

Supplementary Table 3. Related to Figure 3.

Cufflinks predicted exonic bins*

*Cufflinks prediction was flattened from gtf to gff for HTseqcounts.py

exonic bins of min 5nt length, min 6 reads coverage

referenced to UCSC

	total	truly novel exons	LINE-derived
exonic bins	183,361	32,737	3,811
# of genes	9,958	7,604	2,241
with min 15% inclusion in control or MATR3/PTBP1 depleted cells (Whippet)			
exonic bins	149,718	26,717	1,702
# of genes	9,957	7,298	1,085
LINE-derived exons total: 1,702	<div> <div>“cryptic exons”</div> <div> <div>partial-overlap</div> <div>truly novel</div> </div> </div>		
UCSC annotation:	constitutive	alternative	
	211	311	875 305