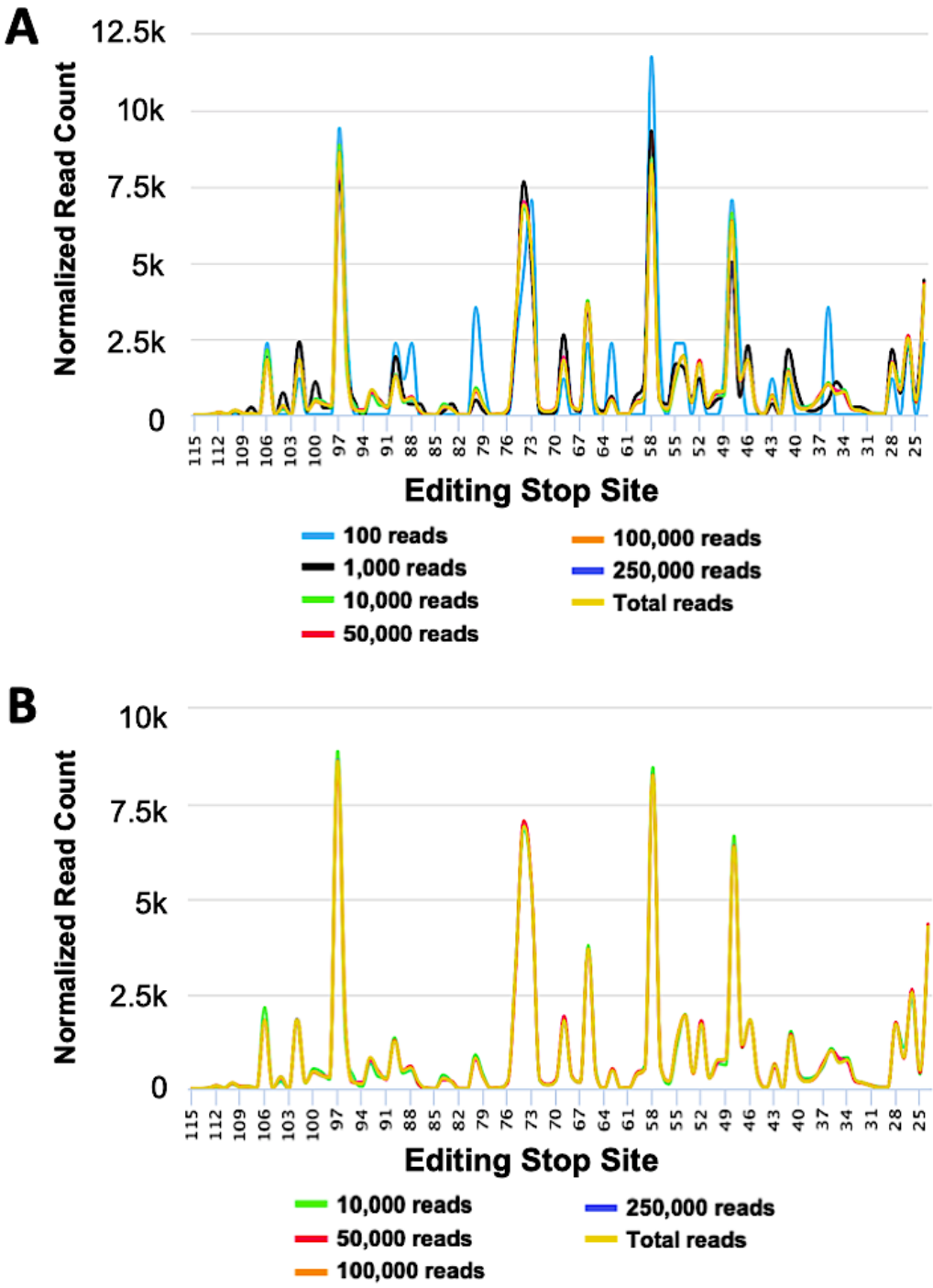
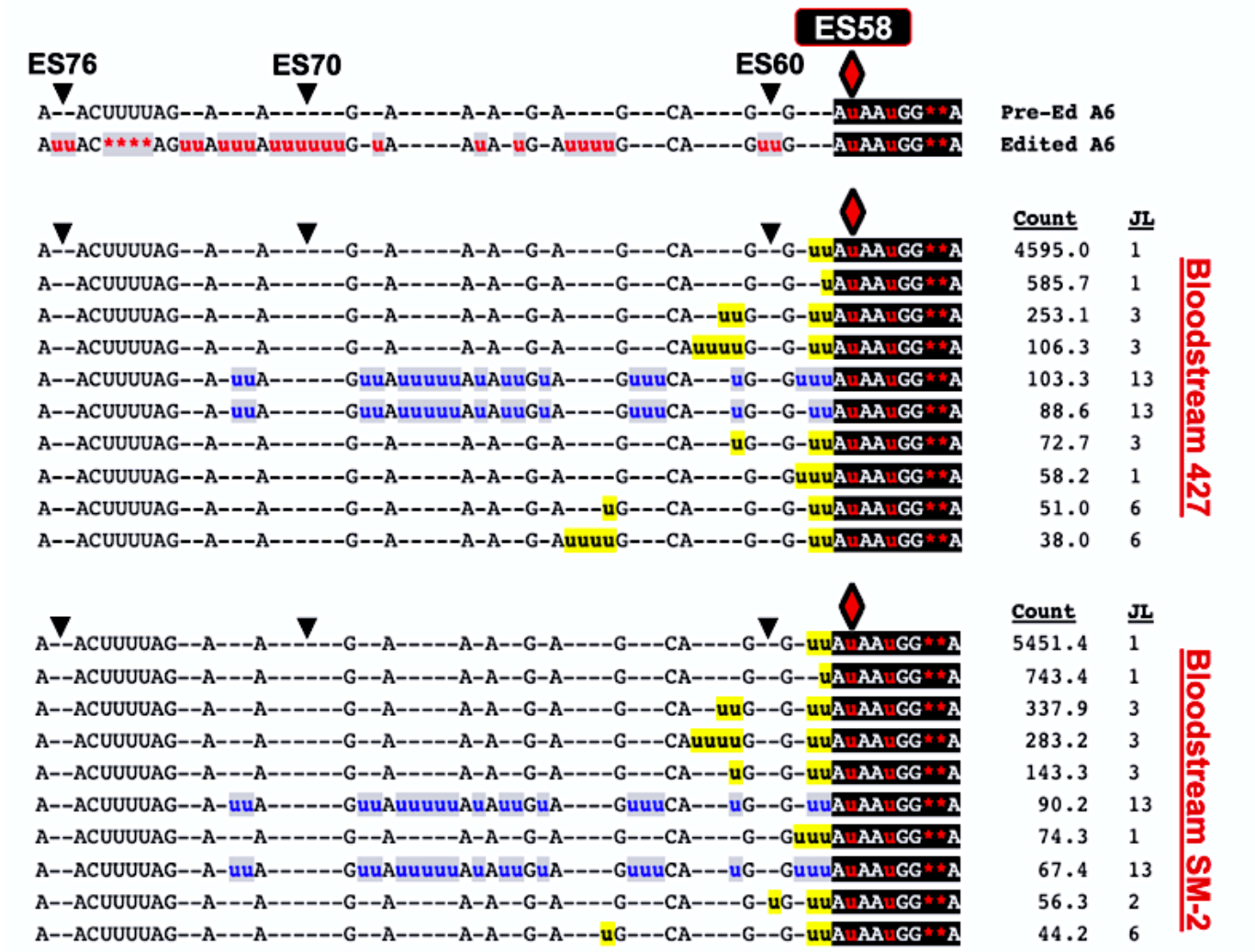


Supplementary Figure 1. Bioinformatic downsampling analysis of PCF A6 mRNA read counts. Standard TREAT processing was followed for read pair merging and adapter trimming. Trimmed sequences were then randomly selected without replacement using a reservoir sampling method found here: https://github.com/alexpreynolds/sample. (**A**) The TREAT peak profiles for 100 reads, 1,000 reads, 10,000 reads, 50,000 reads, 100,000 reads, 250,000 reads and the full dataset were loaded for each sample. For the 100-read and 1,000-read samples, degradation of the signal can be seen. 10,000 and above show nearly identical profiles. (**B**) TREAT peak profiles with the 100-read and 1,000-read samples removed to illustrate the consistency of the peaks among the remaining samples. An editing stop site is the 5'-most ES of continuous and uninterrupted canonical editing in a partially edited mRNA. Every editing site that is 3' of the editing stop site is, therefore, also canonically edited.



Supplementary Figure 2. Statistical and bioinformatics analysis of A6 mRNA editing intermediates at ES58 in BSF 427 and BSF SM-2 cells. Sequence alignments of the 10 most abundant junction sequences at ES58 in A6 mRNA of BSF 427 and SM-2 cells. Symbols and shading as in Fig. 8b.