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Intron analysis of the role of splicing event of Ulp2, a yeast enzyme responsible for yeast SUMO processing

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Splicing of precursor mRNA (pre-mRNA) is a critical step during eukaryotic gene expression. It has recently been shown that many of these exist in the SUMO bound form when bound to the pre-mRNA substrate during the splicing reaction. Although the splicing function of SENPs, which is responsible for human SUMO processing, is well known, Ulp, the yeast enzyme responsible for yeast SUMO processing, has no known slicing function other than its role in chromosome cohesion at centromere regions and replication and repair of DNA damage or DNA. There is no function. We hypothesized that the Ulp sumo protease influences the splicing event. We used bulk RNA sequencing to compare Ulp2 Knockout (KO) and Wild type (WT) mouse models, and made a lot of effort to count introns, as opposed to dealing with exons in normal analysis. We created a count matrix by modifying stringtie2, a fast and efficient assembler for RNA-Seq alignment with potential transcripts, to count introns. Next, using DESeq2, we quantified systematic changes between conditions compared to the variability within conditions, used statistical inference to find DEGs, and even performed gene set enrichment analysis (GSEA) to identify translation related pathways. Specific methods to investigate the splicing event function of Ulp2 are discussed below.