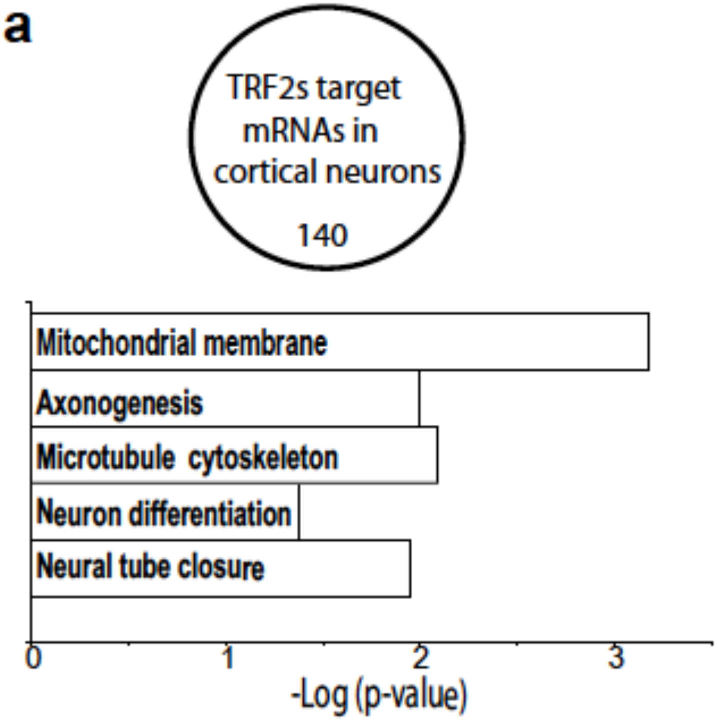
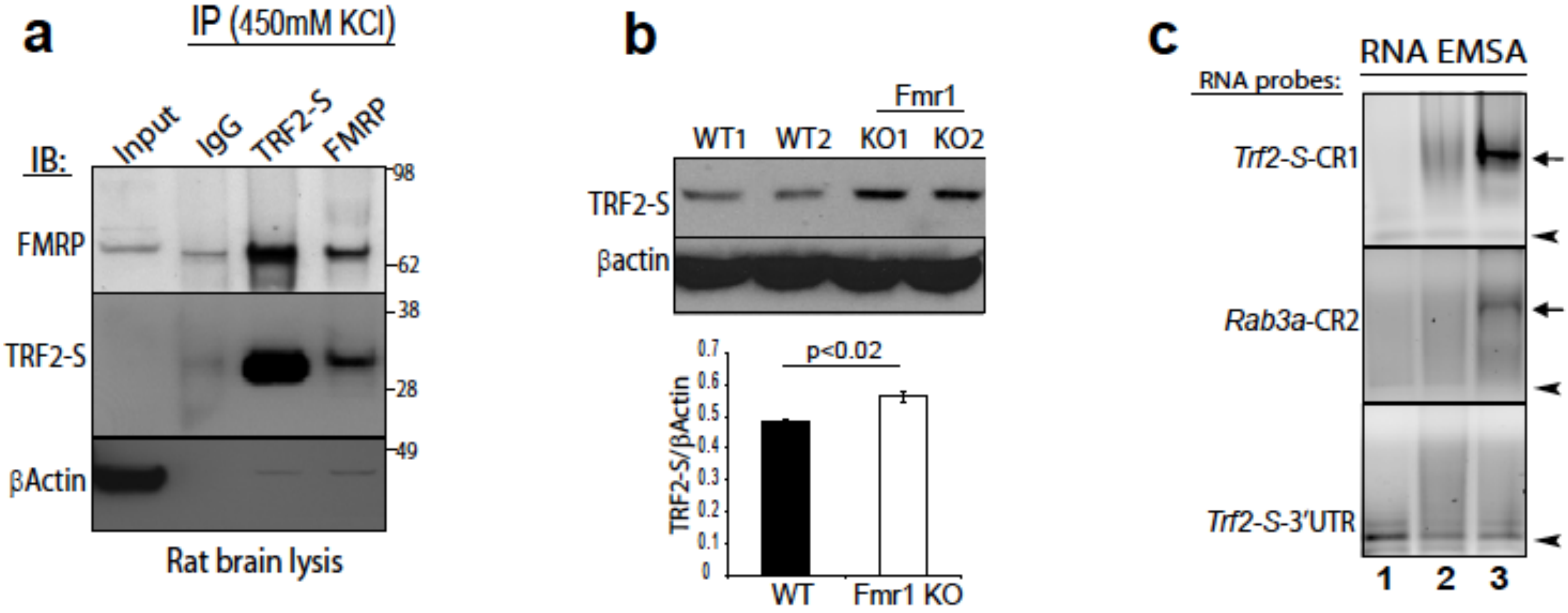


b

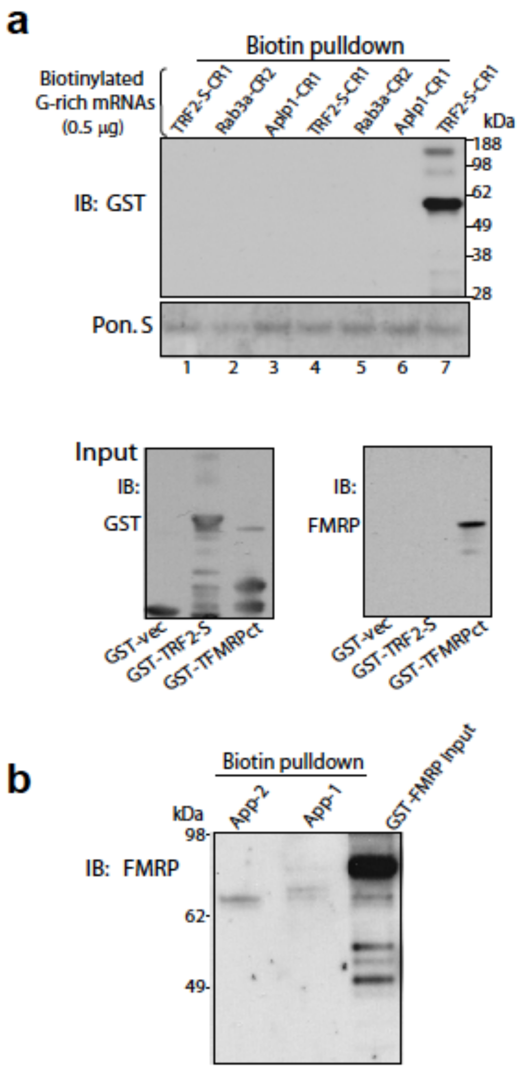
Putative TRF2-S target axonal mRNAs

RAB3A
APLP1
RAB2
SYPL
GDI1
GNG10
NREP
Akt1
Brsk1
PPP2R5B
YY1
HMGB2
TXN1
CIC
Cox7b
TOMM22
RPL18A
RPL13A
LOC499793
Rpl7
NNAT
MAP1B
Map1lc3a
MAPRE1
MTAP2
Nckap1
ATP5G3
SLC25A11
COX7A2L
BAX
Ndufb2
NDUFB3

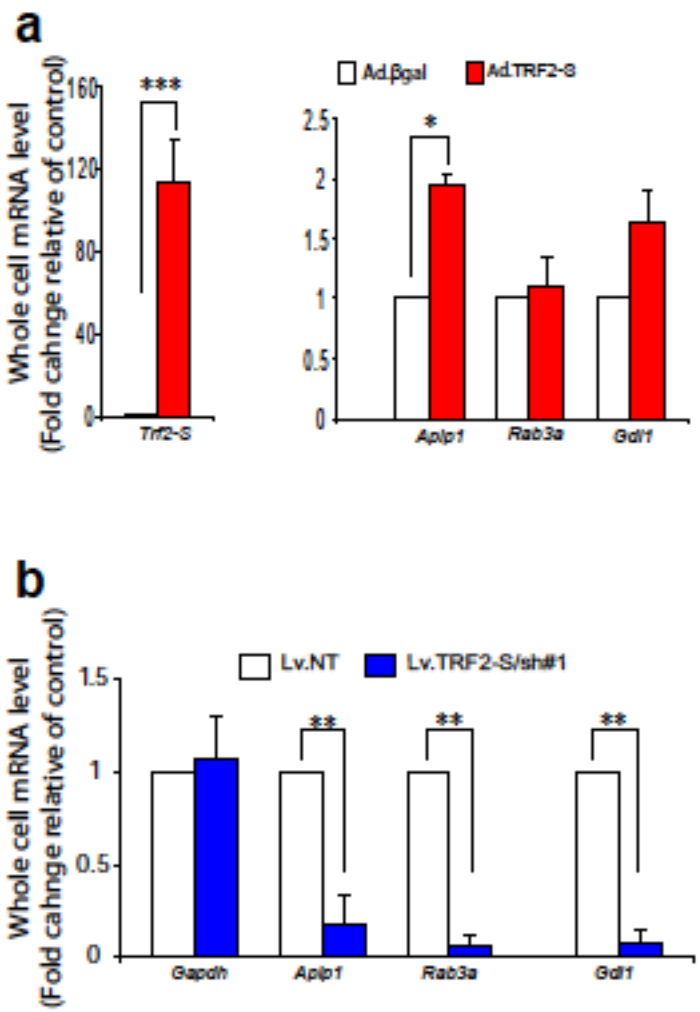
Supplementary Figure 1 | (**a**) Profiling of TRF2-S-associated transcriptomes in cortical neurons. Ribonucleoprotein (RNP) immunoprecipitation (RIP)-assay and subsequent microarray analysis identified 140 putative TRF2-S bound transcripts in cultured rat cerebral cortical neurons. A bar graph shows the top gene ontology (GO) terms that are enriched in TRF2-S targets. The GO terms are ranked by -log *P* values. (**b**) A list of putative TRF2-S target axonal mRNAs.



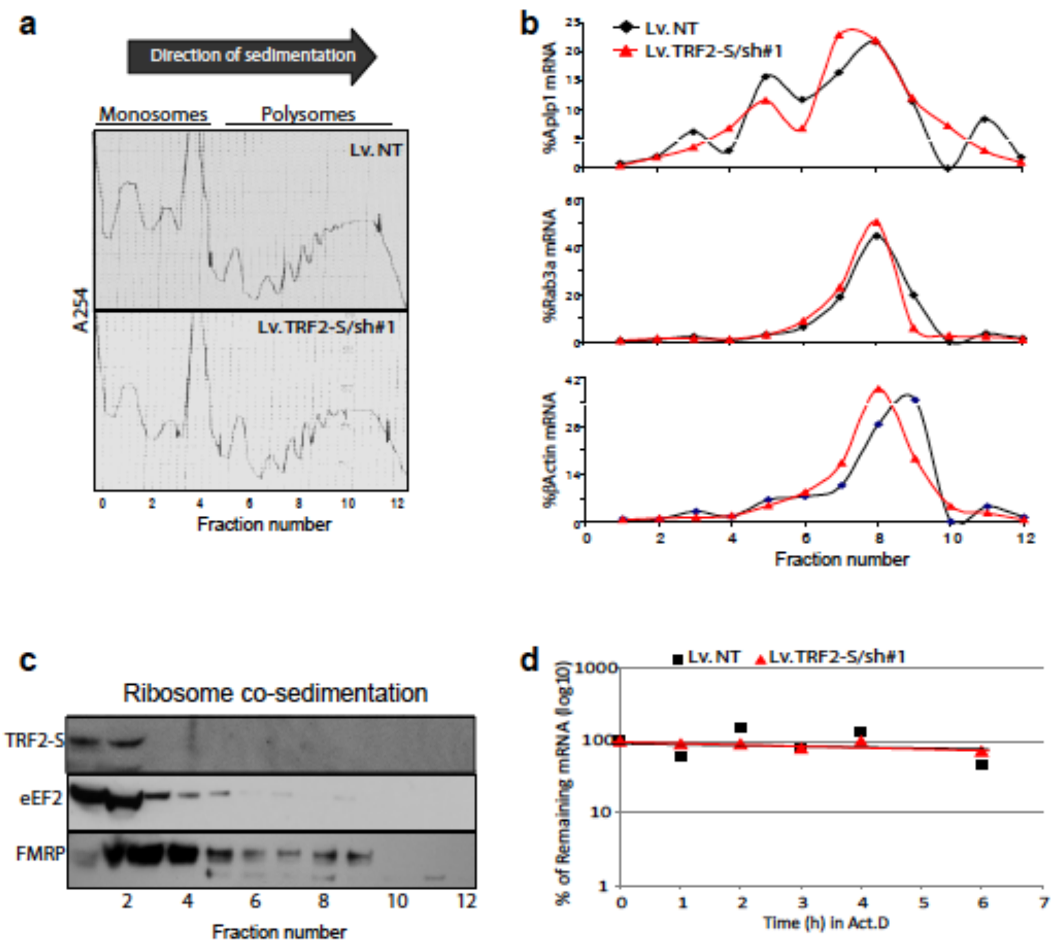
Supplementary Figure 2 | (**a**) CoIP of TRF2-S and FMRP with brain cytoplasmic extracts using 450 mM KCl IP buffer. The immunoblots demonstrate that endogenous TRF2-S and FMRP interact with each other under the high salt IP condition. (**b**) WT and *Fmr1* KO brain lysates were subjected to immunoblotting using FMRP and TRF2-S antibodies. Relative protein loading was assessed by bActin. Bottom, densitometry analysis of TRF2-S normalized to bActin. n=3 per group. All values are mean±SD. P values are based on Student's *t*-test. (**c**) RNA mobility shift assay showing that the binding of FMRP with TRF2-S inhibited the formation of TRF2-S-mRNA complex. The lysate from HEK293 cells expressing HA-TRF2-S was mixed either with or without recombinant GST-FMRP protein prior to HA-CoIP. The purified protein complexes were than incubated with TRF2-S target RNA fragments *Trf2*-S-CR1 (upper), *Rab3*a-CR2 (middle) and a non-target RNA fragment *Trf2*-S-3'UTR (lower) for RNA-EMSA. Lane 1, GST-FMRP only; Lane 2, GST-FMRP plus HA-TRF2-S; lane 3, HA-TRF2-S only. Arrow and arrowhead point to bound and unbound mRNA fragments, respectively.



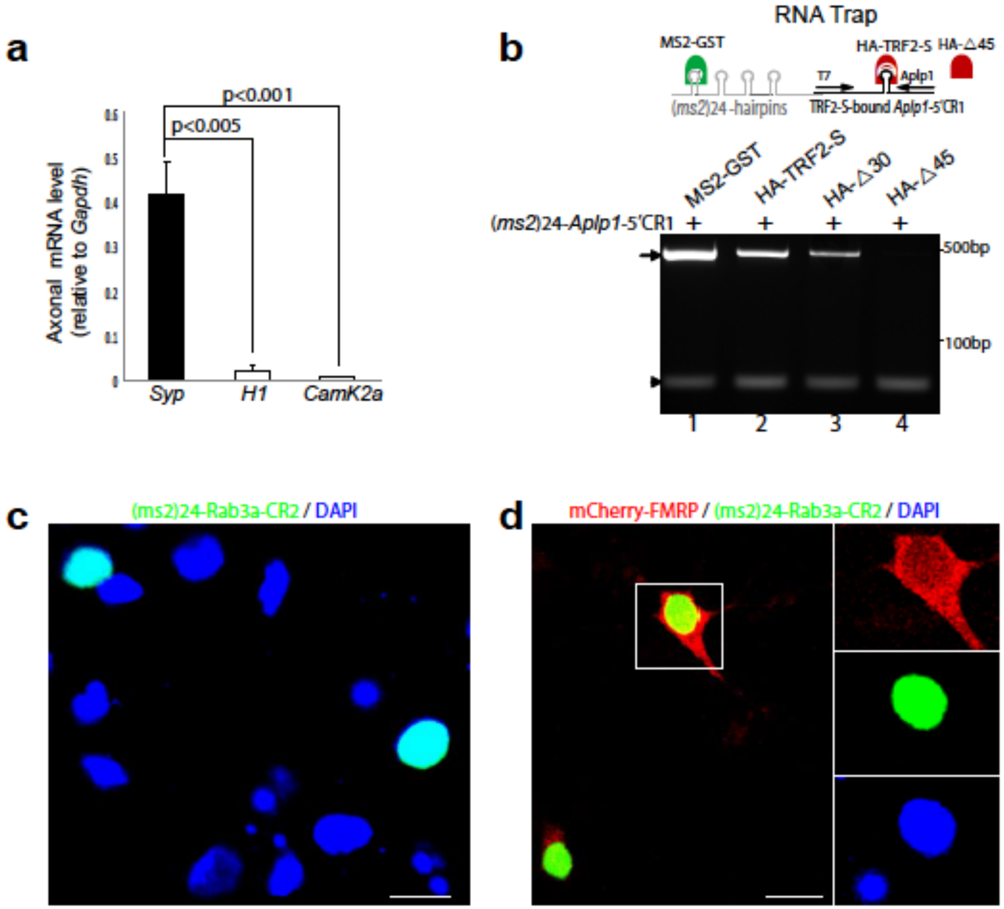
Supplementary Figure 3 | (**a**) Top, biotin pulldown and immunoblotting showing that neither recombinant GST empty vector (lane 1-3) nor GST-FMRPct (lane 4-6) that contains a truncated mouse FMRP with RNA binding RGG box were capable of binding to TRF2-S target mRNAs. GST-TRF2-S (lane7) served as positive control. Bottom, input of GST tagged recombinant proteins. (**b**) Biotin pulldown and immunoblotting showing that recombinant GST-FMRP was capable of binding to biotinylated *App1* and *App2*, two *App* fragments known as FMRP targets[41,42].



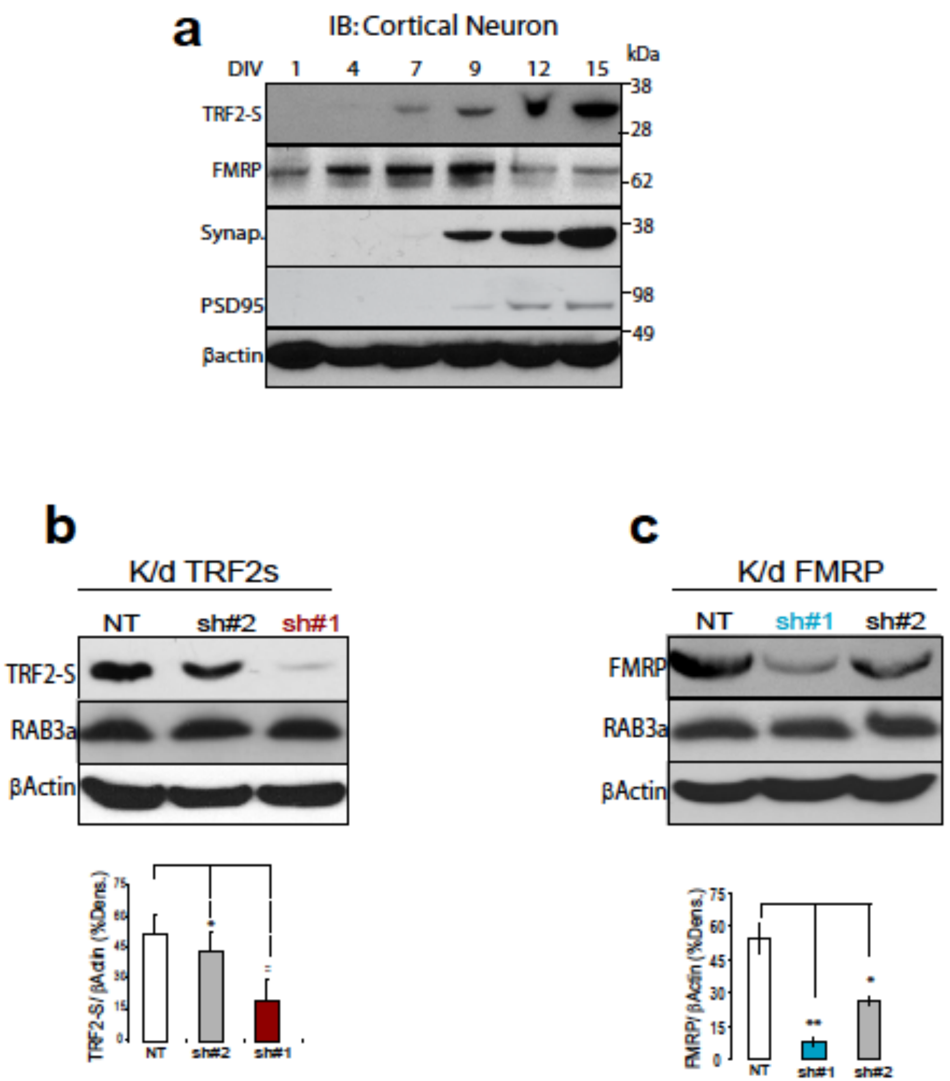
Supplementary Figure 4 | (**a-b**) On culture day 6 cortical neurons were infected for 4 days with adenovirus bearing βGal and TRF2-S (a), and lentivirus bearing shRNA#1 (865) for TRF2-S silencing and non-target control (b). The whole cell extracts were subjected for RT-qPCR analysis of TRF2-S target mRNAs. The values are the fold change normalized to*18S rRNA*. *Gapdh* is a non-target mRNA of TRF2-S. n=3. All values are mean±SD. P values are based on Student's *t*-test.



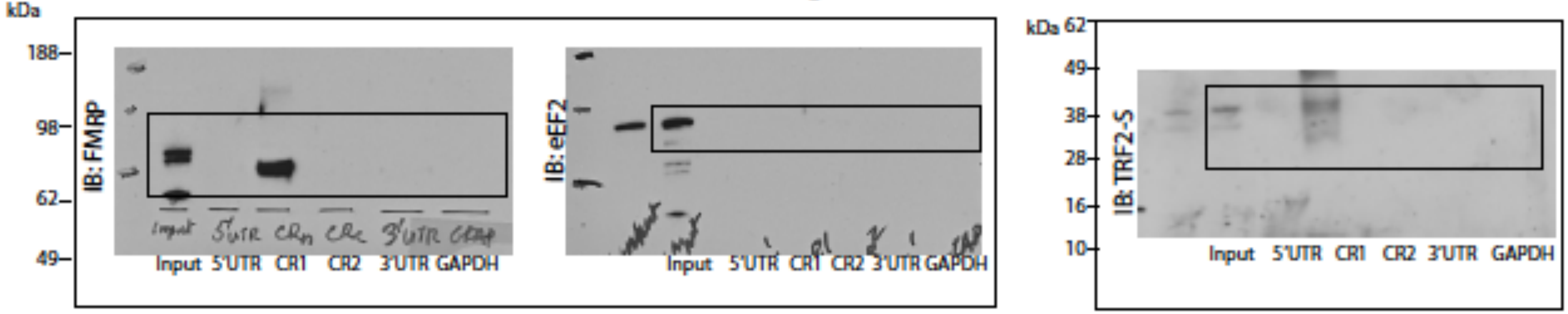
Supplementary Figure 5 | TRF2-S exhibits a monosomal sedimentation profile, and has little or no global effects on translations of its target mRNA. (**a**) On culture day 6 cortical neurons were infected for 4 days with lentivirus carrying non-target (NT) scramble shRNA and TRF2s targeting shRNA#1. Whole cell lysates were fractionated through linear sucrose gradients (15-60%). The arrow indicates the direction of sedimentation from monosomes to polysomes. (**b**) The relative distributions (percentages) of *Aplp1*, *Rab3a* and *Actb* mRNAs were quantified by RT-qPCR analysis of RNA in each of 12 gradient fractions. (**c**) TRF2-S, FMRP and eEF2 protein distributions in each of 12 gradient fractions from the cortical neuron lysate (9 d in culture) were analyzed by immunoblotting. (d) On culture day 6 cortical neurons were subjected to lentiviral mediated TRF2-S silencing as described in a. Four days later neurons were treated with actinomycin D. The RNAs were collected at the indicated times. The half-life of *Aplp1*mRNA was analyzed by RT-qPCR upon normalization to *Gapdh*, defined as the time needed to reach 50% of its original abundance at time 0 h. The linear-fit lines are for Lv. NT-control (black) and Lv. TRF2-S/sh#1(red), respectively. The graph represents two independent experiments.



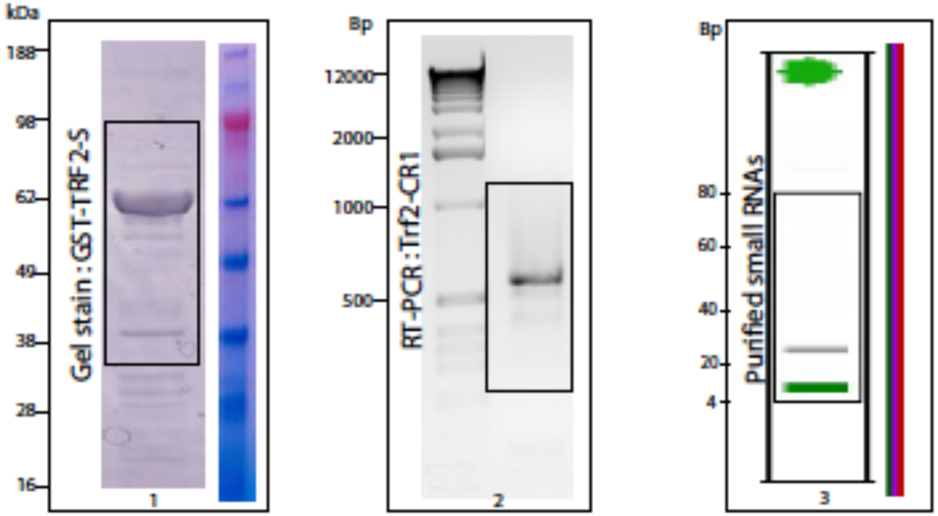
Supplementary Figure 6 | (**a**) RT-qPCR analysis of axonal mRNAs harvested from the high-throughput microfluidic system after 9 d cortical neuron cultures. Upon the normalization with *Gapdh*, the axonal mRNA *synaptophysin* (*Syp*) was readily detectable, whereas the levels of dendritic mRNA *calcium/calmodulin-dependent protein kinase II* (*CamK2a*) and nuclear mRNA *Histone1*(*H1*) were barely measurable (average Ct values are larger than 33.6 and 32.3, respectively). n=3. All values are mean±SD. P values are based on Student's *t*-test. (**b**) Top, schematic of RNA trap assay and necessities of TRF2-S GAR domain and MS2-GST for precipitation of a (*ms2*)24 fused TRF2-S target RNA chimera. Bottom, HEK293 cells were co-transfected with the plasmid expressing (*ms2*)24 tagged *Aplp1*-5'CR1 RNA chimera, accompanied with either MS2-GST or HA-TRF2-S variants. The existence of the exogenous RNA chimera in each GST- or HA-precipitates was assessed by RT-PCR using a primer set (T7 and Aplp1). An arrow points to PCR products; an arrowhead points to primer dimmers. (**c-d**) DIV7 cortical neurons were co-transfected with MS2-YFP-NLS and (*ms2*)24-*Rab3a*-CR2 without (**c**) or with mCherry-FMRP (**d**). Overexpression of mCherry-FMRP failed to translocate YFP labeled RNP from the nucleus. The images are representative from 50 transfected neurons per group. Scale bar=20μm.



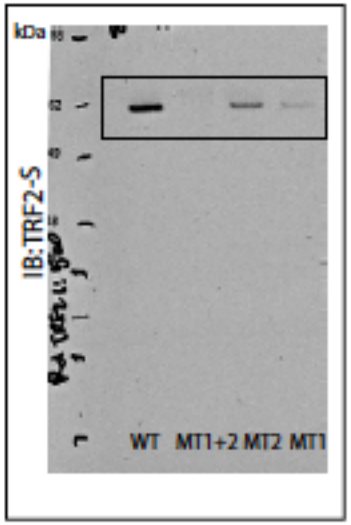
Supplementary Figure 7 | (**a**) Immunoblots showing the expression patterns of TRF2-S and FMRP during the course of neuronal maturation. Synaptophysin (Synap) and PSD95 are pre-and post-synaptic markers, respectively. (**b-c**) Neurons (6 days in culture) were infected for 4 days with lentivirus carrying shRNAs for the silencing of rat TRF2-S (shRNA#1, 865 and shRNA#2, 774) in **b**; for the silencing of rat FMRP (shRNA#1, 2624 and shRNA#2, 2623) in **c**. A non-target (NT) scramble shRNA was used as controls. Cell lysates were then subjected to immunoblot analysis of endogenous levels of Rab3a, along with TRF2-S (**b**) and FMRP (**c**). Densitometry analysis showed as bar graphs at bottom of b and c. n=3; *p<0.05 and **p<0.005. All values are mean±SD. P values are based on Student's *t*-test.



Full scan for western blot in Figure 1 c



Full scan for blots in Figure 1 d

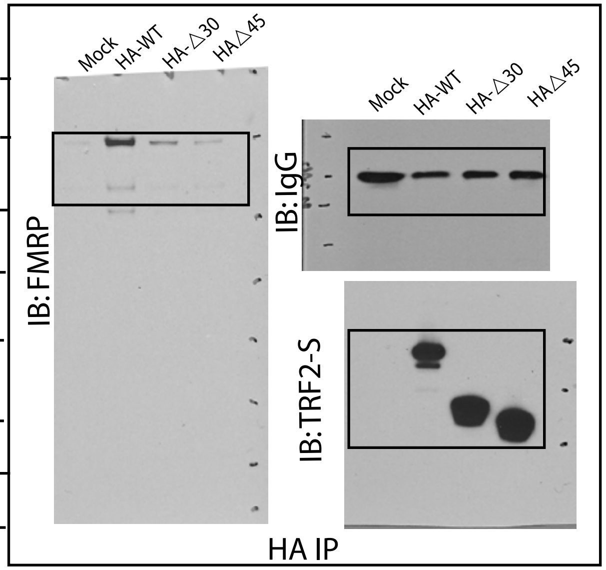


Full scan for blots in Figure 1 e

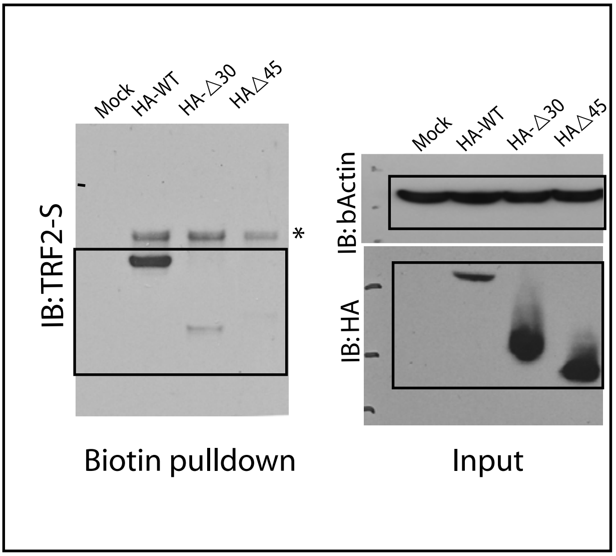
Supplementary Figure 8. Full blots for Figures 1c, d and e**.**

Supplementary Figure 9

Full scan for western blots in Fig. 2a

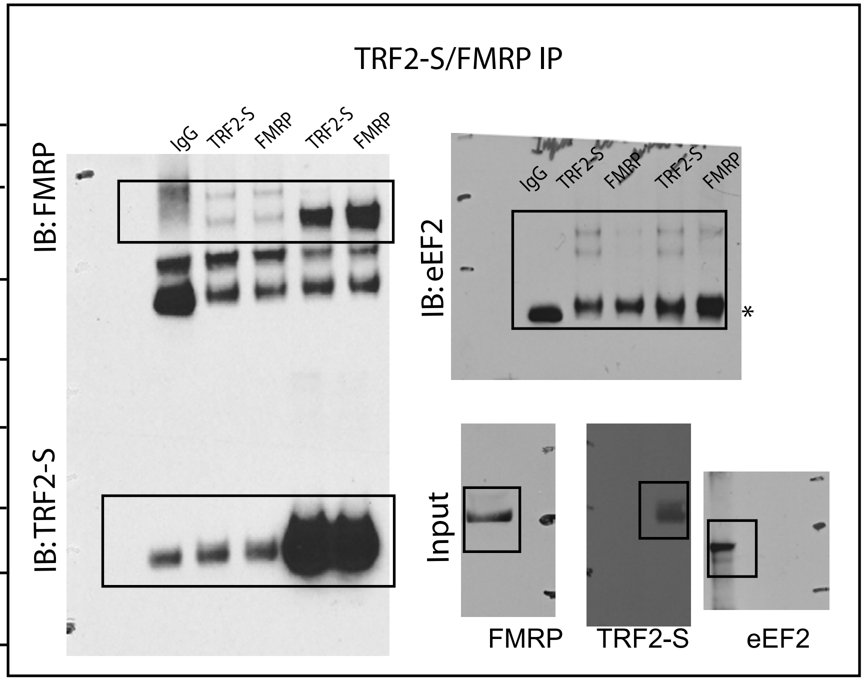


Full scan for western blots in Fig. 2b



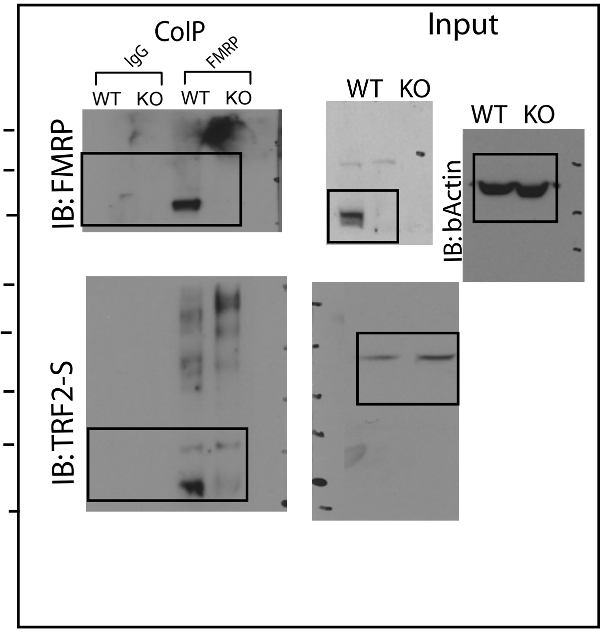
* Endogenous TRF2 in 293 cells

Full scan for western blots in Fig. 2c

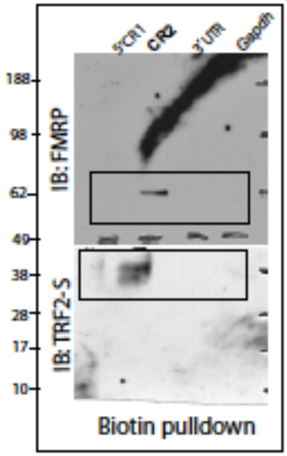


* IgG

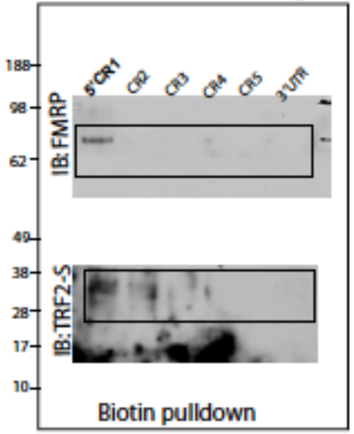
Full scan for western blots in Fig. 2d



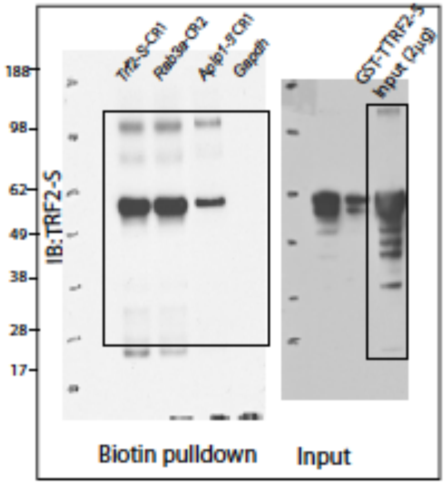
Full scan for western blots in Fig. 3a



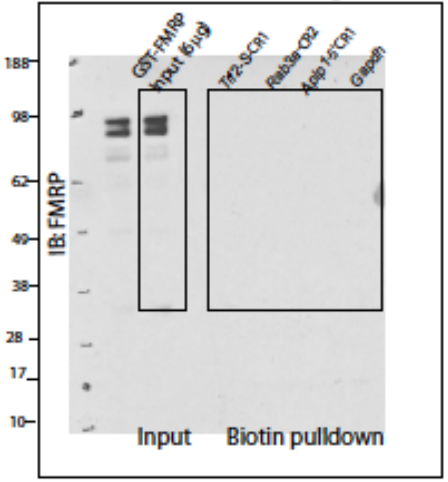
Full scan for western blots in Fig. 3b



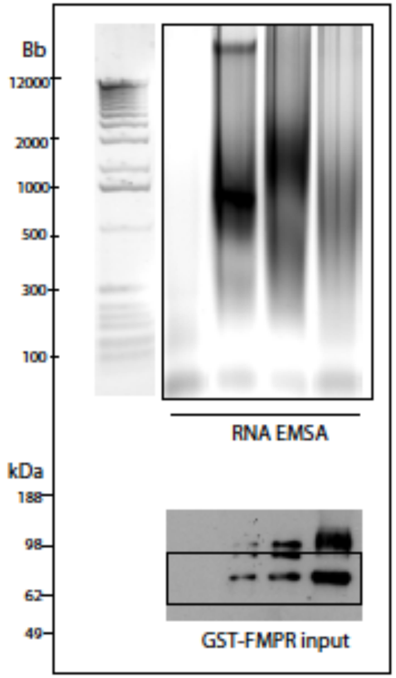
Full scan for western blots in Fig. 3c



Full scan for western blots in Fig. 3d



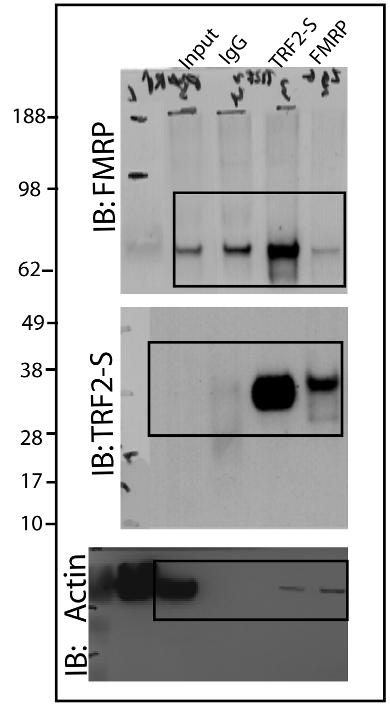
Full scan for blots in Fig. 3e



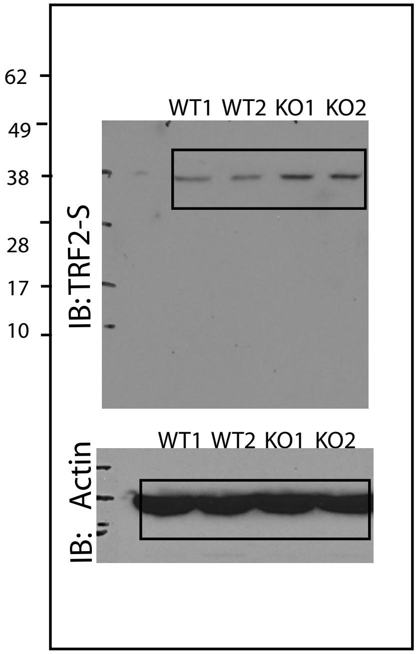
Supplementary Figure 10. Full blots for Figures 3 a, b c, d and e**.**

Supplementary Figure 11

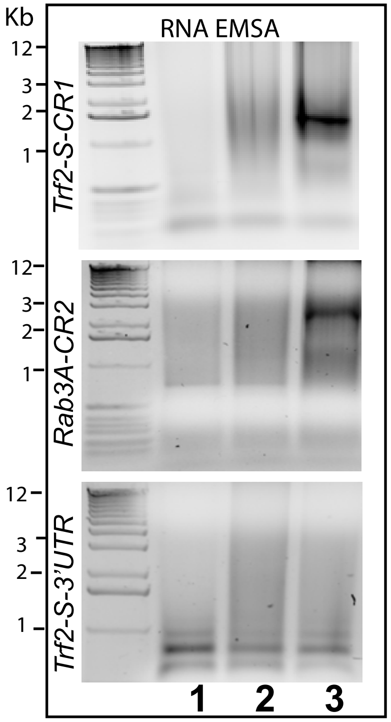
Full scan for western blots in Supplementary Fig. 2a

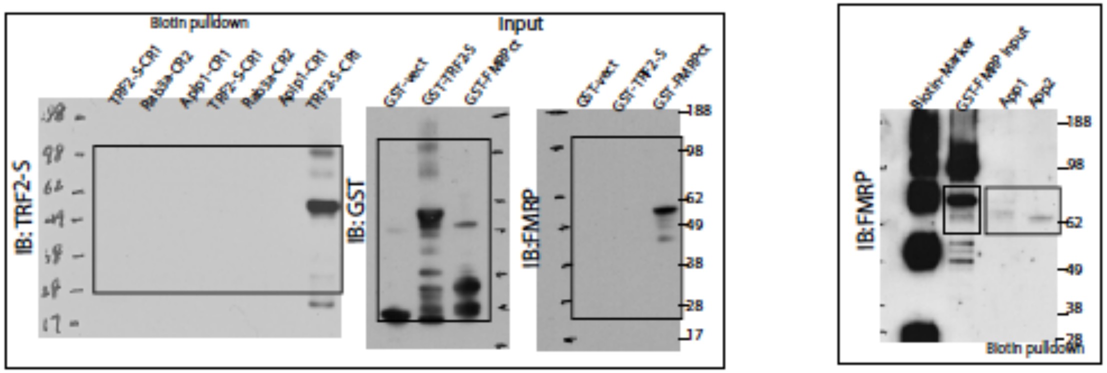


Full scan for western blots in Supplementary Fig. 2b



Full scan for western blots in Supplementary Fig. 2c



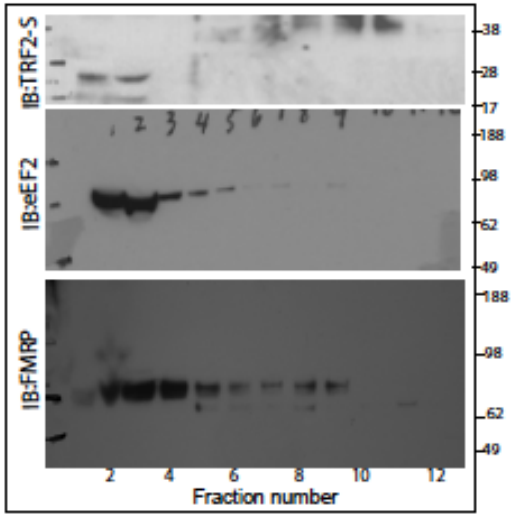


Full scan for western blots in Supplementary Fig. 3a

Full scan for western blots in Supplementary Fig. 3b

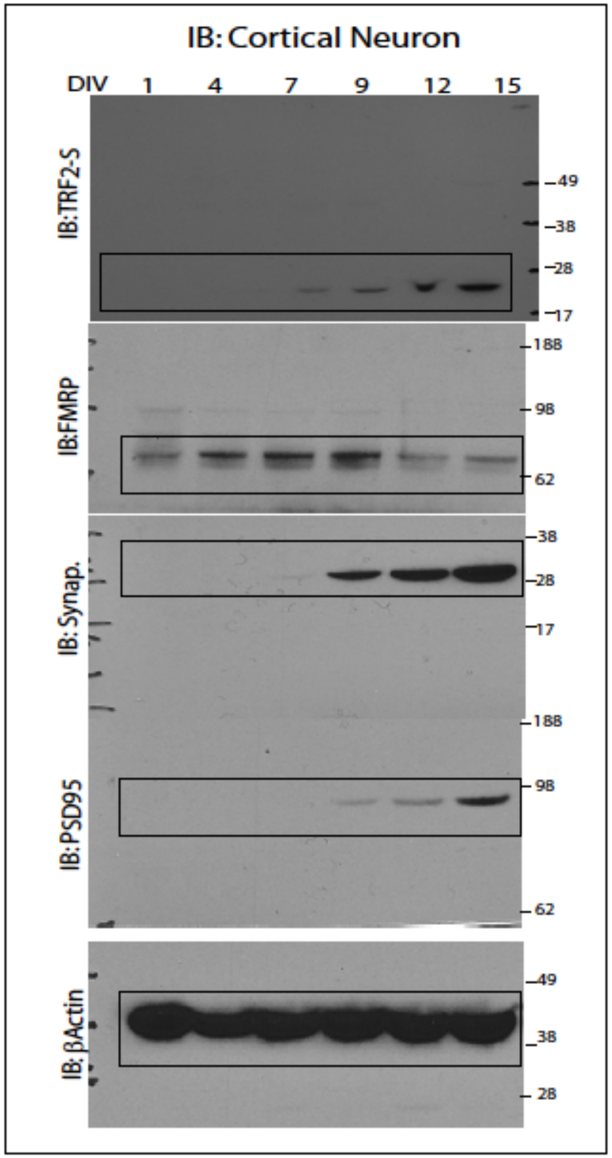
Supplementary Figure 12. Full blots for Supplementary Figures 3 a and b.

Full scan for western blots in Supplementary Fig. 5c

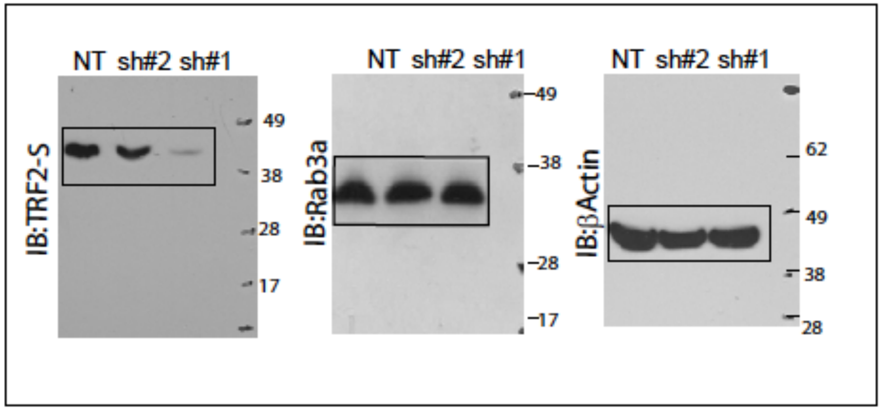


Supplementary Figure 13. Full blot for Supplementary Figure 5c.

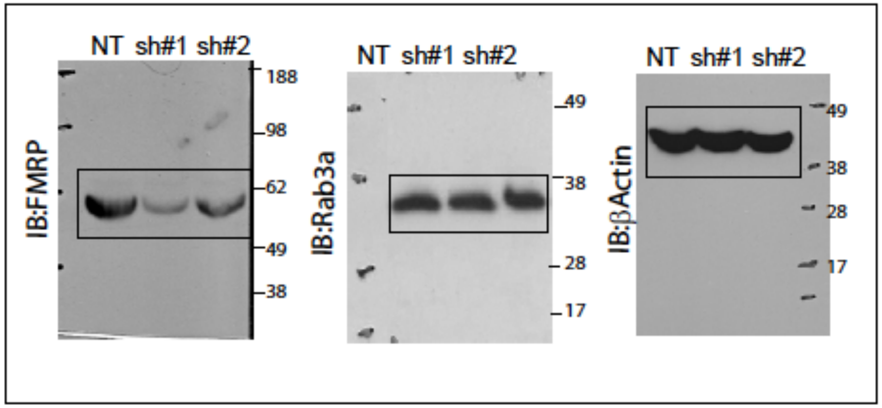
Full scan for western blots in Supplementary Fig. 7a



Full scan for western blots in Supplementary Fig. 7b



Full scan for western blots in Supplementary Fig. 7c



Supplementary Figure 14. Full blots for Supplementary Figures 7a, b and c.

Supplemental table1. **Global analysis of TRF2-S bound neural mRNAs**

Gene Symb	group 1 Z ratio	group 2 Z ratio	**RefSeq ID**	GI	Description
MLPH	14.07	8.5	NM_001012135.1	58865839	melanophilin (Mlph)
Akt1	9.67	5.85	NM_033230	402692490	thymoma viral proto-oncogene 1 (Akt1)
NNAT	9.12	9.85	NM_181687	399498546	neuronatin (Nnat)
Gcfc2	8.79	5.37	NM_001134554	197386558	GC-rich sequence DNA-binding factor 2 (Gcfc2) (RGD1304792_predicted)
LOC501280	8.59	7.88	XR_007805	109486608	similar to myosin regulatory light chain-like (LOC501280)
EIF4EBP2	8.41	6.8	NM_001033069.1	74271858	eukaryotic translation initiation factor 4E binding protein 2 (Eif4ebp2)
MLLT11	8.4	7.71	NM_001013912.1	62078554	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog
LOC500095	8.33	4.95	XM_575446	62647113	similar to T-cell receptor beta chain V region 86T1 precursor (LOC500095)
TEKT1	7.96	3.54	NM_053508.2	51036667	tektin 1 (Tekt1)
EPN1	7.88	8.21	NM_057136.1	16923989	Epsin 1 (Epn1)
MAPK3	7.41	1.95	NM_017347	68537200	mitogen activated protein kinase 3 (Mapk3)
MLF2	7.03	9.95	NM_001107889	157823872	myeloid leukemia factor 2 (predicted) (Mlf2_predicted)
SLC39A2	6.94	4.33	NM_001107260	157822388	solute carrier family 39 (zinc transporter)
R3hdm2	6.54	3.1	NM_001130557	194474025	R3H domain containing 2
PFN1	6.306	7.966	NM_022511.2	42476143	profilin 1
RGD1564087	6.1	2.47	XR_009360.1	109467794	similar to 14-3-3 protein tau (14-3-3 protein theta) (predicted)
RGD1559566	5.99	4.83	XM_001056263.1	293350680	similar to 60S ribosomal protein L9 (predicted) (RGD1559566_predicted)
ATP5G3	5.997	7.804	NM_053756	16758591	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)
CIC	5.98	5.89	NM_001107490.3	215272395	capicua homolog (Drosophila) (predicted) (Cic_predicted)
Brsk1	5.93	7.05	NM_001127337	187960159	BR serine/threonine kinase 1
CAMK2N2	5.63	4.92	NM_021678.1	11067400	calcium/calmodulin-dependent protein kinase II inhibitor 2 (Camk2n2)
RGMA	5.51	4.83	XM_218791.3	157819830	RGM domain family
Ccdc125	5.25	3.49	NM_001134761	197927213	CCDC125 coiled-coil domain containing 125
GNG10	5.21	7.74	NM_053660.1	399154111	guanine nucleotide binding protein (G protein)
P11 protein	5.05	2.51	XM_579635.1	62659845	similar to P11 protein (LOC497693)
Tmem189	5.02	2.58	NM_001113752	166091516	transmembrane protein 189
LOC365025	5.15	6.63	XM_577671.1	62665500	similar to alpha tubulin subunit (LOC365025)
SNURF	5.12	10.02	NM_130738.1	397787561	SNRPN upstream reading frame (Snurf)
LOC300760	5.03	3.57	XM_236308.3	62653977	similar to H3 histone
Yaf2	5.063	5.468	XM_001073895.1	199559858	similar to YY1-associated factor 2 (LOC690262)
LOC500344	4.9	2.49	XM_575696.1	62648245	LOC500344 (LOC500344)
MRPS2	4.88	3.8	NM_001108576	157819458	mitochondrial ribosomal protein S2

TOMM22	4.63	4.9	NM_212514.2	71534292	translocase of outer mitochondrial membrane 22 homolog (yeast) (Tomm22)
Arglu1	4.63	4.5	NM_001024972.1	68163363	arginine and glutamate rich 1 ()
TMEM158	4.61	6.33	NM_057212.1	17933495	transmembrane protein 158 (Tmem158)
LY6H	4.44	8.82	NM_001134839.1	198386344	lymphocyte antigen 6 complex
LENG4	4.31	3.55	NM_001134978	201066394	leukocyte receptor cluster (LRC) member 4
AKT1S	4.25	3.54	NM_001106259	408772021	AKT1 substrate 1 (proline-rich)
Zgc:56193	4.23	5.55	XR_008163.1	109477420	similar to Zgc:56193 (predicted) (RGD1562162_predicted)
WBP2	4.21	3.32	NM_138975.1	20376817	WW domain binding protein 2 (Wbp2)
CYP46A1	4.11	3.77	NM_001108723.	157817886	cytochrome P450
Btbd2	4.11	5.43	XM_001076264.1	392341333	similar to BTB (PO)Z domain containing 2 (predicted) (RGD1566094_predicted)
CSDC2	4.08	3.7	XM_001077363.1	293348836	cold shock domain containing C2
RPL13A	4.05	8.07	NM_173340.1	27545437	ribosomal protein L13A (Rpl13a)
RGD1564980	4.02	4.16	XM_575373.2	293358409	similar to 60S ribosomal protein L29 (P23) (predicted) (RGD1564980_predicted)
Prrc2a	3.99	3.82	NM_212462.2	260166645	proline-rich coiled-coil 2A (Prrc2a)
PPP2R5B	3.93	7.09	NM_181379.2	60593006	protein phosphatase 2
LOC681314	3.91	5.43	XM_001061020.1	109489050	similar to BAX protein
TXN1	3.87	3.53	NM_053800.2	42476285	thioredoxin 1 (Txn1)
MFAP2	3.81	3.89	NM_001107989	157818962	microfibrillar-associated protein 2 (predicted) (Mfap2_predicted)
HMG-2	3.8	3.27	XM_573272.1	392351998	similar to High mobility group protein 2 (HMG-2) (LOC498072)
Hmgb2	3.8	2.76	NM_017187	158711705	high mobility group box 2 (Hmgb2)
LOC364253	3.76	4.27	XM_344296.1	34869079	similar to RIKEN cDNA 1110003E01 (LOC364253)
ADCK2	3.72	1.75	NM_001107855	157822890	aarF domain containing kinase 2 (predicted) (Adck2_predicted)
RPS7	3.71	2.15	XM_213053.2	62650073	ribosomal protein S7 (Rps7)
Ppp1r18	3.69	4.46	NM_001126287.2	261399901	PPP1R18 protein phosphatase 1, regulatory subunit 18
B3GAT1	3.66	4.35	NM_054003.1	16758917	beta-1,3-glucuronyltransferase 1
RGD1565149	3.66	4.35	XM_001077968.1	293343422	similar to chromosome 16 open reading frame 7 (predicted) (RGD1565149_predicted)
Fam57b	3.62	7.49	NM_001106296.2	182888556	family with sequence similarity 57, member B
LOC306766	3.61	3.23	NM_001014007.1	62078742	hypothetical LOC306766 (LOC306766)
RGD1311783	3.59	4.89	XM_001059424.1	197386190	similar to RIKEN cDNA 2010012O05 (predicted) (RGD1311783_predicted)
Ptbp2	3.52	1.87	NM_001005555.1	53850637	polypyrimidine tract binding protein 2 (Ptbp2)
NME2	3.51	4.75	NM_031833.2	55926144	NME/NM23 nucleoside diphosphate kinase 2
Agap3	3.47	5.59	NM_001108616	157824114	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3
Rab2a	3.468	1.64	NM_031718.1	13929005	member RAS oncogene family (Rab2a)
MGST3	3.46	4.62	XM_001076104.1	109498992	microsomal glutathione S-transferase 3 (predicted) (Mgst3_predicted)
Gprin1	3.45	3.49	XM_001070221.1	293342617	G protein-regulated inducer of neurite outgrowth 1 (predicted) (Gprin1_predicted)
LOC500721	3.45	5.65	XM_580114.1	62651251	LOC500721 (LOC500721)
Gstp1	3.45	4.18	NM_012577.1	169646324	glutathione-S-transferase
Nckap1	3.41	2.03	XM_230038.4	158138548	NCK-associated protein 1 (Nckap1)
RRS1	3.394	6.446	NM_001079699.1	119226199	RRS1 ribosome biogenesis regulator homolog (S.cerevisiae)
NREP	3.38	7.02	NM_178096.2	31342528	neuronal regeneration related protein (Nrep)
RGD1561956	3.37	3.52	XM_344287.1	34869055	similar to RIKEN cDNA 1110003E01 (predicted) (RGD1561956_predicted)

GDI1	3.35	5.95	NM_017088.2	71534275	guanosine diphosphate dissociation inhibitor 1 (Gdi1)
RGD1564450	3.35	3.26	XM_001078024.1	157822410	RGD1564450 (predicted) (RGD1564450_predicted)
RGD1560015	3.28	4.26	XM_574311.2	392343688	trans-2,3-enoyl-CoA reductase-like
Npm3	3.26	3.95	XM_001058548.1	392338228	nucleophosmin/nucleoplasmin, 3
Zbtb45	3.26	3.37	NM_001107478	157819040	zinc finger and BTB domain containing 45
SPC25	3.26	2.23	NM_001009654.1	57527006	SPC25, NDC80 kinetochore complex component
LOC311629	3.21	3.81	XM_230844.3	62646356	similar to sorting nexin 21 isoform a; sorting nexin L; sorting nexin 21 (predicted)
PPFIA3	3.21	3.91	NM_001270985	401709972	protein tyrosine phosphatase, receptor type
Cox7b	3.2	2.29	NM_182819.2	65301489	cytochrome c oxidase subunit VIIb
Gtf2h5	3.17	1.82	NM_001126088	186910270	general transcription factor IIH, polypeptide 5
Atxn7l3	3.11	3.88	XM_213493.3	392351635	ataxin 7-like 3, transcript variant 2
MAP1B	3.166	2.525	NM_019217	158749619	microtubule-associated protein 1B
Sypl1	3.106	1.868	NM_001014263	62079260	synaptophysin-like 1
RPL18A	3.09	5.68	NM_212510.1	47059005	Rattus norvegicus ribosomal protein L18A (Rpl18a)
RGD1565784	3.05	2.47	XM_001059479.1	157817212	PREDICTED: Rattus norvegicus RGD1565784 (predicted) (RGD1565784_predicted)
TMEFF1	3.03	5.89	NM_023020.2	121583853	Rattus norvegicus transmembrane protein with two follistatin-like domains 1 (Tmeff1)
Fabp7	3	3.62	NM_030832.1	402744885	fatty acid binding protein 7, brain
Map1lc3a	3	1.68	NM_199500	377652334	microtubule-associated protein 1 light chain 3 alpha
LOC499793	2.97	5.51	XM_575129.1	62645054	similar to 60S ribosomal protein L12
Cbr1	2.94	2.98	NM_019170.2	46048534	carbonyl reductase 1 (Cbr1)
PEA15A	2.896	2.177	NM_001013231.1	61557369	phosphopro cytoch
SLC25A11	2.89	4.96	NM_022398.1	11693169	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier)
Aplp1	2.89	-2.08	XM_001076030.1	198041598	similar to Amyloid beta (A4) precursor-like protein 1 (predicted)
Cox7a2l	2.88	5.51	NM_001106704	157821820	cytochrome c oxidase subunit VIIa polypeptide 2 like
BAX	2.87	3.103	NM_017059	386869282	Bcl2-associated X protein
S100a1	2.85	2.51	NM_001007636.1	218749895	S100 calcium binding protein A1 (S100a1)
Rpl7	2.82	2.53	NM_001100534	198278504	ribosomal protein L7
RGD1564372	2.77	4.31	XM_344301.1	34869098	similar to RIKEN cDNA 1110003E01 (predicted) (RGD1564372_predicted)
Dpp9	2.77	2.28	XM_001061312.1	392342223	dipeptidyl peptidase 9
IL-17D	2.77	2.54	XM_577439.1	62661954	similar to IL-17D (LOC502011)
RGD1565358	2.76	2.29	XM_235062.2	109480494	genes associated with retinoid-IFN-induced mortality 19 (predicted)
C1QL1	2.76	2.8	NM_001108838	157819268	complement component 1,q subcomponent-like 1
Lrrc73	2.75	5.11	NM_001024360.1	119310198	eucine rich repeat containing 73
Actb	2.75	6.06	NM_031144.2	42475962	beta actin
Mapre1	2.742	1.579	NM_138509.3	78097099	microtubule-associate
RAB3A	2.72	3.33	NM_013018.2	61098194	RAB3A, member RAS oncogene family
LOC301444	2.72	3.83	NM_001047872	114145717	pseudogene for diazepam binding inhibitor 1 (LOC301444)
LYPLA2	2.71	4.7	NM_031342.1	13786177	lysophospholipase 2 (Lypla2)
NDUFB8	2.66	5.9	NM_001106360	187937126	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8
Hm13	2.65	3.74	NM_001107789	157823208	histocompatibility 13
Hdac3	2.623	2.343	NM_053448.1	16758191	histone deacetylase 3

SNAP91	2.61	4.12	NM_031728.1	13994176	synaptosomal-associated protein 91 (Snap91)
TERF2	2.61	1.54	NM_001242355.1	334285045	telomeric repeat binding factor 2, transcript variant 2
Nras	2.6	4.8	NM_080766.1	18158430	neuroblastoma ras oncogene (Nras)
LOC691672	2.6	4.06	XM_001079224.1	109513656	similar to Discs large homolog 5 (Placenta and prostate DLG)
MLLT3	2.604	3.286	NM_053718.1	192447427	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosophila)
Zfp513	2.59	4.67	NM_001012110.1	58865789	zinc finger protein 513 (Zfp513)
Mgrn1	2.57	4.76	NM_001013964.1	62078656	mahogunin ring finger 1, E3 ubiquitin protein ligase
Ndufb2	2.56	2.54	XM_001070173.1	219277691	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
Stk11	2.55	4.6	XM_234901.4	157823728	downstream of Stk11 (predicted) (Dos_predicted)
Hes5	2.55	4.53	NM_024383.1	13242286	hairy and enhancer of split 5 (Drosophila) (Hes5)
VAMP8	2.491	4.002	NM_031827	13929181	vesicle-associated membrane protein 8
Lmo3	2.43	3.91	NM_139112.1	20806164	LIM domain only 3 (Lmo3)
Mkrn3	2.41	3.8	XM_001057262.1	392337728	makorin, ring finger protein, 3
Gnal	2.357	2.641	NM_001191836	300797436	guanine nucleotide binding protein, alpha, stimulating, olfactory type
NDUFB3	2.259	3.999	NM_001106912	157824070	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3
Lemd2	2.18	4.78	NM_001039032.1	84781657	Rattus norvegicus LEM domain containing 2 (Lemd2)
Ube2c	2.18	1.86	NM_001106542	157818348	ubiquitin-conjugating enzyme E2C
Efna2	2.15	2.53	NM_001168670	274327666	ephrin A2 (Efna2)
LOC361128	2.08	4.17	XM_341415.2	62662451	similar to TR4 orphan receptor associated protein TRA16 (LOC361128)
Hnrpa2b1	1.97	4.15	XM_342684.3	157265558	heterogeneous nuclear ribonucleoprotein A2/B1 (predicted) (Hnrpa2b1_predicted)
MTAP2	1.939	1.862	NM_013066.1	6981181	microtubule-associated protein 2
Sdhb	1.82	2.12	NM_001100539	209915613	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)

Supplemental Table 2: **TRF2-S targets related to axonogenesis**

mRNA identified in DIV 13 cortical axons[8]

RPL18A	Ribosomal protein L18A
RPL13A	Ribosomal protein L13A
LOC499793	60S ribosomal protein L12
Rpl7	Ribosomal protein L7
Hnrpa2b1	Heterogeneous nuclear ribonucleoprotein A2/B1
NNAT	Neuronatin
MAP1B	Microtubule-associated protein 1B
Map1lc3a	Microtubule-associated protein 1 light chain 3 alpha
ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit 9
Cox7b	Cytochrome c oxidase subunit VIIb
COX7A2L	Cytochrome c oxidase subunit VIIa polypeptide 2
CAMK2N2	Calcium/calmodulin-dependent protein kinase II inhibitor 2
GNG10	Guanine nucleotide binding protein (G protein)
TXN1	Thioredoxin 1
NME2	Non-metastatic cells 2
NREP	Neuronal regeneration related protein
LOC691672	Discs large homolog 5

mRNA indentified in embryonic axons[11]

RPL18A	Ribosomal protein L18A
RPL13A	Ribosomal protein L13A
LOC499793	60S ribosomal protein L12
Rpl7	Ribosomal protein L7
NNAT	Neuronatin
MAP1B	Microtubule-associated protein 1B
Map1lc3a	Microtubule-associated protein 1 light chain 3 alpha
MAPRE1	Microtubule-associated protein
MTAP2	Microtubule-associated protein 2
Nckap1	NCK-associated protein
ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit 9
SLC25A11	Solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier)
COX7A2L	Cytochrome c oxidase subunit VIIa polypeptide 2
BAX	Bcl2-associated X protein
Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3
Cox7b	Cytochrome c oxidase subunit VIIb
TOMM22	Outer mitochondrial membrane 22 homolog (yeast)
RAB3A	RAB3A
APLP1	Amyloid beta (A4) precursor-like protein 1
RAB2	RAB2
SYPL	Synaptophysin-like 1
GDI1	Guanosine diphosphate dissociation inhibitor 1
GNG10	Guanine nucleotide binding protein (G protein)
NREP	Neuronal regeneration related protein
Akt1	Thymoma viral proto-oncogene 1
Brsk1	BR serine/threonine kinase 1

PPP2R5B	Protein phosphatase 2
YY1	YY1-associated factor 2
HMGB2	High mobility group box 2
TXN1	Thioredoxin 1
CIC	Capicua homolog (Drosophila)

Supplemental Table 3

Oligomer pairs for biotin pull-down assays

	Forward	Reverse
Trf2s:		
5'UTR	CCAAGCTTCTAATACGACTCACTATAGGGAGAAACAGCGGGCCCTGCTTC	CGTGTTCGACCGCCGAG
CR1	CCAAGCTTCTAATACGACTCACTATAGGGAGAATGGCGGGAGGAGGCG	ATTTTTGAAGCCTTTTCAAATTCTT
CR2	CCAAGCTTCTAATACGACTCACTATAGGGAGATTTGTATCAAAAACAAAGAATTTGA	TTAGGGCTGTTCCACTTG
3'UTR	CCAAGCTTCTAATACGACTCACTATAGGGAGACGGGCTTGAAGAAAAGGAAG	CCCGCACTTCAAACAGCT
Clip-WT	CCAAGCTTCTAATACGACTCACTATAGGGAGAGGTCTGCGGGCCTTTCGGAGTAGCCGGTACCGGGACTTCAGGCAGATCCG	CGGATCTGCCTGAAGTCCCGGTACC
Clip-MT1	CCAAGCTTCTAATACGACTCACTATAGGGAGAGGT CTGCGGGCCTAAGCCTCATCCCGGTACCGGGACTTCAGGCAGATCCG	CGGATCTGCCTGAAGTCCCGGTACC
Clip-MT2	CCAAGCTTCTAATACGACTCACTATAGGGAGAGGT CTGCGGGCCTTTCGGAGTAGCCGGTACCGGGACTTCACCGTCTAGCG	CGCTAGACGGTGAAGTCCCGGTACC
ClipMT1+2	CCAAGCTTCTAATACGACTCACTATAGGGAGAGGT CTGCGGGCCTAAGCCTCATCCCGGTACCGGGACTTCACCGTCTAGCG	CGCTAGACGGTGAAGTCCCGGTACC
Aplp1		
5'CR1	CCAAGCTTCTAATACGACTCACTATAGGGAGAGCAGGGCCGGGCGGGAGCGCA	AGGCAATGGAAGGGCACAACC
CR2	CCAAGCTTCTAATACGACTCACTATAGGGAGAGGTTGTGCCCTTCCATTGCCT	GTGGGAGTGACTCTGCTGACC
CR3	CCAAGCTTCTAATACGACTCACTATAGGGAGAGGTCAGCAGAGTCACTCCCAC	CTCAGGGCCATCAGAACTCTC
CR4	CCAAGCTTCTAATACGACTCACTATAGGGAGAGAGAGTTCTGATGGCCCTGAG	GGAAGGGTCACTGGGGCATCT
CR5	CCAAGCTTCTAATACGACTCACTATAGGGAGAAGATGCCCCAGTGACCCTTCC	AGCTAGGGTTGGGGTCAAGGT
3'UTR	CCAAGCTTCTAATACGACTCACTATAGGGAGAGAAGAACGACCTTGACCCCAACCCT	GAAGAGGACTTTATTGGGATGTTAG
Rab3a		
5'CR1	CCAAGCTTCTAATACGACTCACTATAGGGAGAGAGCCTCCACCGCCGCCTGCA	ACATTAGAATGAAGCCCATGG
CR2	CCAAGCTTCTAATACGACTCACTATAGGGAGACCATGGGCTTCATTCTAATGT	GGTGGGGAAGGGAAGTGTGGT
3'UTR	CCAAGCTTCTAATACGACTCACTATAGGGAGAACCACACTTCCCTTCCCCACC	TTCTCTCTTTAATGTCAAGGACTGC
App		
887-1150	CCAAGCTTCTAATACGACTCACTATAGGGAGAtgcagatgggagtgaagacaaag	tggaaatgggcatgttcattctc
1944-2150	CCAAGCTTCTAATACGACTCACTATAGGGAGAccgccctgctgccgaccgagga	cttcttcagcatcaccaaggtg