**TABLE S1.**  p-values for all parameters tested for both MJESs and IPSs in RPS12.

**TABLE S2.** p-values for all parameters tested for both MJESs and IPSs in ND7-5’.

**TABLE S3.** Oligonucleotides used in this study.

**FIGURE S1.** Screenshots of TREAT program web-based user interface. *(A)* Screenshot of the Overview page where constrainable graphs can be generated based on user-defined search parameters. Multiple samples can be viewed on the same graphs (not shown). The graph image can be exported in several file formats via a dropdown box at the top right of each graph. The data used to generate the graph can be exported as a csv file using the Export button at the top left of each graph. *(B)* Search page where queries return a list of sequences meeting the criteria entered into the search bar by the user. Each unique sequence is depicted in a row where basic data is summarized. This includes both the merge count and normalized count for the sequences, as well as junction sequence, junction end, and Editing Stop Site. Each unique sequence is clickable to allow the user examine the full length sequence aligned with the templates. The tables in the search pages are exportable as .csv files for further analysis. *(C)* Appearance of an individual sequence alignment following selection from the Search page. Blue represents fully edited sequence, green pre-edited, and yellow the optional alternatively edited templates as input by the user. The color of each editing site in the unique sequence (bottom line, RD) is set to match the template to which it corresponds, and the matching editing site in the template is bolded for ease of identification. The junction region is coded purple.

**FIGURE S2.** The distribution of pausing across ESs suggests a non-normal distribution and the presence of outliers within the data. The density plot of the number of sequences that pause at any given Editing Stop Site is shown for all three replicates of RPS12 (top row) and ND7-5’ (bottom row). The Outlier Threshold, calculated as described in the Materials and Methods section, is shown as a vertical red line in each graph.

**FIGURE S3.**  Distribution of junction lengths shown in nucleotides. Each unique sequence is depicted as an open circle graphed to show its junction length in nucleotides (NT) versus its ESS. RPS12 (A); ND7-5’ *(B).*

**FIGURE S4.** MJESs requiring deletion have undergone a mix of canonical and non-canonical deletion action. *(A)* The percentage of sequences at the MJESs requiring deletions that have received any deletion action. *(B)* The breakdown by site for the percentage of sequences at