

**Table S12: RNA-seq expression in fragments per kilobase per million (FPKM) for wild-type and mutant transcript.** Table shows the FPKM expression values for both the wild-type (Wt) and mutant (exon-skipping) transcript.

Hap.	Carrier identifiers	Gene	Transcript IDs (Effect)	Wild-type	Mutant
LA1	711604	<i>POLR1B</i>	TCONS_35434 (Wt), TCONS_35427 (exon skipping)	627.35	126.24
LA1	781828	<i>POLR1B</i>	TCONS_35434 (Wt), TCONS_35427 (exon skipping)	568.95	136.61
LA1	924455	<i>POLR1B</i>	TCONS_35434 (Wt), TCONS_35427 (exon skipping)	483.44	99.21
LA1	928519	<i>POLR1B</i>	TCONS_35434 (Wt), TCONS_35427 (exon skipping)	451.92	128.61
DU1	768945	<i>TADA2A</i>	TCONS_9105 (Wt), TCON_9101(intron retention), TCONS_9107 (exon skipping)	495.56	39.33, 195.53
DU1	780181	<i>TADA2A</i>	TCONS_9105 (Wt), TCON_9101(intron retention), TCONS_9107 (exon skipping)	517.72	61.84, 159.46
DU1	906564	<i>TADA2A</i>	TCONS_9105 (Wt), TCON_9101(intron retention), TCONS_9107 (exon skipping)	310.01	83.59, 269.6