Table S1.
Number of RPFs from 26 to 32 nt long that map the transcriptome, excluding rRNA, tRNA, snoRNA, snRNA and misc RNA. The percentage of reads per size is indicated.

Table S2.
(A) All smORFs (from all possible isoforms), defined as actively translated by ORFscore (strict + relaxed) in Zebrafish.
(B) PhyloCSF results for all conserved smORFs in zebrafish
(C) All smORFs (from all possible isoforms), defined as actively translated by ORFscore (strict) in human.
(D) PhyloCSF results for all conserved smORFs in human

File S1.
Subcodon profiles for genes with non-redundant smORFs in Zebrafish. A selected coding smORF in each gene is marked with an asterisk and its amino acid sequence shown below.

File S2.
Subcodon profiles for genes with non-redundant smORFs in Human. A selected coding smORF in each gene is marked with an asterisk and its amino acid sequence shown below.