



Figure 1-figure supplement 2: The proportion of altORFs with a translation initiation site (TIS) with a Kozak motif in hg38 is significantly different from 100 shuffled hg38 transcriptomes.

Percentage of altORFs with a TIS within an optimal Kozak sequence in hg38 (dark blue) compared to 100 shuffled hg38 (light blue). Mean and standard deviations for sequence shuffling are displayed, and significant difference was defined by using one sample t test. **** $P < 0.0001$. Note that shuffling all transcripts in the hg38 transcriptome generates a total of 489,073 altORFs on average, compared to 539,134 altORFs in hg38. Most transcripts result from alternative splicing and there are 183,191 unique altORFs in the hg38 transcriptome, while the 489,073 altORFs in shuffled transcriptomes are all unique. Figure 1g shows the percentage of unique altORFs with a kozak motif (15%), while the current Fig. shows the percentage of altORFs with a kozak motif relative to the total number of altORFs (14%).