

**Table S2. Selected pathways enriched among genes with differential exon usage associated with *SF3B1* mutations (FDR = 0.1).**

pathway	# genes	p-value	gene names
Antigen processing-Cross presentation	4	$3.6 \cdot 10^{-3}$	<i>HLA-F, B2M, CYBA</i>
Interferon Signaling	4	$2.8 \cdot 10^{-3}$	<i>HLA-F, GBP2, B2M, EIF4A2</i>
Translation	4	$2.6 \cdot 10^{-3}$	<i>RPL24, RPL31, EIF4A2, EIF5</i>
mRNA Splicing	3	$1.09 \cdot 10^{-2}$	<i>SRSF7, FUS, HN-RNPH2</i>

The first column indicates the *REACTOME* pathway name. The second column depicts the number of genes in that specific pathway with DEU associated to mutations in *SF3B1*. The third column shows the *p*-value resulting from testing for over-representation of hits on that pathway compared to a background set of genes with high expression (Fisher's exact test). The fourth column list the genes with DEU associated with the mutation in *SF3B1* among those in the pathway.