



Figure 4 - Supplemental Figure 12: Global characterization of AFE. (A) Length distribution of first exon from exclusion (CTL) exon and inclusion (LPS) exon. (B) Graph of the length difference between the exclusion and inclusion exons, also known as ΔAFE . (C) All potential UTR motifs were identified using RegRNA2.0 for either the exclusion (CTL) or inclusion (LPS) specific first exons.