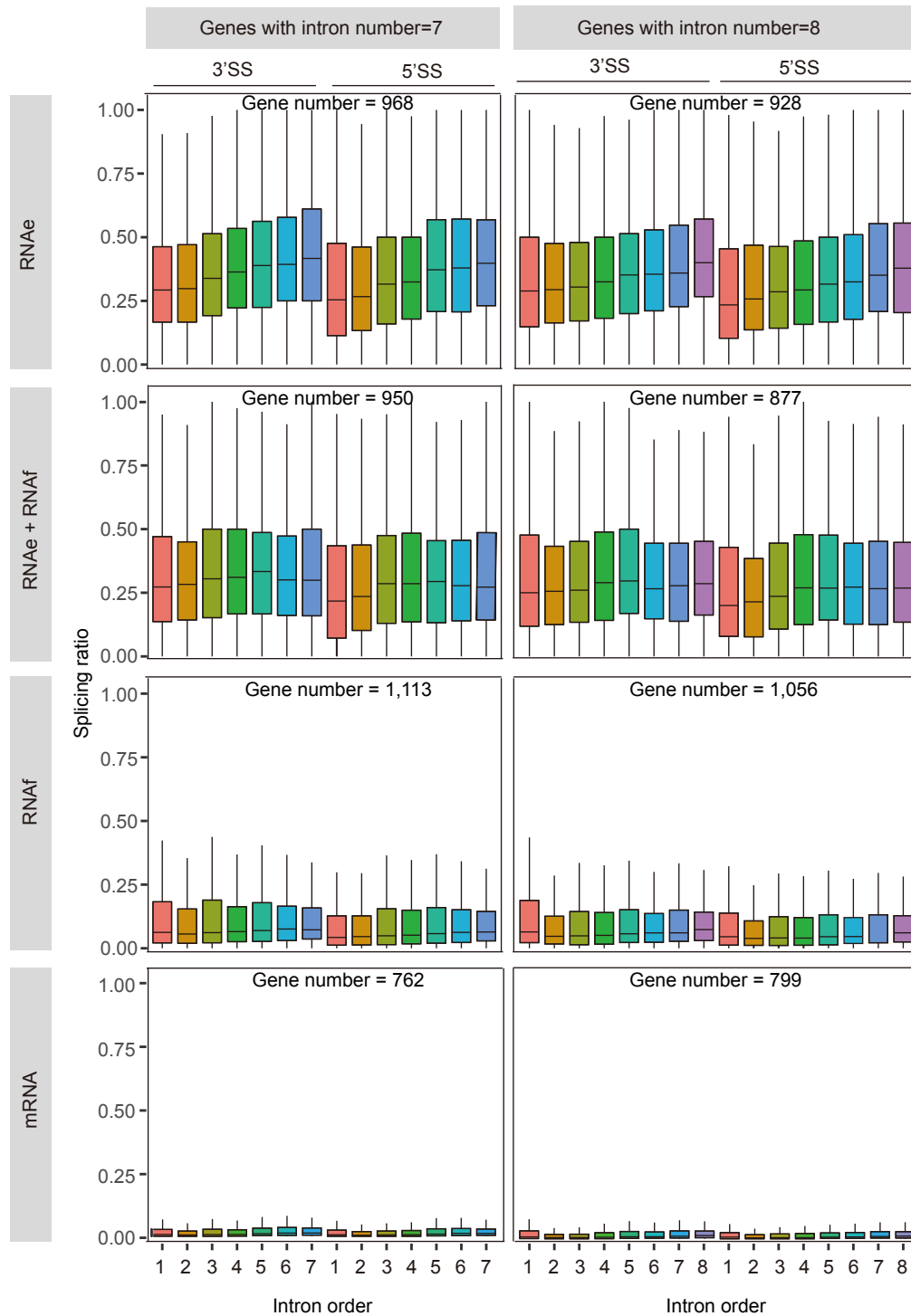




FigureS1. The relationship between co-transcriptional splicing (CTS) efficiency and intron order in RNAe, RNAf, RNAe+RNAf and mRNA.

The genes with length between 2k bp to 5k bp, containing 7 and 8 introns were selected as representatives. X-axis indicates the the intron order from 1st to 7th and 1st to 8th. The analyzed gene number was indicated at the top of each box.