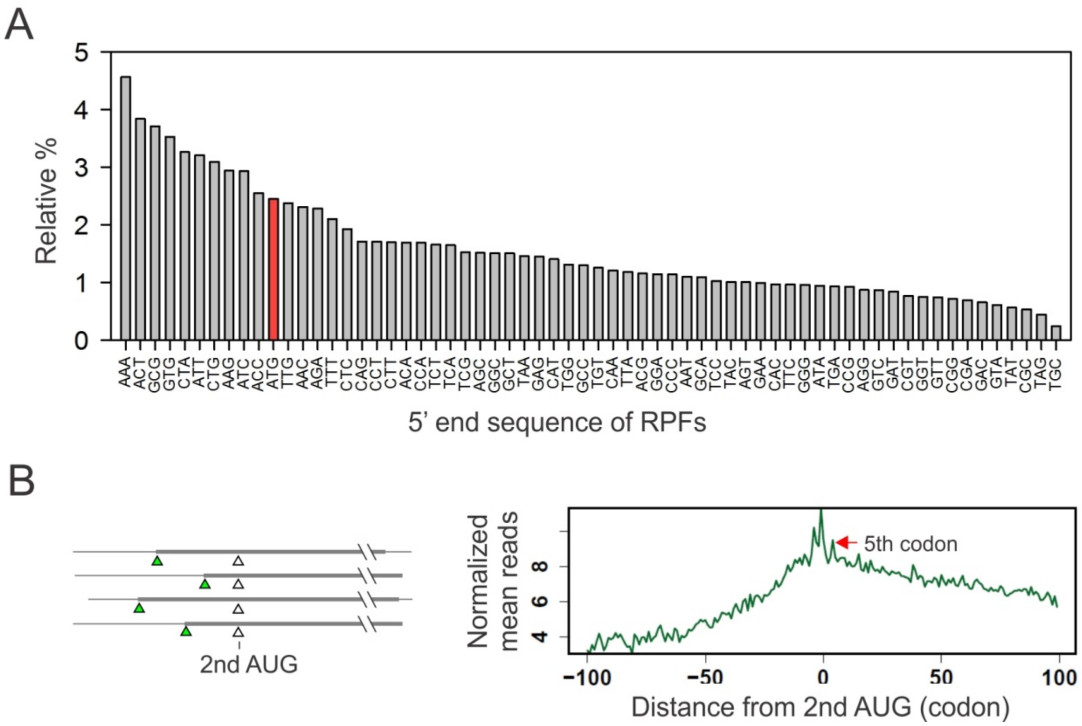

Figure S4. Characterizing RPFs starting with AUG.

(**A**) Relative percentage of RPFs with all possible triplet sequences is computed across the entire mapped RPF reads. The red bar indicates the RPF starting with AUG.

(**B**) Metagene analysis of RPFs obtained from HEK293 cells treated with CHX. All mapped reads are aligned at the second AUG after the annotated start codon. The reads density at each codon position is averaged using the P-site of RPFs. The red arrow indicates the 5th codon position.