rates and their determinants in Arabidopsis thaliana. Plant Cell 19, 3418-36.

Sharova, L.V., Sharov, A.A., Nedorezov, T., Piao, Y., Shaik, N., and Ko, M.S., 2009. Database for mRNA half-life of 19 977 genes obtained by DNA microarray analysis of pluripotent and differentiating mouse embryonic stem cells. DNA Res 16, 45-58.

Tani, H., Mizutani, R., Salam, K.A., Tano, K., Ijiri, K., Wakamatsu, A., Isogai, T., Suzuki, Y., and Akimitsu, N., 2012. Genome-wide determination of RNA stability reveals hundreds of short-lived noncoding transcripts in mammals. Genome Res 22, 947-56.