

多重化 RNA モチーフライブラリを用いた RNA 構造総体における  
機能的相互作用の発見

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RNA structure-wide discovery of functional interactions with  
multiplexed RNA motif library

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Biochemical assays and computational analyses have discovered RNA structures throughout various transcripts. However, the roles of these structures are mostly unknown. Here we develop folded RNA element profiling with structure library (FOREST), a multiplexed affinity assay system to identify functional interactions from transcriptome-wide RNA structure datasets. We generate an RNA structure library by extracting validated or predicted RNA motifs from gene-annotated RNA regions. The RNA structure library with an affinity enrichment assay allows for the comprehensive identification of target-binding RNA sequences and structures in a high-throughput manner. As a proof-of-concept, FOREST discovers multiple RNA-protein interaction networks with quantitative scores, including translational regulatory elements that function in living cells. Moreover, FOREST reveals different binding landscapes of RNA G-quadruplex (rG4) structures-binding proteins and discovers rG4 structures in the terminal loops of precursor microRNAs. Overall, FOREST serves as a versatile platform to investigate RNA structure-function relationships on a large scale.