

Supplementary Table S4. Over-represented 5mers in flanking introns of Matrin3 repressed exons.

The splicing event region, pentamer, total sites found, number of sequences with sites, log₂(fold-ratio), p-value, FDR and logo are shown. Enriched pentamers were selected after multiple test correction (FDR < 0.05). 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.

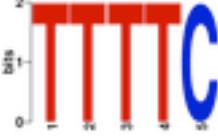
5mer enrichment analysis: Matrin3 NEG (-PTB)(Skipping)

region		5mer	sites	seq w/ sites	log ₂ (ratio)	p-value	FDR	Logo
5IA	1	TCTTG	112	85 (44.7%)	1.22	3.65e-8	3.73e-5	
5IA	2	TTTGT	166	106 (55.8%)	1.06	7.29e-7	3.29e-4	
5IA	3	TTCAT	101	82 (43.2%)	1.07	1.24e-6	3.29e-4	
5IA	4	TTTAT	150	102 (53.7%)	1.03	1.28e-6	3.29e-4	
5IA	5	TCATT	103	80 (42.1%)	0.97	1.08e-5	2.20e-3	
5IA	6	TTCTT	158	101 (53.2%)	0.93	1.37e-5	2.34e-3	

5IA	7	CTTTG	105	83 (43.7%)	0.92	2.43e-5	3.55e-3	
5IA	8	TTTCT	182	112 (58.9%)	0.89	3.17e-5	4.05e-3	
5IA	9	CTCTA	60	52 (27.4%)	1.03	4.64e-5	5.28e-3	
5IA	10	CTCTT	95	78 (41.1%)	0.89	5.21e-5	5.34e-3	
5IA	11	TGTGA	88	74 (38.9%)	0.88	1.08e-4	8.49e-3	
5IA	12	TCTCT	107	80 (42.1%)	0.84	1.37e-4	1.00e-2	
5IA	13	GTTCT	78	63 (33.2%)	0.9	1.47e-4	1.00e-2	
5IA	14	CATTG	68	58 (30.5%)	0.91	1.68e-4	1.00e-2	
5IA	15	TTCTG	122	88 (46.3%)	0.81	1.76e-4	1.00e-2	
5IA	16	TGTCT	103	79 (41.6%)	0.83	1.76e-4	1.00e-2	

5IA	17	TTGTC	73	59 (31.1%)	0.89	2.10e-4	1.13e-2	
5IA	18	CTGTA	65	61 (32.1%)	0.84	3.06e-4	1.49e-2	
5IA	19	TGACT	64	57 (30%)	0.83	5.82e-4	2.31e-2	
5IA	20	ATAGT	53	48 (25.3%)	0.87	5.88e-4	2.31e-2	
5IA	21	TTATT	127	89 (46.8%)	0.74	6.63e-4	2.52e-2	
5IA	22	ATACT	51	47 (24.7%)	0.88	7.19e-4	2.60e-2	
5IA	23	CTTCT	99	74 (38.9%)	0.75	7.36e-4	2.60e-2	
5IA	24	TCTTT	160	95 (50%)	0.71	8.76e-4	2.79e-2	
5IA	25	TATCT	66	54 (28.4%)	0.82	8.82e-4	2.79e-2	
5IA	26	ATTCT	89	72 (37.9%)	0.74	8.96e-4	2.79e-2	

5IA	27	TATTT	153	99 (52.1%)	0.71	9.46e-4	2.79e-2	
5IA	28	TTATC	55	48 (25.3%)	0.84	9.50e-4	2.79e-2	
5IA	29	GTTTA	69	58 (30.5%)	0.8	9.73e-4	2.79e-2	
5IA	30	TTGTA	78	66 (34.7%)	0.75	1.08e-3	2.96e-2	
5IA	31	CGTAC	9	9 (4.7%)	1.93	1.10e-3	2.96e-2	
5IA	32	CTGAT	59	53 (27.9%)	0.81	1.16e-3	3.04e-2	
5IA	33	TTATA	90	67 (35.3%)	0.73	1.22e-3	3.09e-2	
5IA	34	ATGTG	81	64 (33.7%)	0.75	1.27e-3	3.09e-2	
5IA	35	ACTTC	53	48 (25.3%)	0.83	1.31e-3	3.13e-2	
5IA	36	GTATT	72	58 (30.5%)	0.76	1.47e-3	3.42e-2	

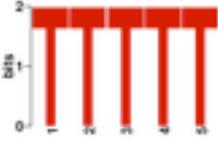
5IA	37	GATGA	51	49 (25.8%)	0.81	1.56e-3	3.54e-2	
5IA	38	TACTG	49	47 (24.7%)	0.79	1.98e-3	4.31e-2	
5IA	39	GTCTT	82	61 (32.1%)	0.72	2.07e-3	4.43e-2	
5IA	40	TCCTT	95	72 (37.9%)	0.68	2.35e-3	4.91e-2	
3ID	1	TTCTT	171	114 (59.1%)	1.09	2.48e-7	2.54e-4	
3ID	2	TCCTT	125	90 (46.6%)	1.06	9.22e-7	4.72e-4	
3ID	3	CCTTA	70	58 (30.1%)	1.17	1.52e-6	5.19e-4	
3ID	4	TCTTT	168	110 (57%)	1	2.47e-6	6.31e-4	
3ID	5	TTTTC	201	115 (59.6%)	0.99	3.11e-6	6.31e-4	

3ID	6	TTTCT	230	124 (64.2%)	1	3.70e-6	6.31e-4	
3ID	7	CTTAC	56	51 (26.4%)	1.14	8.87e-6	1.30e-3	
3ID	8	CATCT	97	76 (39.4%)	0.97	1.61e-5	2.06e-3	
3ID	9	TCTCT	132	90 (46.6%)	0.87	4.99e-5	5.29e-3	
3ID	10	CTTTT	183	113 (58.5%)	0.86	5.17e-5	5.29e-3	
3ID	11	TCTGT	119	95 (49.2%)	0.85	6.85e-5	5.85e-3	
3ID	12	TGTCT	102	82 (42.5%)	0.85	1.12e-4	8.85e-3	
3ID	13	TTCAT	115	81 (42%)	0.82	1.58e-4	1.15e-2	
3ID	14	TTCTC	123	88 (45.6%)	0.8	1.85e-4	1.26e-2	
3ID	15	ATCTT	99	72 (37.3%)	0.83	2.08e-4	1.33e-2	

3ID	16	TCTTC	108	74 (38.3%)	0.8	2.74e-4	1.57e-2	
3ID	17	TATCT	71	61 (31.6%)	0.87	2.75e-4	1.57e-2	
3ID	18	ATCCT	67	59 (30.6%)	0.87	3.18e-4	1.72e-2	
3ID	19	ATCTG	78	66 (34.2%)	0.81	3.84e-4	1.96e-2	
3ID	20	CTCTT	100	80 (41.5%)	0.77	4.29e-4	2.09e-2	
3ID	21	TTTCC	113	87 (45.1%)	0.74	4.85e-4	2.26e-2	
3ID	22	CATTC	68	60 (31.1%)	0.81	5.81e-4	2.31e-2	
3ID	23	TTCTG	126	92 (47.7%)	0.73	5.96e-4	2.31e-2	
3ID	24	TACTT	84	67 (34.7%)	0.78	6.09e-4	2.31e-2	
3ID	25	TTACT	73	67 (34.7%)	0.78	6.09e-4	2.31e-2	

3ID	26	GTTTT	146	97 (50.3%)	0.71	7.32e-4	2.68e-2	
3ID	27	CTATC	36	34 (17.6%)	0.99	8.46e-4	2.99e-2	
3ID	28	GTACA	42	41 (21.2%)	0.91	9.52e-4	3.25e-2	
3ID	29	TTGGT	85	64 (33.2%)	0.74	1.35e-3	4.45e-2	
3ID	30	TTTAC	73	61 (31.6%)	0.75	1.43e-3	4.58e-2	
3IA	1	TCTTA	86	71 (36.8%)	1.02	7.20e-6	3.69e-3	
3IA	2	TTATT	128	94 (48.7%)	0.88	4.30e-5	9.18e-3	
3IA	3	GATAG	47	41 (21.2%)	1.12	4.63e-5	9.18e-3	
3IA	4	GTTTT	127	95 (49.2%)	0.86	4.77e-5	9.18e-3	

3IA	5	ATTCA	86	65 (33.7%)	0.94	5.38e-5	9.18e-3	
3IA	6	ATTAA	108	74 (38.3%)	0.89	7.38e-5	1.08e-2	
3IA	7	AATTC	63	58 (30.1%)	0.92	1.17e-4	1.50e-2	
3IA	8	ATATT	122	85 (44%)	0.81	1.55e-4	1.60e-2	
3IA	9	TATTT	163	106 (54.9%)	0.8	1.57e-4	1.60e-2	
3IA	10	ATGAC	51	46 (23.8%)	0.98	1.98e-4	1.60e-2	
3IA	11	TTCTT	137	96 (49.7%)	0.79	2.03e-4	1.60e-2	
3IA	12	TCAAT	48	44 (22.8%)	0.96	3.59e-4	2.35e-2	
3IA	13	TATGT	84	67 (34.7%)	0.82	3.86e-4	2.35e-2	
3IA	14	CATTC	64	54 (28%)	0.87	3.88e-4	2.35e-2	

3IA	15	TTTTT	186	106 (54.9%)	0.75	3.90e-4	2.35e-2	
3IA	16	TAAAT	112	83 (43%)	0.76	5.04e-4	2.87e-2	
3IA	17	CGTTG	17	16 (8.3%)	1.44	6.85e-4	3.44e-2	
3IA	18	GATAA	58	48 (24.9%)	0.85	8.84e-4	4.00e-2	
3IA	19	AAGTT	78	64 (33.2%)	0.77	8.98e-4	4.00e-2	
3IA	20	AAATG	121	89 (46.1%)	0.7	9.77e-4	4.17e-2	
3IA	21	TTTAA	152	97 (50.3%)	0.69	1.27e-3	4.99e-2	
3IA	22	CGGTA	10	10 (5.2%)	1.78	1.28e-3	4.99e-2	
3IA	23	TATCT	61	54 (28%)	0.78	1.39e-3	4.99e-2	
3IA	24	ACTTT	90	74 (38.3%)	0.71	1.46e-3	4.99e-2	

3IA	25	TAAAA	138	93 (48.2%)	0.68	1.48e-3	4.99e-2
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5' Exon (5E), # sequences = 198, # 5mers = 0
5' Intron Donor (5ID), # sequences = 190, # 5mers = 0
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3' Intron Acceptor (3IA), # sequences = 193, # 5mers = 25
3' Exon (3E), # sequences = 198, # 5mers = 0