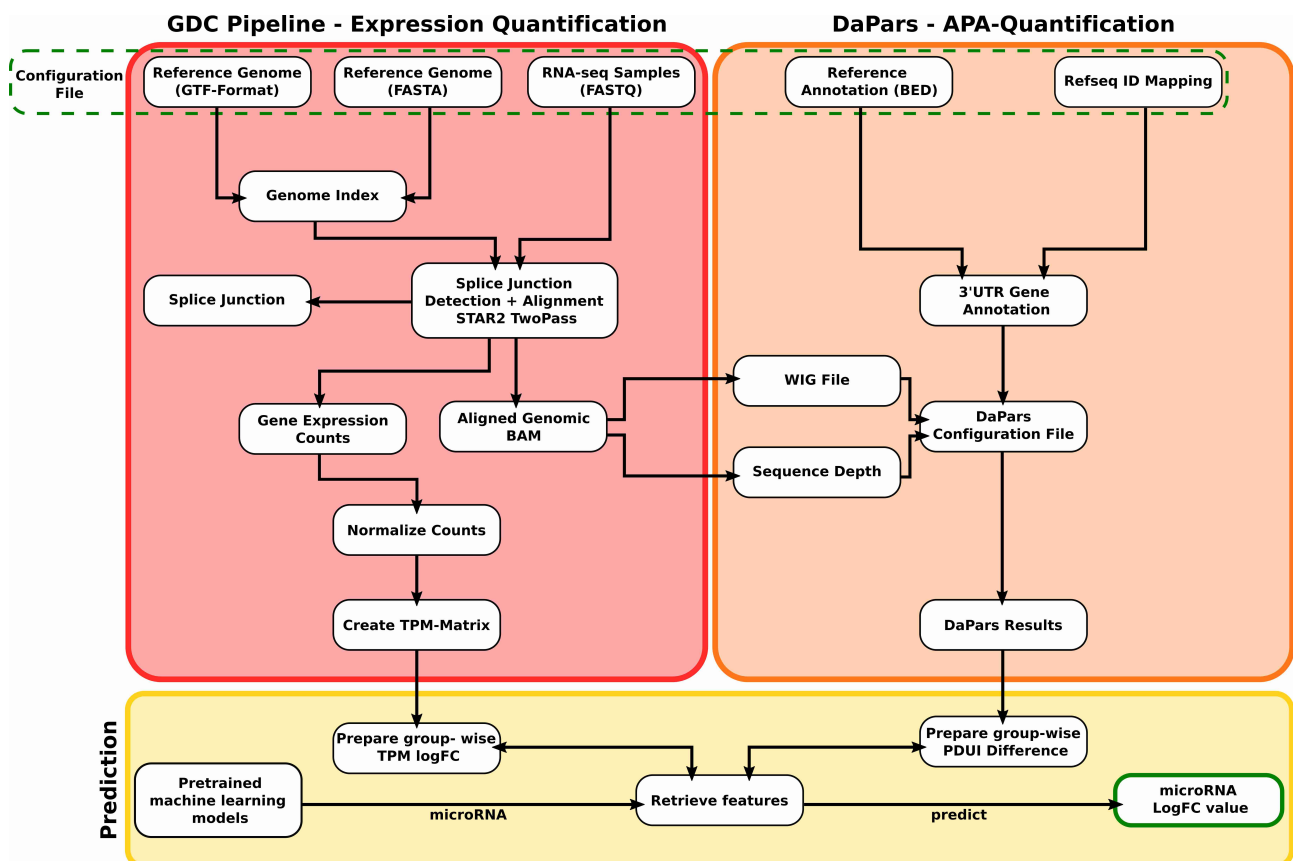




Supplementary Figure 1. MIRNAPEX workflow.

Schematic of the MIRNAPEX pipeline, showing how RNA-seq reads are aligned and quantified, 3'UTR usage is estimated with DaPars, and expression and APA features are combined with reference annotations to feed the pre-trained models that predict miRNA log-fold changes.