










Supplementary Table S5. Over-represented RBP binding motifs obtained by RNA-compete (Ray *et al.* 2013) in flanking introns of Matrin3 repressed exons.

The splicing event region, RBP gene name, RNA-compete id, species of the RBP, total sites found, number of sequences with sites, log₂(fold-ratio), p-value, FDR and sites logo are shown. Enriched motifs were selected after multiple test correction (FDR < 0.05). Motifs shown here include those for all RBPs (multiple species) from Ray *et al.* 2013, whereas Figure 4 shows only the enriched motifs for human proteins. See further details in main text Materials and Methods. Abbreviations, number of sequences comprised and over-represented RBP motifs for each splicing event region analyzed are shown at the foot of the table.

RBP motifs enrichment analysis: Matrin3 NEG (-PTB)(Skipping)

region	gene name	RBP id	species	sites	seq w/ sites	log ₂ (ratio)	p-value	FDR	Logo	
5IA	1	MATR3	MATR3_00037	<i>Homo sapiens</i>	83	67 (35.3%)	1.1	1.85e-6	4.52e-4	
5IA	2	Tv_0258	Tv_0258_00258	<i>Trichomonas vaginalis</i>	124	86 (45.3%)	0.77	4.15e-4	3.38e-2	
3ID	1	PTBP1	PTBP1_00269	<i>Homo sapiens</i>	222	124 (64.2%)	1.24	6.80e-9	1.66e-6	
3ID	2	PCBP1	PCBP1_00239	<i>Mus musculus</i>	143	96 (49.7%)	0.94	1.05e-5	7.32e-4	
3ID	3	PTBP1	PTBP1_00268	<i>Homo sapiens</i>	255	120 (62.2%)	0.94	1.08e-5	7.32e-4	
3ID	4	Tb_0220	Tb_0220_00220	<i>Trypanosoma brucei</i>	181	112 (58%)	0.93	1.20e-5	7.32e-4	
3ID	5	FNE	FNE_00120	<i>Drosophila melanogaster</i>	102	76 (39.4%)	0.86	1.02e-4	3.55e-3	
3ID	6	CG5213	CG5213_00010	<i>Drosophila melanogaster</i>	128	93 (48.2%)	0.78	2.49e-4	7.59e-3	
3ID	7	U2AF50	U2AF50_00080	<i>Drosophila melanogaster</i>	377	74 (38.3%)	0.8	3.65e-4	9.91e-3	
3ID	8	MATR3	MATR3_00037	<i>Homo sapiens</i>	89	64 (33.2%)	0.83	4.09e-4	9.98e-3	