



**Additional file 2: Supplementary Figure 1. Schematics of the initial ADAR site identification pipeline used in this study.** The pipeline shown here was used to generate annotated and unannotated sites shown in the Figure 2 prior to the subsequent refinement based on the Sanger validation. The diagram shows the 3 major steps in pipeline: (1) the initial calling of the candidate editing sites from RNA-seq data, (2) filtration of false positives and (3) overlap with annotated databases.