Additional data file 4

Distribution of changing exons per transcript under KCl treatment.

The average number of exons called as changing per transcript for transcripts of a given number of exons is shown. Note the different y-axis for the Transcript dataset. Greater numbers of exons per transcript were called as changing among those transcripts in the KCl-Transcript list. Error bars represent the standard deviation for all transcripts of the same exon number. Datasets used to generate each histogram were A) KCl-Transcript dataset, B) Transcripts of the KCl-Exon dataset (includes those transcripts in both the Transcript and Exon datasets), and C) Transcripts unique to the KCl-Exon dataset. Similar results were obtained for the TPG datasets (data not shown).