

\*acgcgacggggcatttcccgttcgtcattagcagtaggtaatgaagatgtttgtttct

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atgagctagttagatcaacagttacaactcatcaacacgccttcttctcgttaaatgtaca

796 2,806 38 351 36 13 2 1 1 1 225 2 5

caatcttgatcctccacctttatgggtccattgtttgcctcttccgctgtgtggagtgc

gcctacacgcacttctcacttcgtaagtgggtggcgtaagtattccctaattgttgact

ctatgttctcctctcctcaccctcgcggtgctgatttctgacagatcttcaaacacta

2,108 192 64 450 18 37,588 2 2 2

gtttaagcaaaggactattcatccgtttatattagcaacagtaggtactagcaccactaa

caacaacaacaagcacttctattttatttc\*

**Figure S10. Comparison between RNA-seq mapped processing sites with sites mapped by previous sequencing of cDNA clones [8].** Polyadenylation sites and 3'-trans-splice sites mapped by cDNA clones sequencing in the  $\beta$ -tubulin/ $\alpha$ -tubulin inter-ORF region are indicated by dark red and dark blue upward arrows, respectively. Polyadenylation sites and 3'-trans-splice sites mapped by end-reads in our RNA-seq for all  $\beta$ -tubulin/ $\alpha$ -tubulin regions are indicated by red and blue downward arrows, respectively. The numbers on top of the arrows designate the number of reads. Asterisk at the beginning of the sequence indicates the  $\beta$ -tubulin stop codon and asterisk at the end of the sequence indicates the  $\alpha$ -tubulin start codon.