



Figure 1 - Supplemental Figure 1: Computational Pipeline and comparison of t-test and DRIMSeq alternative splicing events. (A) Bioinformatic pipeline for Human and Mouse RNA-seq data. Alternative splicing event type classification of significant differential splicing events ($|\Delta\text{PSI}| \geq 10$ and corrected $p\text{-value} \leq 0.25$) in Human and Mouse macrophages +/- LPS as identified and quantified using the (B) t-test with JuncBASE or (C) the Dirichlet-multinomial framework applied by DRIMSeq. Venn Diagrams representing the unique and overlapping AFE events from (D) Human or (E) Mouse macrophage alternative splicing analysis.