HCV IRES Secondary Structure Search in Human 5’UTRs

Cap-independent translation is a well-known mechanism that viral RNAs use to promote their transcription at the expense of cellular mRNAs. Though typical for viruses, a fraction of human genes has been shown in vitro to use this mechanism as well. Key to this process is a so-called internal ribosomal entry site (IRES) - an RNA element able to recruit ribosomes without the canonical set of transcription factors. The function of IRESs is closely tied to their structure and until now, 4 major types of IRESs have been described, differing in the structural organization. Type IV is also known as HCV-like IRES - named after the notorious human pathogen - Hepatitis C virus (HCV). This work

hypothesizes, that a structure similar to the one of HCV IRES can be found in human 5’UTR sequences and proposes a computational pipeline that outputs potential candidates resembling the target structure. The keystones of the pipeline are programs RSEARCH and NA2Dsearch. RSEARCH provides a fast and broad collection of preliminary matches, NA2DSearch subsequently filters the

matches via folding and structural matching. We present 118 findings in 5’UTR regions that contain structural motifs, which in silico may exhibit transcription regulatory capabilities of HCV IRES.