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Imaging translation dynamics in live embryos reveals spatial heterogeneities.

The translation of individual mRNA molecules is a key biological process, yet this multi-step process has never been imaged in living multicellular organisms. Here we deploy the recently developed Suntag method to visualize and quantify translation dynamics of single mRNAs in living Drosophila embryos. By focusing on the translation of the conserved major epithelial-mesenchymal transition (EMT)-inducing transcription factor Twist, we identified spatial heterogeneity in mRNA translation efficiency and reveal the existence of translation factories, where clustered mRNAs are co-translated preferentially at basal perinuclear regions. Simultaneous visualization of transcription and translation dynamics in a living multicellular organism opens exciting new avenues for understanding of gene regulation during development.