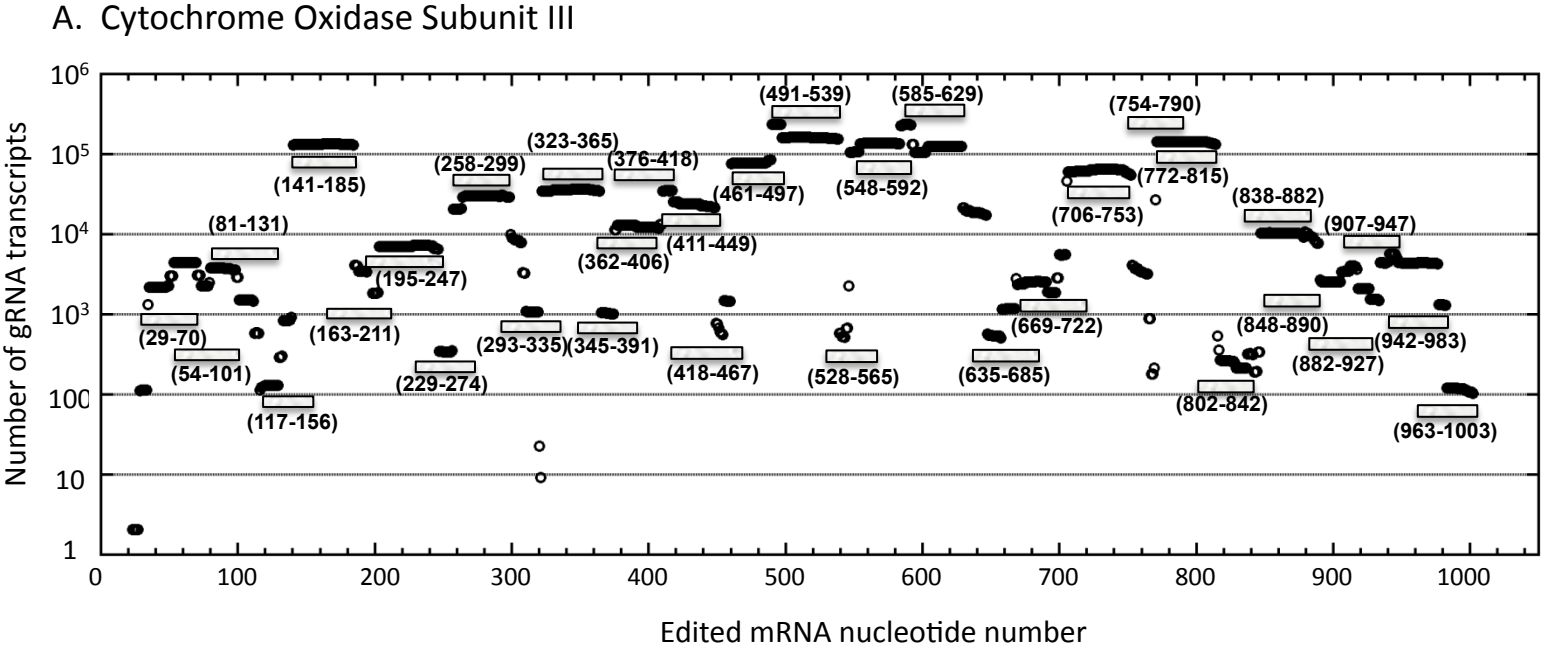
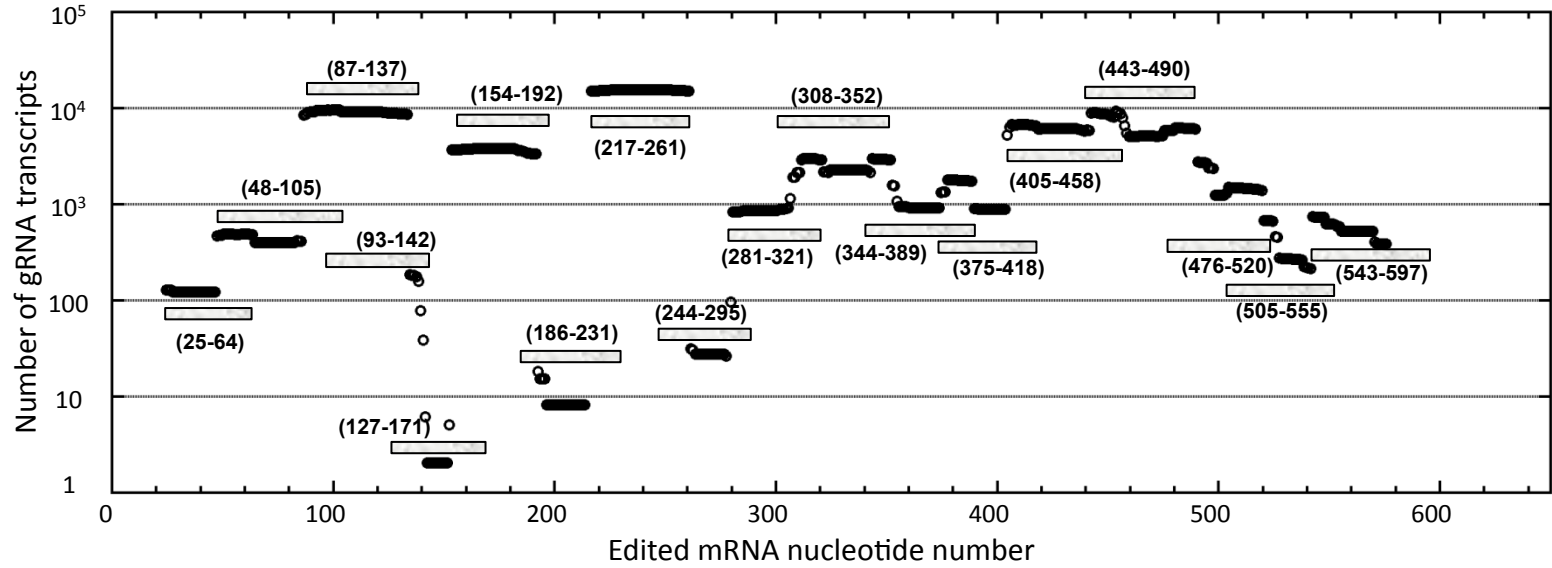


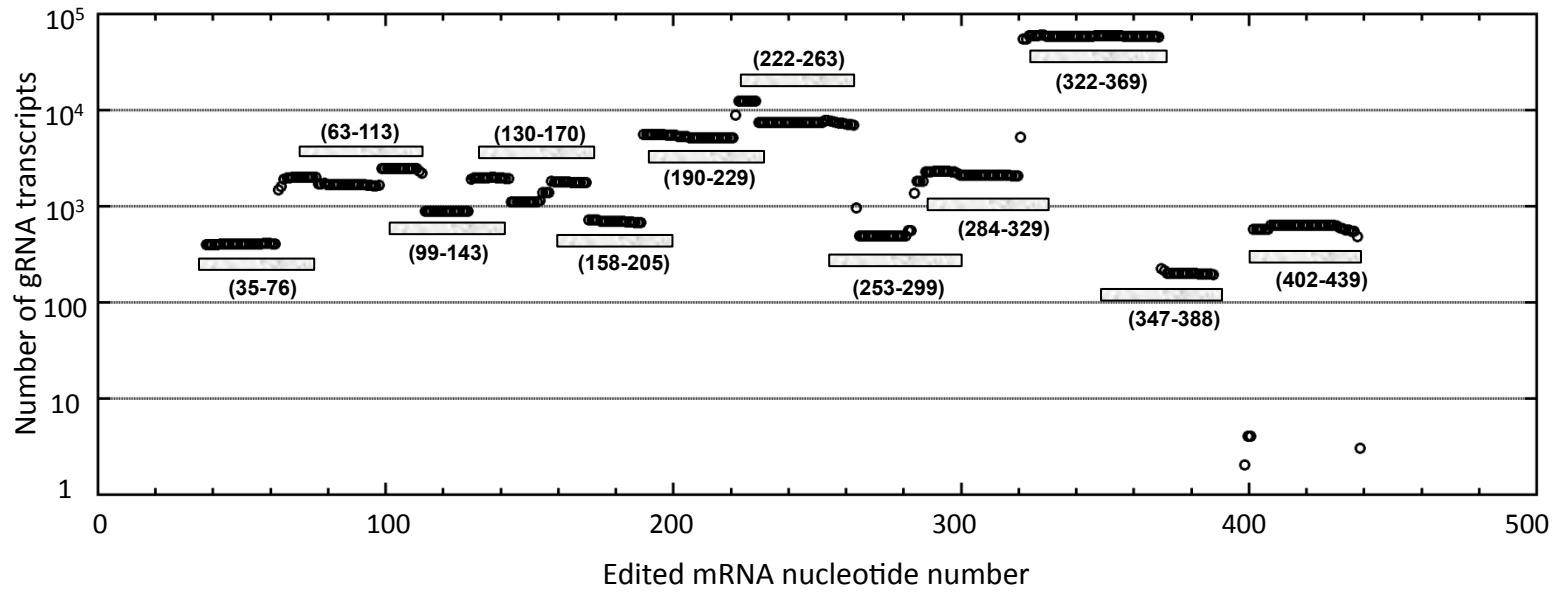
Supplementary Figure 2: gRNA transcript quantification. Abundance of gRNA transcripts (y-axis, note log scale) that align to a respective nucleotide in the fully edited mRNA. Both nucleotides and deletion sites in the fully edited mRNA were numbered starting from the 5' end (+1 = 0). Shaded boxes indicate identified gRNAs that guide specific editing sites (numbers in parentheses). A.) Cytochrome Oxidase III; B.) C-Rich Region 4; C.) NADH Dehydrogenase Subunit 3; D.) NADH Dehydrogenase Subunit 7; E.) NADH Dehydrogenase Subunit 8; F.) NADH Dehydrogenase Subunit 9. All individual data points were designated using an open circle.



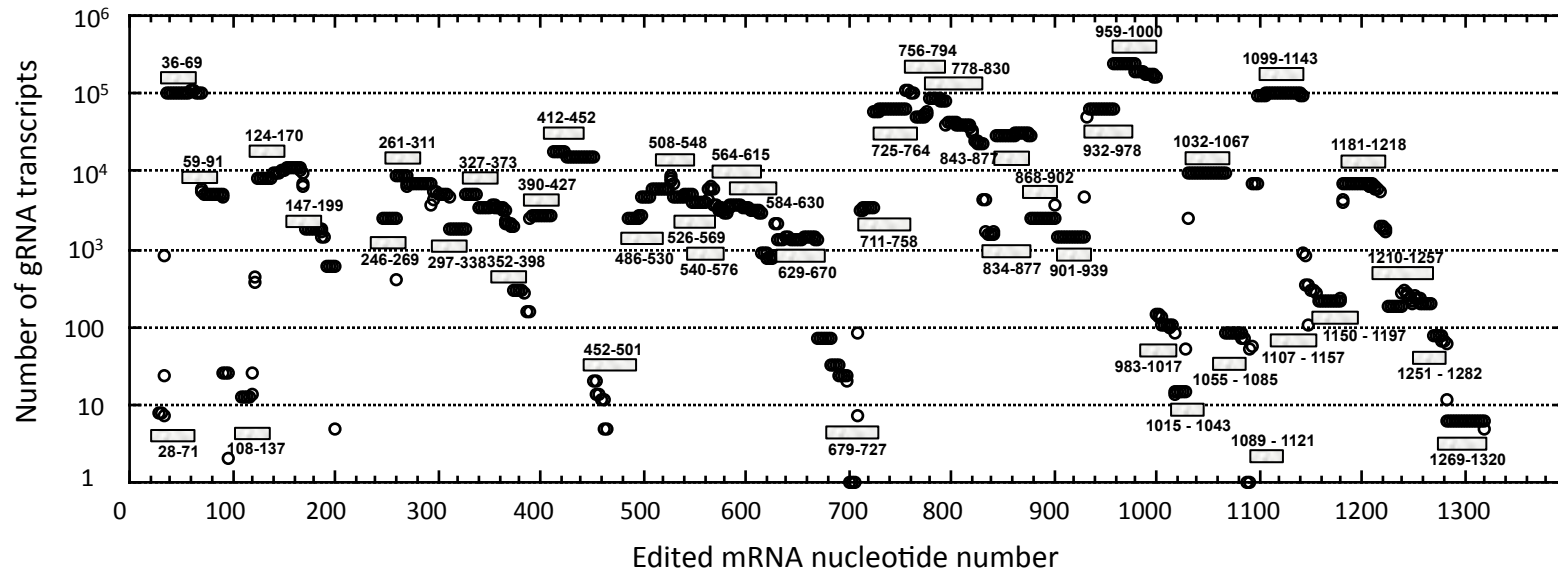
### B. C-Rich Region 4



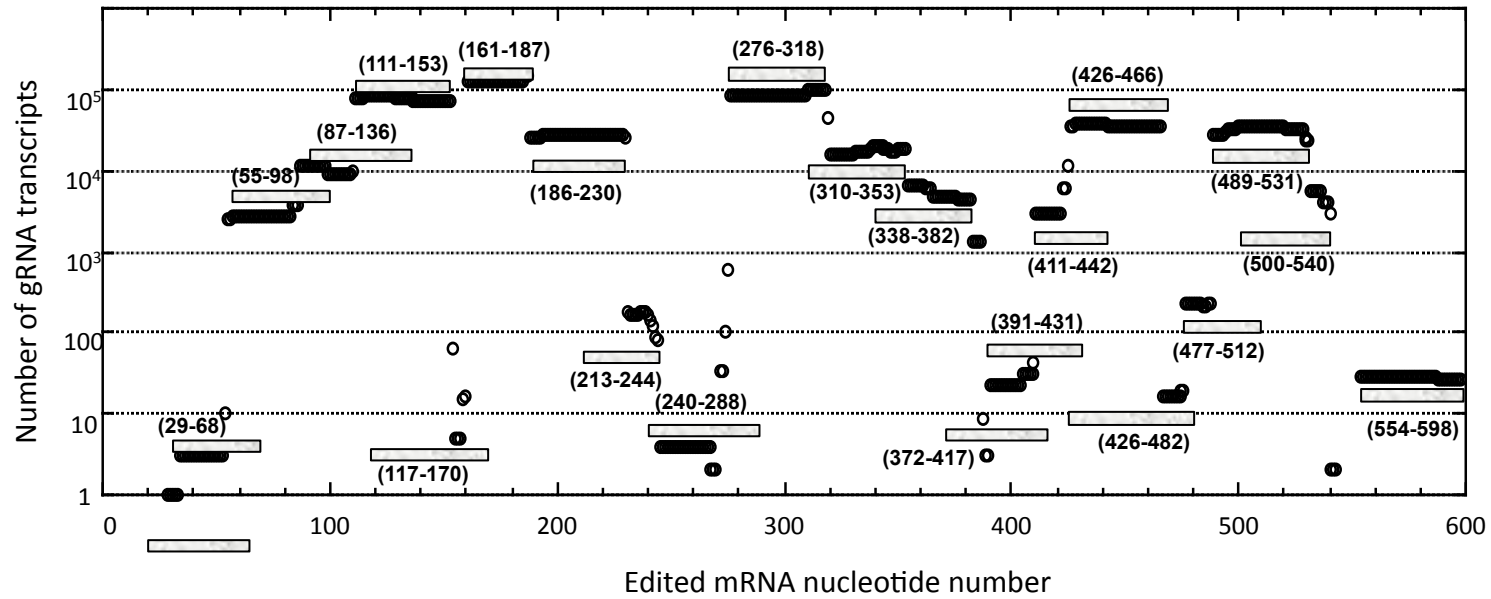
### C. ND3



D. ND7



E. ND8



F. ND9

