



**Table S2: Peptide identification by mass spectrometric in-gel digestion analysis of INTS3 band  
(Corresponding to 110 kDa on SDS-PAGE, amino acid coverage: 65.3%)**

#	Sequence	Protein Group Accessions	Modifications	Parent Charge	Parent Mass to Charge Ratio (m/z) (Da)
1	AAASGAAGGGGGGAGAGAPGGGR	Q68E01		2	806.3853
2	AALSSPR	Q68E01		2	351.2026
3	ACQEDDVR	Q68E01		2	496.7103
4	CDLIR	Q68E01		2	338.6771
5	CmSIVTsmTAGVSER	Q68E01	m:Oxidized methionine	3	554.2525
6	DELEER	Q68E01		2	395.6834
7	DGmNIVLNK	Q68E01	m:Oxidized methionine	2	510.2635
8	DIIHNPQ	Q68E01		2	418.7181
9	DLALVSR	Q68E01		2	387.2303
10	EAnDALNAYVCK	Q68E01	n:Deamidated	2	684.8197
11	EANDALNAYVCK	Q68E01		3	456.5484
12	EKPSEEmVK	Q68E01	m:Oxidized methionine	3	364.8488
13	EWVLK	Q68E01		2	337.6981
14	FHPIK	Q68E01		2	321.1942
15	FLACR	Q68E01		2	333.6742
16	GAAAAAASGAAGGGGGGAGAGAPGGGR	Q68E01		2	976.9698
17	HDELLAEHIK	Q68E01		3	402.2185
18	IIEPVSmEmDNHmSDK	Q68E01	m:Oxidized methionine	3	647.2655
19	IIEPVSmEmDnHmSDK	Q68E01	m:Oxidized methionine n:Deamidated	3	647.5988
20	ILTEPAQAQK	Q68E01		2	549.8131
21	INQILmEK	Q68E01	m:Oxidized methionine	2	502.7764
22	INQILMEk	Q68E01	k:Carbamylated lysine	2	516.2829
23	INQILMEK	Q68E01		2	494.7798
24	InQILmEK	Q68E01	n:Deamidated m:Oxidized methionine	2	503.2734
25	InQILMEK	Q68E01	n:Deamidated	2	495.2799

26	INQILMEK	Q68E01	k:Carbamylated lysine	2	516.2829
27	LAPLFDNPK	Q68E01		2	507.7853
28	LDESLR	Q68E01		2	366.7
29	LLFmTSR	Q68E01	m:Oxidized methionine	2	442.2395
30	LLLSTSLDAK	Q68E01		2	530.8173
31	LLQNVAR	Q68E01		2	407.2517
32	LLQSR	Q68E01		2	308.6944
33	LLTTCTSNVAASNAK	Q68E01		2	775.8981
34	LNLNTNK	Q68E01		2	402.2367
35	LQDTCR	Q68E01		2	396.688
36	LTPDMETK	Q68E01		2	467.7325
37	LTPDmETK	Q68E01	m:Oxidized methionine	2	475.73
38	LTPDMETk	Q68E01	k:Carbamylated lysine	2	489.2362
39	NATQPPNAEEESGSSSASEEEDTKPKPTK	Q68E01		4	762.1014
40	NNSLPR	Q68E01		2	350.6926
41	QYLSTPDSQSLR	Q68E01		3	465.5719
42	qYLSTPDSQSLR	Q68E01	q:Pyroglutamic acid	2	689.3359
43	SGVLGADGVCmTFmK	Q68E01	m:Oxidized methionine	2	802.8621
44	SSDILPR	Q68E01		2	394.2207
45	SSLNHIVEK	Q68E01		3	342.8594
46	SSPSPPEVK	Q68E01		2	513.7774
47	TAGVSER	Q68E01		2	360.1897
48	TLILTEPAQAQK	Q68E01		2	656.8798
49	TQLVWLVR	Q68E01		2	507.8107
50	TSNVAASNAK	Q68E01		2	481.7503
51	VAASNAK	Q68E01		2	330.69
52	VLAHLAPLFDNPK	Q68E01		3	478.9437
53	VLQLQK	Q68E01		2	364.739
54	YQDWFQR	Q68E01		2	521.7396

**Table S3: Peptide identification by mass spectrometric in-gel digestion analysis of INTS3 band  
(Corresponding to 60 kDa on SDS-PAGE, amino acid coverage: 35.6%)**

#	Sequence	Protein Group Accessions	Modifications	Parent Charge	Parent Mass to Charge Ratio (m/z) (Da)
1	AAASGAAGGGGGGAGAGAPGGGR	Q68E01		2	806.3853
2	AALSSPR	Q68E01		2	351.2026
3	ACQEDDVR	Q68E01		2	496.7103
4	CDLIR	Q68E01		2	338.6771
5	CmSIVTSmTAGVSER	Q68E01	m:Oxidized methionine	3	554.2525
6	DELEER	Q68E01		2	395.6834
7	DGmNIVLNK	Q68E01	m:Oxidized methionine	2	510.2635
8	DIIHNPQ	Q68E01		2	418.7181
9	DLALVSR	Q68E01		2	387.2303
10	EAnDALNAYVCK	Q68E01	n:Deamidated	2	684.8197
11	EANDALNAYVCK	Q68E01		3	456.5484
12	EKPSEEmVK	Q68E01	m:Oxidized methionine	3	364.8488
13	EWVLK	Q68E01		2	337.6981
14	FHPIK	Q68E01		2	321.1942
15	FLACR	Q68E01		2	333.6742
16	GAAAAAASGAAGGGGGGAGAGAPGGGR	Q68E01		2	976.9698
17	HDELLAEHIK	Q68E01		3	402.2185
18	IIEPVSmEmDNHmSDK	Q68E01	m:Oxidized methionine	3	647.2655
19	IIEPVSmEmDnHmSDK	Q68E01	m:Oxidized methionine n:Deamidated	3	647.5988
20	ILTEPAQAQK	Q68E01		2	549.8131
21	INQILmEK	Q68E01	m:Oxidized methionine	2	502.7764
22	INQILMEK	Q68E01	k:Carbamylated lysine	2	516.2829
23	INQILMEK	Q68E01		2	494.7798
24	InQILmEK	Q68E01	n:Deamidated m:Oxidized methionine	2	503.2734
25	InQILMEK	Q68E01	n:Deamidated	2	495.2799

26	INQILMEk	Q68E01	k:Carbamylated lysine	2	516.2829
27	LAPLFDNPK	Q68E01		2	507.7853
28	LDESLR	Q68E01		2	366.7
29	LLFmTSR	Q68E01	m:Oxidized methionine	2	442.2395
30	LLLSTSLDAK	Q68E01		2	530.8173
31	LLQNVAR	Q68E01		2	407.2517
32	LLQSR	Q68E01		2	308.6944
33	LLTTCTSNVAASNAK	Q68E01		2	775.8981
34	LNLNTNK	Q68E01		2	402.2367
35	LQDTCR	Q68E01		2	396.688
36	LTPDMETK	Q68E01		2	467.7325
37	LTPDmETK	Q68E01	m:Oxidized methionine	2	475.73
38	LTPDMETk	Q68E01	k:Carbamylated lysine	2	489.2362
39	NATQPPNAEEESGSSSASEEEDTKPKPTK	Q68E01		4	762.1014
40	NNSLPR	Q68E01		2	350.6926
41	QYLSTPDSQSLR	Q68E01		3	465.5719
42	qYLSTPDSQSLR	Q68E01	q:Pyroglutamic acid	2	689.3359
43	SGVLGADGVCmTFmK	Q68E01	m:Oxidized methionine	2	802.8621
44	SSDILPR	Q68E01		2	394.2207
45	SSLNHIVEK	Q68E01		3	342.8594
46	SSPSPPEVK	Q68E01		2	513.7774
47	TAGVSER	Q68E01		2	360.1897
48	TLILTEPAQAQK	Q68E01		2	656.8798
49	TQLVWLVR	Q68E01		2	507.8107
50	TSNVAASNAK	Q68E01		2	481.7503
51	VAASNAK	Q68E01		2	330.69
52	VLAHLAPLFDNPK	Q68E01		3	478.9437
53	VLQLQK	Q68E01		2	364.739
54	YQDWFQR	Q68E01		2	521.7396

**Table S4: Peptide identification by mass spectrometric in-gel digestion analysis of C9ORF80  
(amino acid coverage: 80.7%)**

#	Sequence	Protein Group Accessions	Parent Charge	Parent Mass to Charge Ratio (m/z) (Da)
1	VAILAELDK	Q9NRY2	2	486.294
2	AILAELDKEK	Q9NRY2	2	565.328
3	LILPVLPR	Q9NRY2	2	460.8208
4	VAILAELDKEK	Q9NRY2	3	410.2454
5	GNLILPVLPR	Q9NRY2	2	546.353
6	ILPVLPR	Q9NRY2	2	404.2774
7	AALQHA	Q9NRY2	2	305.67
8	AALQHAHAH	Q9NRY2	3	319.1697
9	SIALSR	Q9NRY2	2	323.6992
10	AANSSGQGFQNK	Q9NRY2	3	403.528
11	NSSGQGFQNK	Q9NRY2	2	533.7514
12	AANSSGQGFQNKNR	Q9NRY2	3	493.5774
13	DHAEQQH	Q9NRY2	2	432.6861
14	ILPVLPR	Q9NRY2	2	404.2774
15	HPGASIALSR	Q9NRY2	2	504.783
16	SSTNHPGASIALSR	Q9NRY2	2	699.362
17	HIAAQK	Q9NRY2	2	398.229
18	PGASIALSR	Q9NRY2	2	436.2549
19	QHIAAQK	Q9NRY2	2	462.2581
20	ANSSGQGFQNK	Q9NRY2	2	569.2695
21	ILPVLPR	Q9NRY2	2	404.2774
22	AALQHAH	Q9NRY2	2	374.1996
23	ASIALSR	Q9NRY2	2	359.2183
24	LLMQNQSSTNHPGAS	Q9NRY2	3	528.9217
25	STNHPGASIALSR	Q9NRY2	3	437.5677
26	DHAEQQHIAAQ	Q9NRY2	2	624.2934
27	QSSTNHPGASIALSR	Q9NRY2	2	763.3917
28	AALQHAHAHSSGY	Q9NRY2	3	450.552
29	DFRDHAEQQHIAAQK	Q9NRY2	4	481.2411
30	DHAEQQHIAAQK	Q9NRY2	2	752.3689
31	TNHPGASIALSR	Q9NRY2	3	408.5565

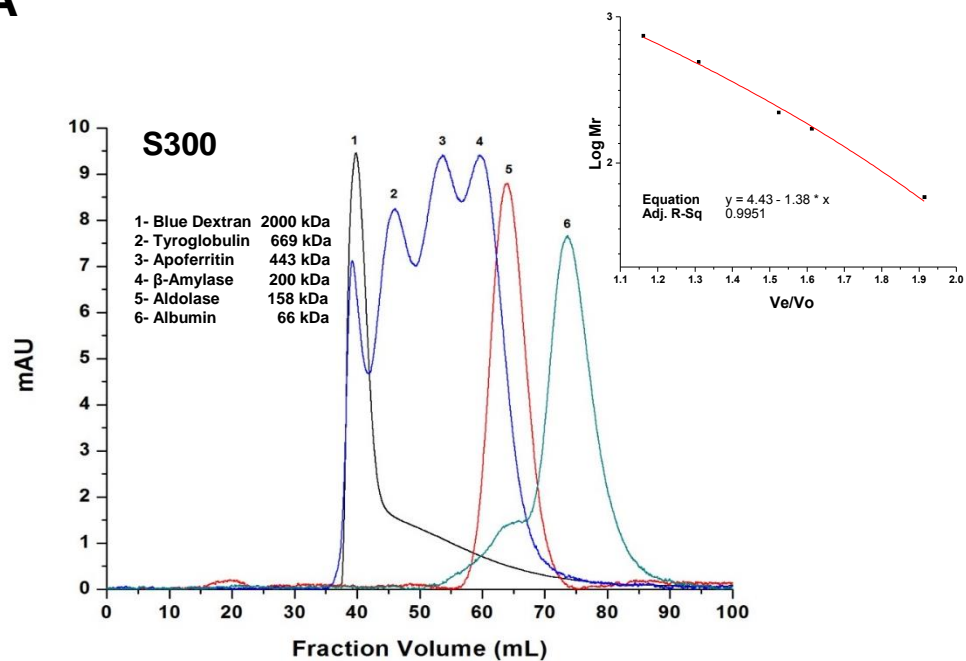
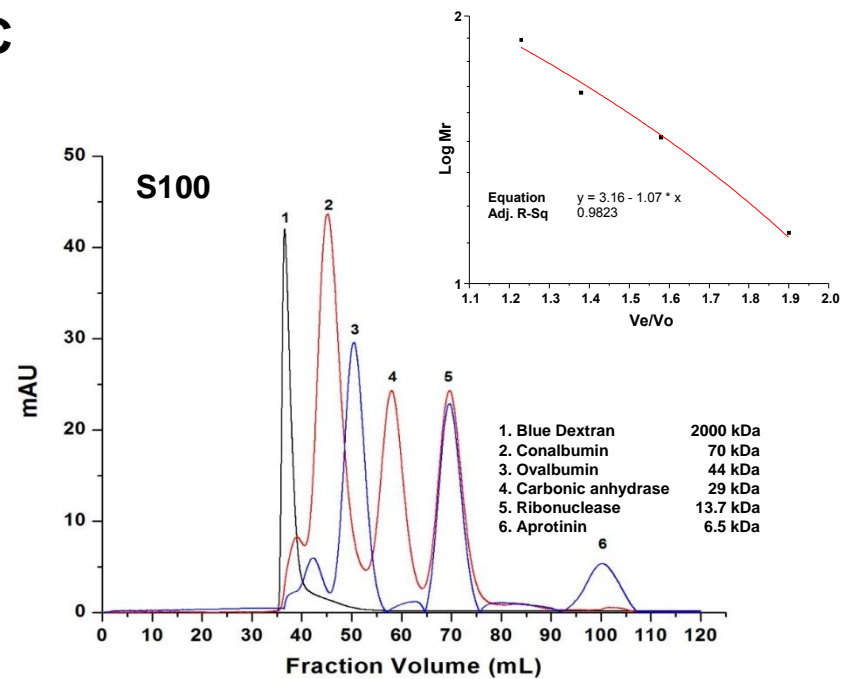
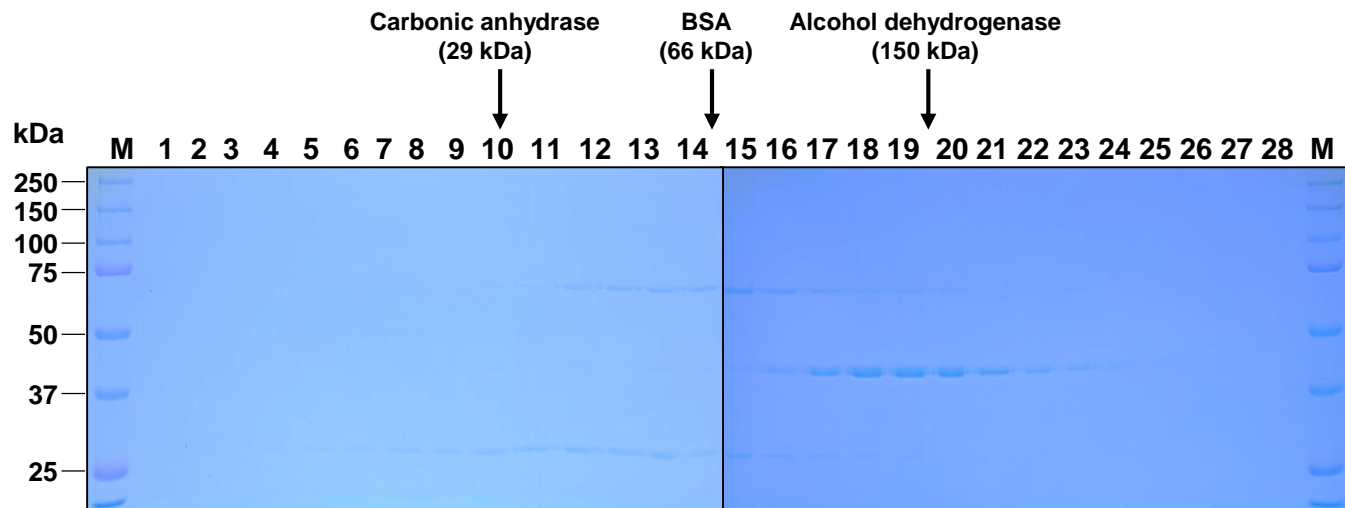
**Table S5: Mass spectrometric analysis of proteins pull down with an anti-hNABP2 antibody**

<b>Accession</b>	<b>Description</b>	<b>Score</b>	<b>Coverage</b>	<b># Peptides</b>	<b>MW [kDa]</b>
P25398	40S ribosomal protein S12	4.13	15.15	2	14.5
P62277	40S ribosomal protein S13	13.78	16.56	3	17.2
P62263	40S ribosomal protein S14	9.99	23.84	4	16.3
P62244	40S ribosomal protein S15a	6.31	13.85	2	14.8
P62249	40S ribosomal protein S16	22.12	47.26	7	16.4
P62269	40S ribosomal protein S18	45.63	48.68	9	17.7
P39019	40S ribosomal protein S19	11.3	17.93	3	16.1
P60866	40S ribosomal protein S20	5.49	19.33	2	13.4
P62266	40S ribosomal protein S23	5.36	13.29	2	15.8
P62847	40S ribosomal protein S24	5.82	20.3	2	15.4
P62851	40S ribosomal protein S25	4.61	8.8	2	13.7
P62854	40S ribosomal protein S26	6.7	20.87	2	13
P05388	60S acidic ribosomal protein P0	11.76	17.67	4	34.3
P05387	60S acidic ribosomal protein P2	9.17	53.04	3	11.7
P30050	60S ribosomal protein L12	10.68	24.24	3	17.8
P35268	60S ribosomal protein L22	10.8	38.28	4	14.8
P62829	60S ribosomal protein L23	10.08	32.14	3	14.9
P61353	60S ribosomal protein L27	4.29	12.5	2	15.8
P62888	60S ribosomal protein L30	13.71	34.78	4	12.8
P62899	60S ribosomal protein L31	7.07	18.4	2	14.5
P62910	60S ribosomal protein L32	7.88	20	2	15.8
Q9Y3U8	60S ribosomal protein L36	4.43	20	2	12.2
P61204	ADP-ribosylation factor 3	9.56	19.89	3	20.6
P07355	Annexin A2	5.48	8.26	2	38.6
O95831	Apoptosis-inducing factor 1, mitochondrial	5.24	3.92	2	66.9
P46063	ATP-dependent DNA helicase Q1 (RECQ1)	4.99	3.85	2	73.4
Q9H3F6	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3 (BACD3)	4.87	9.27	2	35.4
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	7.62	6.07	3	74.1
Q16630	Cleavage and polyadenylation specificity factor subunit 6	10.2	7.44	3	59.2
Q8N684	Cleavage and polyadenylation specificity factor subunit 7	6.79	8.07	3	52
Q14258	E3 ubiquitin/ISG15 ligase TRIM25	5.53	3.97	2	70.9
Q15717	ELAV-like protein 1	8.44	10.43	3	36.1
P05198	Eukaryotic translation initiation factor 2 subunit 1	6.32	11.11	3	36.1
P51114	Fragile X mental retardation syndrome-related protein 1	6.14	4.19	2	69.7
P08107	Heat shock 70 kDa protein 1A/1B	26.75	15.91	8	70

P11142	Heat shock cognate 71 kDa protein	67.49	32.2	19	70.9
P08238	Heat shock protein HSP 90-beta	4	3.18	2	83.2
P09651	Heterogeneous nuclear ribonucleoprotein A1	14.97	6.99	2	38.7
P61978	Heterogeneous nuclear ribonucleoprotein K	9.17	8.21	3	50.9
P52272	Heterogeneous nuclear ribonucleoprotein M	33.5	21.64	13	77.5
O43390	Heterogeneous nuclear ribonucleoprotein R	8.56	6	3	70.9
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1	4.53	4.56	2	95.7
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	13.32	17	4	37.4
P16403	Histone H1.2	4.58	11.27	2	21.4
Q96KK5	Histone H2A type 1-H	10.05	21.09	3	13.9
O60814	Histone H2B type 1-K	12.45	13.49	3	13.9
P62805	Histone H4	4.44	17.48	2	11.4
Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1	40.47	23.92	10	63.4
O00425	Insulin-like growth factor 2 mRNA-binding protein 3	39.62	26.08	11	63.7
P19525	Interferon-induced, double-stranded RNA-activated protein kinase	5.24	4.54	2	62.1
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	6	5.42	2	48.2
Q4G0J3	La-related protein 7	4.9	4.3	2	66.9
Q8N1G4	Leucine-rich repeat-containing protein 47	4.81	5.15	2	63.4
Q15233	Non-POU domain-containing octamer-binding protein	64.65	22.29	10	54.2
Q7Z3B4	Nucleoporin p54	5.02	4.34	2	55.4
Q6P1J9	Parafibromin	4.09	3.77	2	60.5
P11940	Polyadenylate-binding protein 1	91.72	41.04	22	70.6
Q13310	Polyadenylate-binding protein 4	38.14	15.37	9	70.7
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	4.28	5.39	2	66.5
Q92841	Probable ATP-dependent RNA helicase DDX17	25.9	16.19	10	80.2
Q99623	Prohibitin-2	4.87	7.02	2	33.3
Q8NCA5	Protein FAM98A	11.42	5.78	3	55.4
Q9P258	Protein RCC2	6.72	6.51	3	56
Q92734	Protein TFG	14.19	17	6	43.4
Q13283	Ras GTPase-activating protein-binding protein 1	38.31	21.46	7	52.1
Q9UN86	Ras GTPase-activating protein-binding protein 2	22.07	13.49	5	54.1
P27694	Replication protein A 70 kDa DNA-binding subunit	7.29	5.52	3	68.1
Q96PK6	RNA-binding protein 14 (RBM14)	7.23	5.83	3	69.4
A0AV96	RNA-binding protein 47 (RBM47)	4.67	4.05	2	64.1
P35637	RNA-binding protein FUS	19.62	11.22	6	53.4
Q13501	Sequestosome-1	23.37	24.09	6	47.7
Q01130	Serine/arginine-rich splicing factor 2	6.31	11.31	2	25.5



P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	7.55	5.26	3	65.3
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial	4.74	6.57	2	32
P37108	Signal recognition particle 14 kDa protein	8.18	28.68	2	14.6
Q9UHB9	Signal recognition particle subunit SRP68	4.97	3.51	2	70.7
P62316	Small nuclear ribonucleoprotein Sm D2	6.2	24.58	3	13.5
<b>Q9BQ15</b>	<b>SOSS complex subunit B1</b>	<b>6.82</b>	<b>14.69</b>	<b>2</b>	<b>22.3</b>
Q15637	Splicing factor 1	4.98	4.07	2	68.3
P51571	Translocon-associated protein subunit delta	5.03	13.87	2	19
P12956	X-ray repair cross-complementing protein 6	41.22	30.05	15	69.8
Q9Y5A9	YTH domain-containing family protein 2	5.63	4.66	2	62.3

**A****C****B****Fig. S1**

**Figure S1.** (A) Calibration of Sephacryl S-300 HR columns with various standard globular proteins and their calibration curve (right top). (B) Coomassie blue stained gels of protein standards (fractions 1-28) collected from sucrose gradient centrifugation. The positions of standards are indicated at the top. Note: Alcohol dehydrogenase is a tetramer containing four equal subunits. (C) Calibration of Sephacryl S-100 HR columns with various standard globular proteins and their calibration curve (right top).

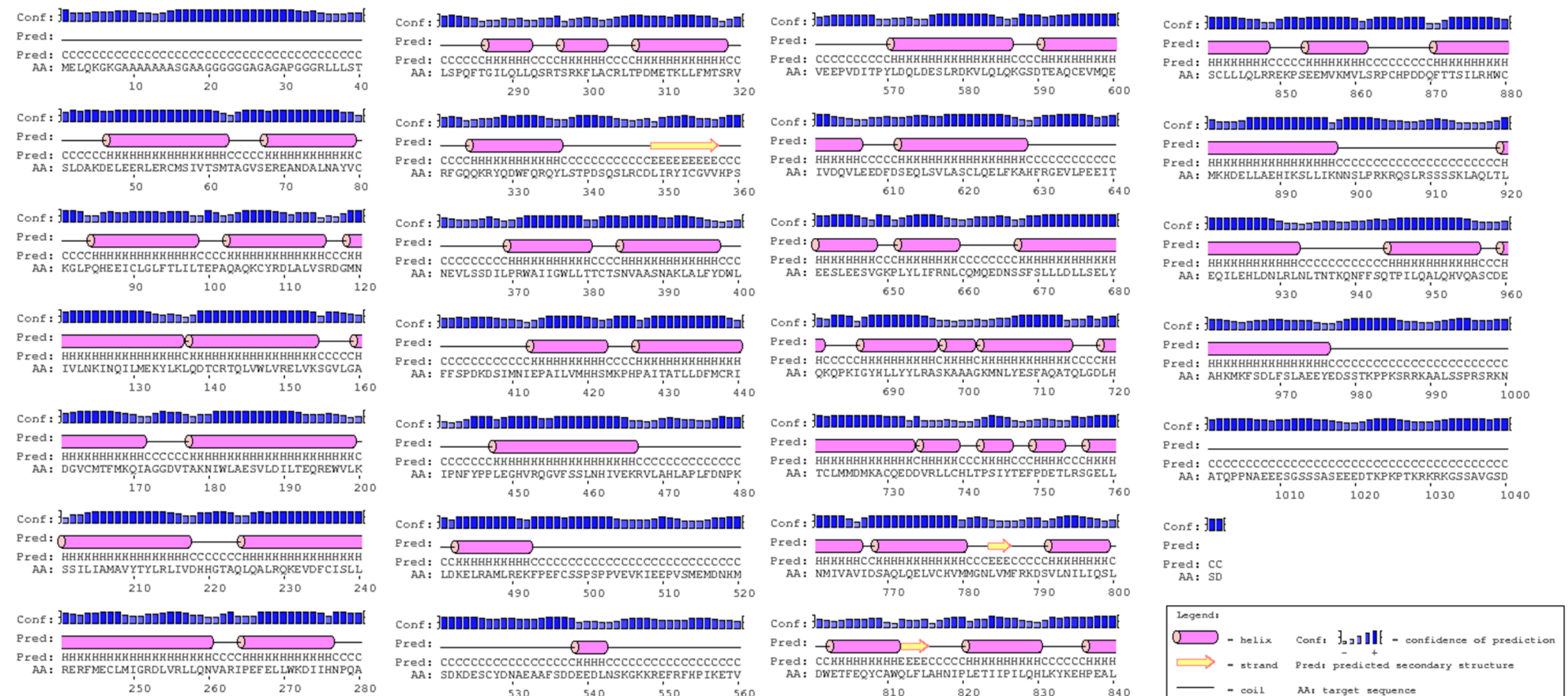
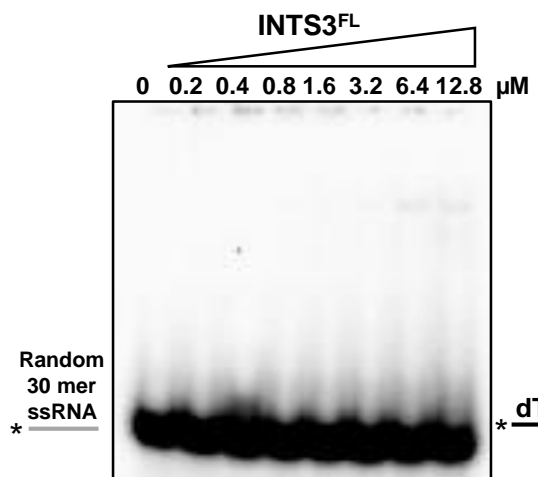
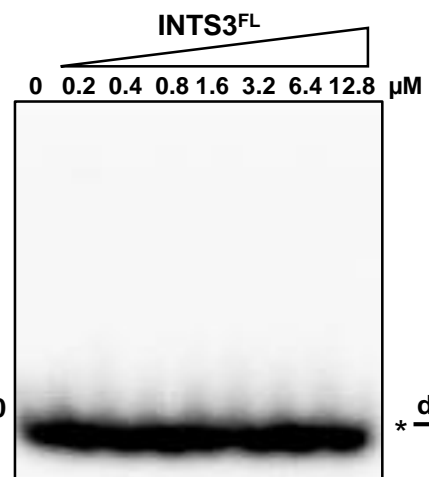
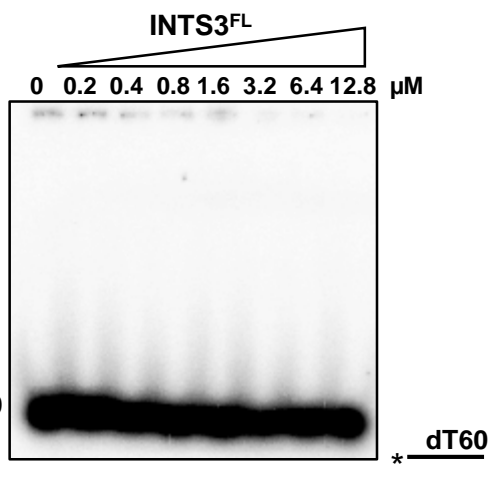
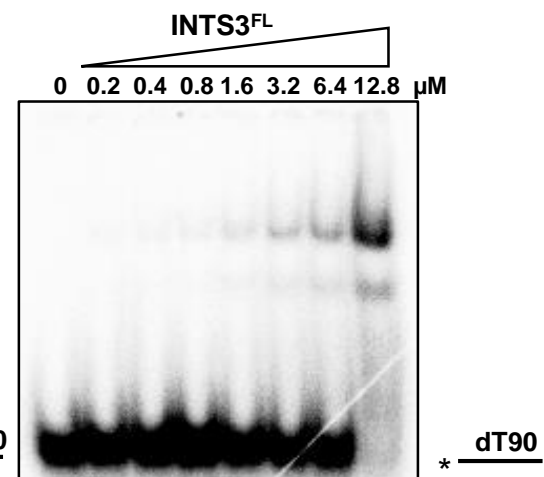
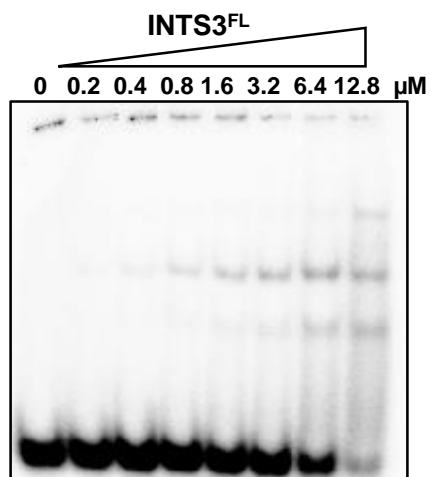
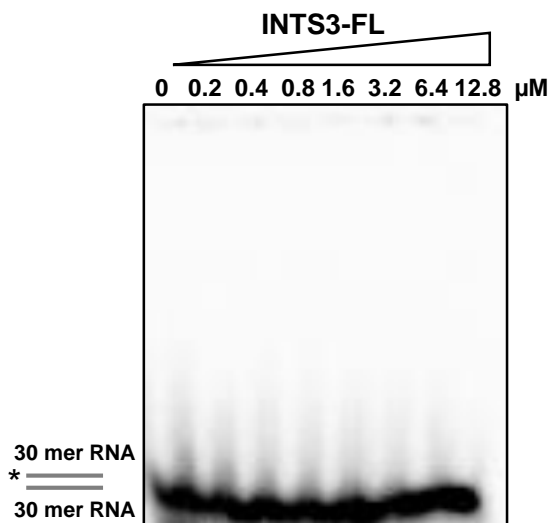
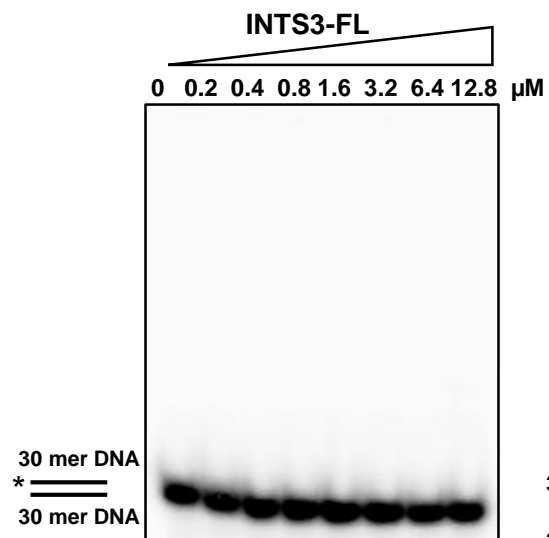
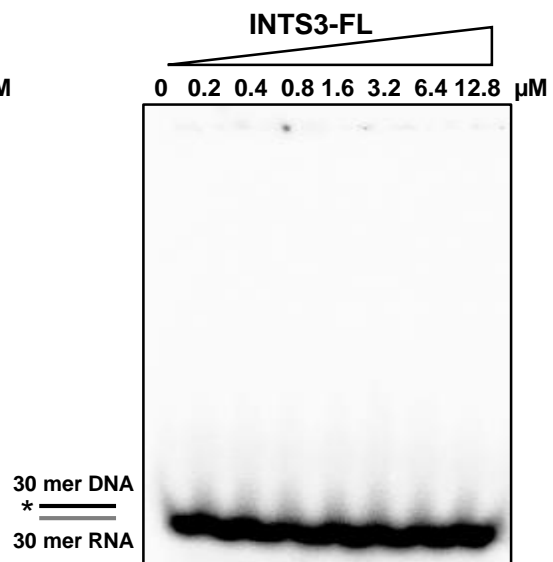
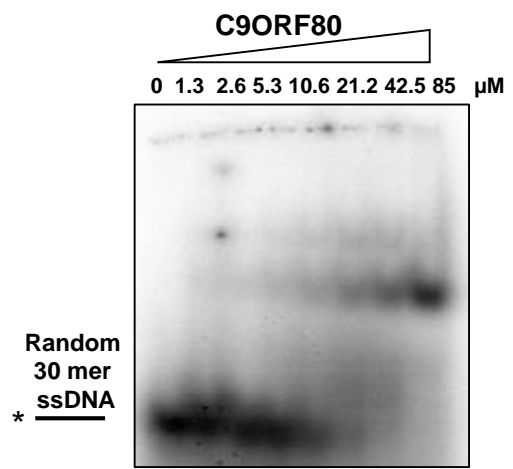
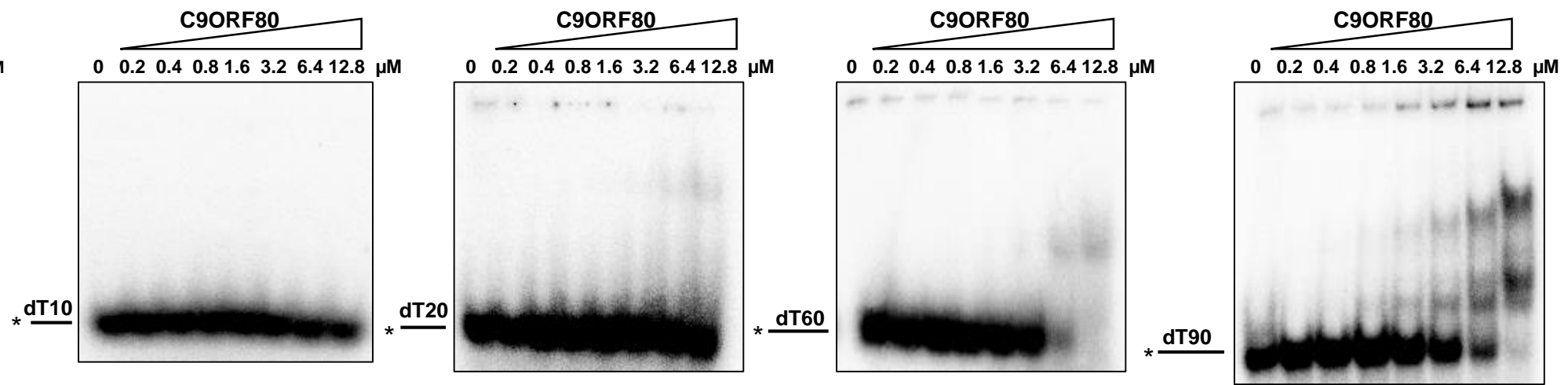
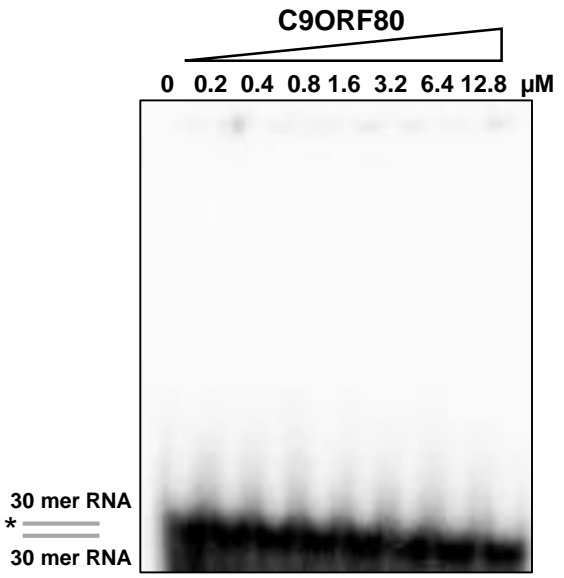
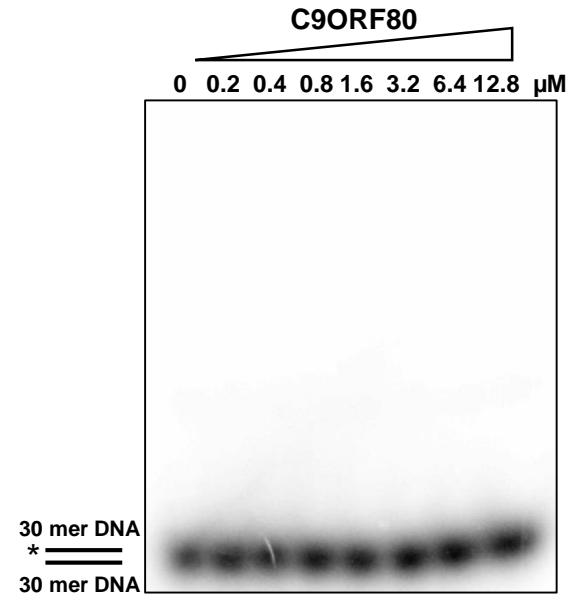
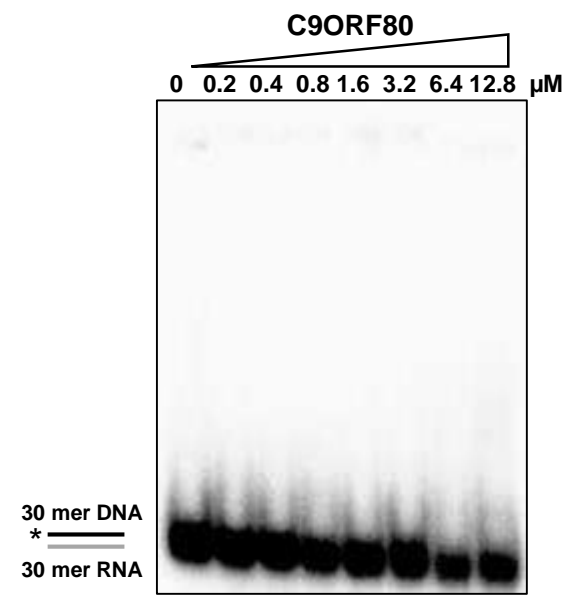


Figure S2. Secondary structure prediction of INTS3<sup>FL</sup> protein by PSIPRED.

**A****B****INTS3<sup>FL</sup>****INTS3<sup>FL</sup>****INTS3<sup>FL</sup>****C****D****E****Fig. S3**

**Figure S3.** Representative EMSA images for INTS3 full length protein binding with random 30 mer ssRNA (**A**), various lengths of dT (10, 20, 60 and 90, **B**), dsRNA (**C**), dsDNA (**D**), or DNA:RNA hybrid (**E**).



**A****B****C****D****E****Fig. S5**



**Figure S5.** Representative EMSA images for increasing protein concentration of C9ORF80 protein binding with random 30 mer ssDNA (**A**), various lengths of dT (10, 20, 60 and 90, **B**), dsRNA (**C**), dsDNA (**D**), or DNA: RNA hybrid (**E**).

Sequence: MELQKGKGAATAAASGAAGGGGGGAGAGAPGGGRLLLSTSLDAKDELEERLERCMSIVT  
 Prediction: -----+-----+-----++-----+-----  
 Confidence: 847274823332444722211116111111762394452214551577674966862763

Sequence: SMTAGVSEREANDALNAYVCKGLPQHEEICLGLFTLILTEPAQAQKCYRDLALVSRDGMN  
 Prediction: -----+-----+-----+---+-----+-----  
 Confidence: 352215126462577373866555477898999939994454647831687567374753

Sequence: IVLNKINQILMEKYLKLDTCRTQLVWLVRELVKSGVLGADGVCMTFMKQIAGGDVTAKN  
 Prediction: -----+-----+-----  
 Confidence: 888639438998549262224723964992797125754766877589369845366614

Sequence: IWLAEVLDILTEQREWVLKSSILIAMAVYTYLRLIVDHHGTAQLQALRQKEVDFCISLL  
 Prediction: -----+-----+-----  
 Confidence: 948966996963763645815488887993339299986651613636653584899379

Sequence: RERFMECLMIGRDLVRLQNVARIPEFELLWKDI IHNPQALSPQFTGILQLLQSRTRSKE  
 Prediction: -----+-----+-----+-----+-----  
 Confidence: 283997999991788199348978689699769996762651547279936621987961

Sequence: LACRLTPDMETKLLFMTSRVRFQKRYQDFQRYLSTPDSQSLRCDLIRYICGVVHPS  
 Prediction: -----+-----+-----+-----+-----+-----  
 Confidence: 557183457523874522868668178121155242566218864824791698869453

Sequence: NEVLSSDILPRWAIIGWLLTTCTSNVAASNAKLALFYDWLFFSPDKDSIMNIEPAILVMH  
 Prediction: -----+-----+-----+-----  
 Confidence: 446523478638999989833521654361566889899998666353786987999997

Sequence: HSMKPHPAITATLLDFMCRIIPNFYPPLEGHVRQGVFSSLNHIVEKRVLAHLAPLFDNPK  
 Prediction: -----+-----+-----  
 Confidence: 535162357273996999399669566844386256523963688539865996886441

Sequence: LDKELRAMLREKFPEFCSSPSPVEVKIEEPVSMEMDNHMSDKDESCYDNAEAAFSDDDE  
 Prediction: -----+-----+-----+-----+-----  
 Confidence: 631587548163864742111225372984783768734624244152648566536775

Sequence: DLNSKGGKREFRFHPIKETVVEEPPVDITPYLDQDESRLRDKVLQQLKGSDETAQCEVMQE  
 Prediction: -----+-----+-----+-----+-----  
 Confidence: 451697999637564937699898989463995955376537837364131263889979

Sequence: IVDQVLEEDFDSEQLSVLASCLQELFKAHFRGEVLP EEITEESLEESVKGPLYLIFRNLC  
 Prediction: -----+-----+-----+-----+-----  
 Confidence: 999899998774838288627946972737165975889468486446716918993698

Sequence: QMQEDNSSFSLLLDLLSELYQKQPKIGYHLLYYLRASKAAAGKMNLYESFAQATQLGDLH  
 Prediction: -----+-----+-----+-----+-----  
 Confidence: 363551225289999945823622756159844967173222742636569473374395

Sequence: TCLMMDMKACQEDDVRLCHLTPSIYTEFPDET LRSGELLNMIVAVIDSAQLQELVCHVM  
 Prediction: -----+-----+-----+-----+-----  
 Confidence: 389899937746759297879343832486554773557859999996363956999798

**Fig. S6**

```

Sequence:      MGNLVMFRKDSVLNLIQSLDWETFEQYCAWQLFLAHNIPLLETIIPILQHLKYKEHPEAL
Prediction:    -----
Confidence:    896886734737849994376564886589689999778597499899557122532577

Sequence:      SCLLLQLRREKPSSEEMVKMVLSPCHPDDQFTTSSILRHWCMKHDELLAEHIKSLLIKNNNS
Prediction:    -----++-+-----+-----+-----+
Confidence:    379771667162136792898373533554621279144884997989969226671317

Sequence:      LPRKRQSLRSSSSKLAQLTLEQILEHLDNLRNLNTNTKQNFSSQTPILQALQHVQASCDE
Prediction:    -+++++-----+--+-----
Confidence:    168898969887773418498699989649771367112126344786399669373653

Sequence:      AHKMKFSDLFSLAEYEDSSTKPPKSRKAALSSPRSRKNATQPPNAEEESGSSSAESEE
Prediction:    -----+++++-----+++++-----+++-----
Confidence:    52282735985798634317899999997119899899968821132321287721112

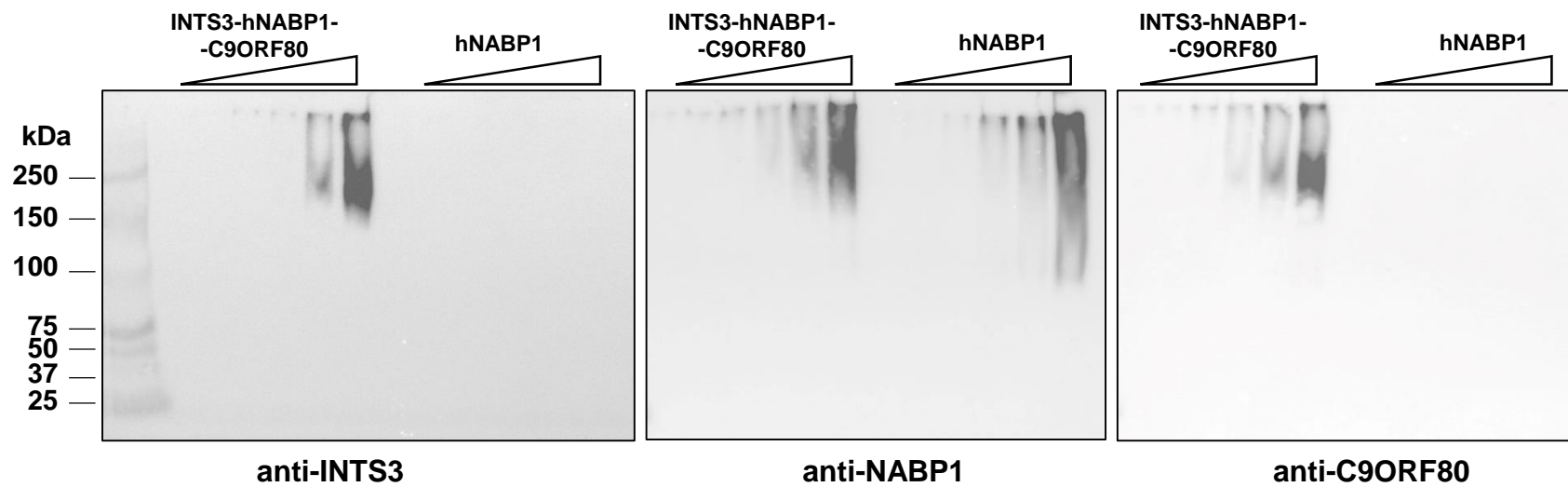
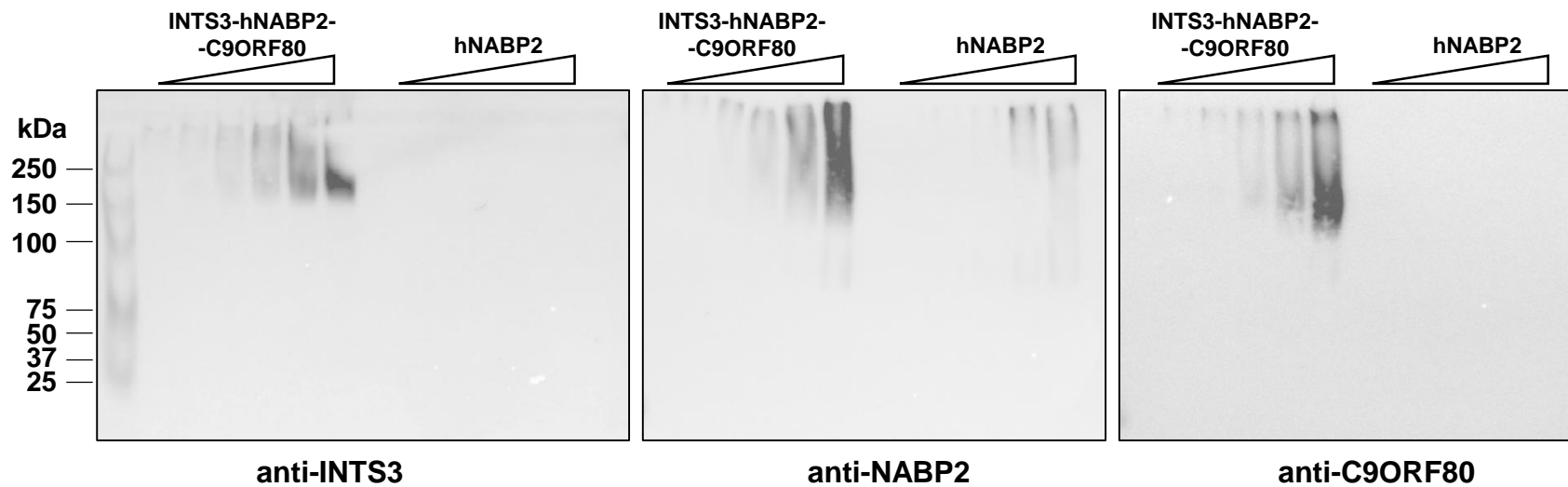
Sequence:      DTKPKPTKRKRKGSSAVGSDSD
Prediction:    -+++++-----+----
Confidence:    268699999998981116214

```

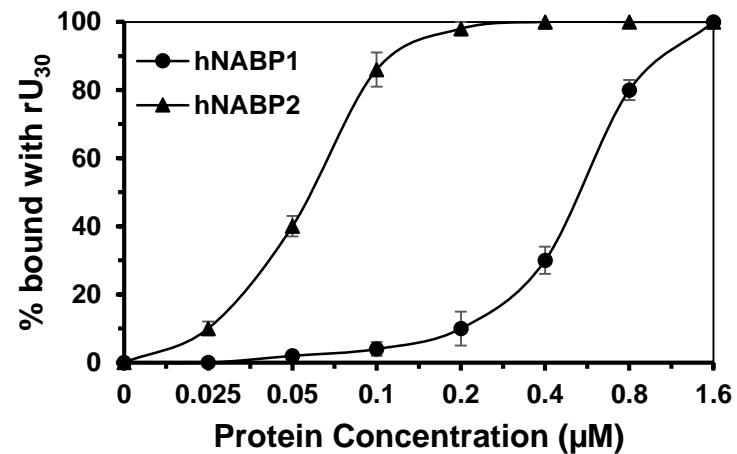
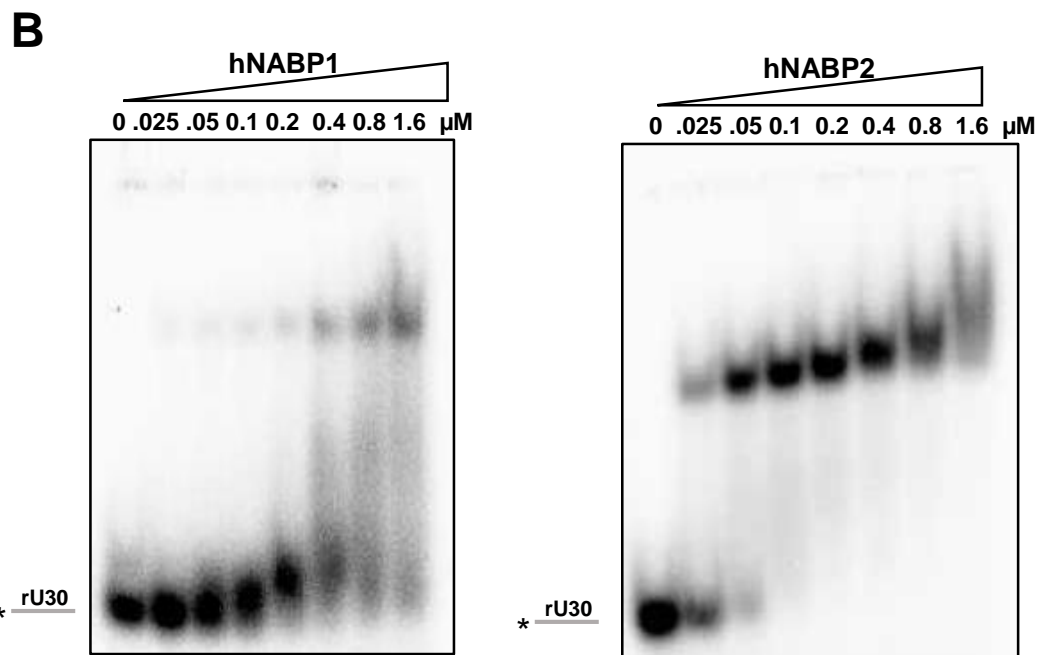
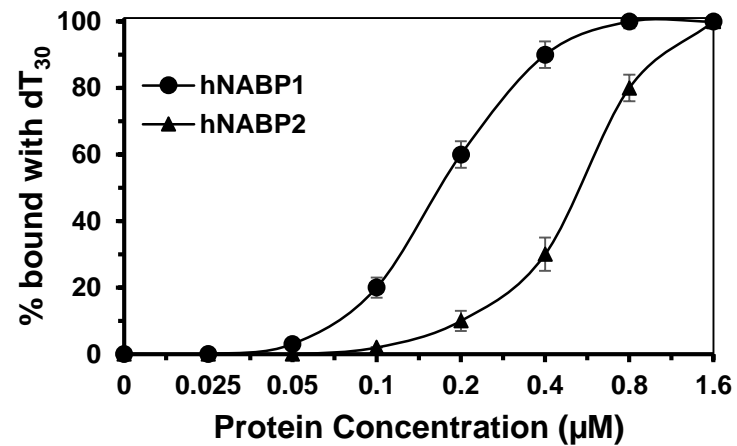
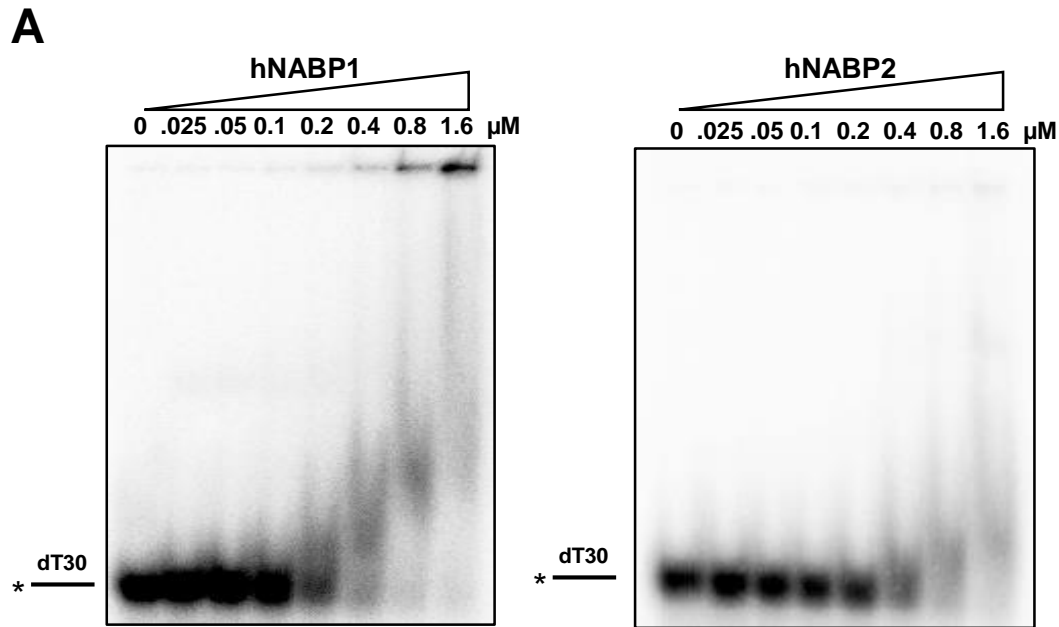
\*\*\* Prediction: binding residues are labeled with '+' and in red;  
non-binding residues labeled with '-' and in green.  
\*\*\* Confidence: from level 0 (lowest) to level 9 (highest).

## Fig. S6 (cont'd)

**Figure S6.** Prediction of INTS3 protein binding with ssDNA using BindN with 90% expected specificity.

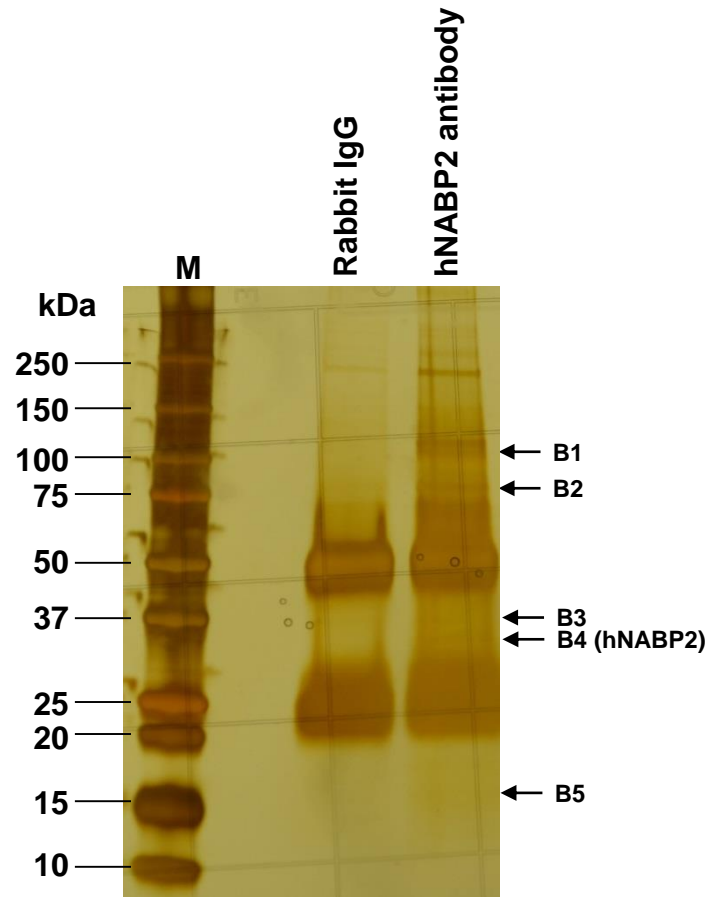
**A****B****Fig. S7**

**Figure S7.** Western blot detection of individual protein with indicated antibodies in the INTS3<sup>FL</sup>-hNABP1-C9ORF80 complex binding with dT<sub>30</sub>(**A**), and INTS3<sup>FL</sup>-hNABP2-C9ORF80 complex with rU<sub>30</sub> (**B**).



**Fig. S8**

**Figure S8.** Representative EMSA images for hNABP1 and hNABP2 binding with dT<sub>30</sub> (**A**) and rU<sub>30</sub> (**B**), and their quantitative analysis (right).



**Figure S9.** Silver staining of immunoprecipitated proteins using a hNABP2 antibody and rabbit IgG. Samples were separated on a gradient (4-20%) SDS-PAGE gel. M: protein marker. The excised bands are indicated as B1-5.