

# Tissue-specific landscape of translation machinery components

P-02.1-31

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Protein synthesis is vital for the majority of cell types. Diversely differentiated cells require specific translation regulation, which suggests specialization of translation machinery across tissues and organs. Using data from GTEx, FANTOM, and Gene Atlas we systematically explored the abundance of transcripts coding for translation factors and aminoacyl-tRNA synthetases (ARSases) in normal and cancer human tissues. We recovered a few known and identified several novel cases of a strict tissue-specific expression of particular transcripts. Among those there were eEF1A1, eEF1A2, PABPC1L, PABPC3, eIF1B, eIF4E1B, eIF4ENIF1, and eIF5AL1. Furthermore, our analysis revealed pervasive tissue-specificity of relative abundance of transcripts encoding components of the translation machinery (e.g. paralogs of PABP, eRF3, and eIF5MP, as well as eIF2B subunits and some ARSases), suggesting presumptive variance in composition of translation initiation, elongation, and termination complexes. These conclusions were largely confirmed by the analysis of proteomic data. Finally, we paid attention to a sex-specific difference in the repertoire of translation factors encoded in sex chromosomes (eIF1A, eIF2 $\gamma$ , and DDX3) and identified ovary, testis, and brain as organs with the most diverged expression patterns.

N.M.K., A.A.E., and S.E.D. are part of the Interdisciplinary Scientific and Educational School of Moscow University «Molecular Technologies of the Living Systems and Synthetic Biology». The work was supported by the Russian Science Foundation (grant no. 18-14-00291 to S.E.D.)

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