Fox-3	1
Fox-2	1 NEKKKNVTOGNOEPTTIPDANVOPFTTIPFPPPPONGIPTEYG. VPH.T
Fox-1	.: . : . 1 Mincerequergingeaa aapdtwaqpyasaqf. Appqng ipaeytaphiphpa
Fox-3	31. QDYSGQTPVPPFHGHTLYTPAQTHPEQPGT. EASTQPIAGTQTVPQADEAA
Fox-2	48 QDYAGQTSEHNLTLYGSTOPHGEQSSN.SPSNQNGSLTQTEGGA
Fox-1	: . : 50 PEYTGQTTVP.DHTLNLYPPTQTHSEQSADTSAQTVSGTATQTDDAA
Fox-3	81 QTDNQQLHPSDPTE.KQQPKRLHVSNIPFRFRDPDLRQMFGQFGKILD
Fox-2	
Fox-1	96 PTDG. QPQTQPSENTESKSQPKRLHVSN IPFRFRDPDLRQMFGQFGKILD
Fox-3	128 VEIIFNERGSKGFGFVTFETSSDADRAREKINGTIVEGRKIEVNNATARV
Fox-2	141 VELIFNERGSKGFGFVTFENSADADRAREKLIGTVVEGRKTEVNNATARV
Fox-1	145 VELIFNERGSKGFGFVTFENSADADRAREKLHGTVVEGRKIEVNNATARV
Fox-3	178 NTNKKPGNPYANGWKINPYWGTYYGPEFYAVTSFPYPTT.GTAVAYRGAH
Fox-2	191 NTNKKHYTPYANGVKLSPYVGAVYGPELYAASSFOADVSLGNFAAVP
Fox-1	195 HTNKKTVNPYTNGWKLNPVVGAVYSPDFYAGTVLLCQANQEGSSH
Fox-3	227 IRGRGRAVYNTFRAAPPPPPIPTYGAALEQTLVKHPVPVAGLAPCPIPPQ
Fox-2	238 LSGRGG. INTYIPLI IPGEPYPTAATTAAAFRGAHLR
Fox-1	: . : 240 YSGPSSL.VY TS.AMPGFPYP.AATAAAAYRGAHLR
Fox-3	277 QTPEPAYPTSP.AFPPISCPFASRVVYQDGFYGAEIYGGYAAYRYAQPAAA
Fox-2	274 GRGRTVYGAVR.AVPPTAIPAYPGVVYQDGFYGADLYGGYAAYRYAQPATA
Fox-1	111111 111111111111111111111111111111111111
Fox-3	327 TAAAYSDSYGRYYAAADPYHHTIGPTATYSIGTH
Fox-2	1 111111 1111 1
Fox-1	. . 324 T
Fox-3	361
Fox-2	374
Fox-1	: 366 KTRSHADDVGLVLSSLQASIYRGGYNRFAPY* 396

Figure S1. Amino acid alignment of the Fox-1 gene family. Among several isoforms for Fox-2 and Fox-1, F011 and A016 published previously (Nakahata & Kawamoto, 2005, *Nucleic Acids Res* **33**, 2078) are shown as Fox-2 and Fox-1, respectively. The underlined amino acids in Fox-3 indicate the sequences obtained by MS analysis. The blue and green letters in Fox-3 can be included or excluded depending on alternative pre-mRNA splicing, therefore potentially 4 isoforms exist. The red letters indicate the RNA recognition motif. The vertical lines and colons between sequences indicate identical and similar aa, respectively, compared to Fox-2.

Α

MTQALPR GSHSQSSSPGALTLGR QTTAAAAATFSEQVGGGSGGAGR EMLSSTTYPVVVK DHIIEVVGSSMPLIGDHQDEDK TYATAEPFIDAK **SLKPDFVLIR** VLLVIDEPHTDWAK KLGTEEFPLIDQTFYPNHK VDNQHDFQDIASVVALTK QLIVELVVNK ASTAAPVASPAAPSPGSSGGGGFFSSLSNAVK LWVDTCSEIFGGLDICAVEALHGK TNTGSAMLEQIAMSDR QGPPQKPPGPAGPTR QTSQQPAGPPAQQRPPPQGGPPQPGPGPQR QSRPVAGGPGAPPAARPPASPSPQR TSVSGNWK LPSPTAAPQQSASQATPVTQGQGR SQSLTNAFNLPEPAPPRPSLSQDEVKAETIR

B

MTQALPR QASISGPAPTK QTSQQPAGPPAQQRPPPQGGPPQPGPGPQR QSRPVAGGPGAPPAARPPASPSPQR **TSVSGNWK** LPSPTAAPQQSASQATPVTQGQGR GSHSQSSSPGALTLGR QTTAAAAATFSEQVGGGSGGAGR **EMLSSTTYPVVVK TYATAEPFIDAK** DHIIEVVGSSMPLIGDHQDEDK SLKPDFVLIR VLLVIDEPHTDWAK KLGTEEFPLIDQTFYPNHK VDNQHDFQDIASVVALTK QLIVELVVNK ASTAAPVASPAAPSPGSSGGGGFFSSLSNAVK VEQAEFSDLNLVAHANGGFSVDMEVLR LGTEEFPLIDQTFYPNHK TNTGSAMLEQIAMSDR

Figure S2. Tryptic peptide sequences of the 70 kDa proteins identified as synapsin I by MS analysis. Each of the doublet band proteins immunoprecipitated with anti-NeuN was subjected to MS analysis. The peptide sequences obtained from the upper band (A) and the lower band (B) are shown. The sequence shown in bold letters is unique to the isoform synapsin Ia, and all other sequences are common to two alternatively spliced isoforms of synapsin I, Ia and Ib.