

Fig. S1: Nebulin SH3 pulldown assay. A. Experimental scheme for the nebulin SH3 pulldown assay on cell lysate from differentiated C2C12 cells. B. SDS-PAGE gel on unbound and pulled down fractions using H6-GST-3C tagged nebulin SH3 domain (SH3) and H6-GST-3C tag (tag).

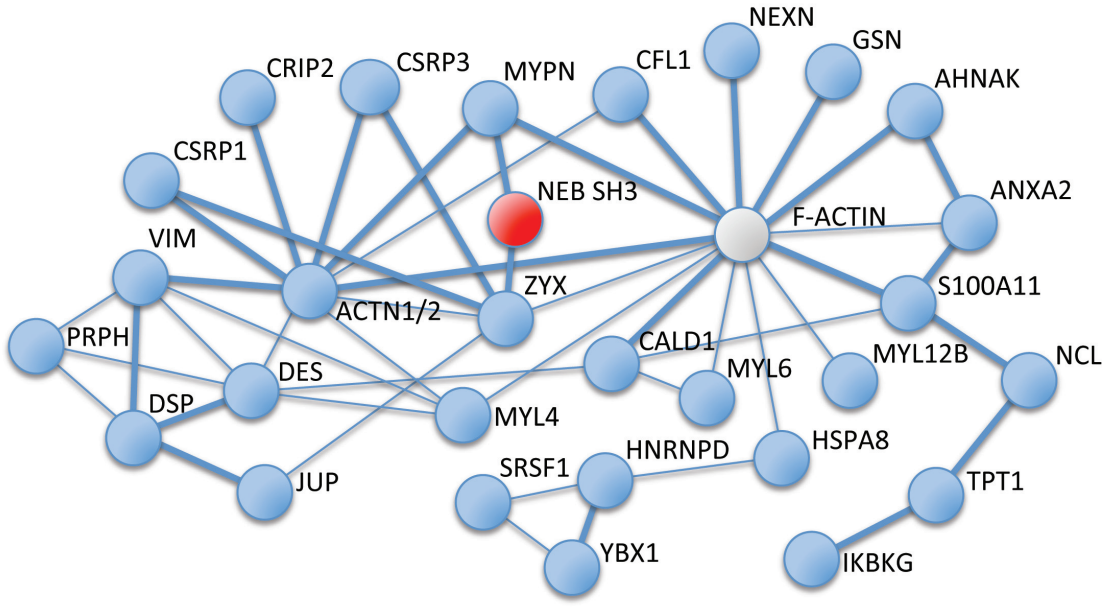


Fig. S2. Protein association network based on the proteins identified in the nebulin SH3 pulldown using STRING 9.05 software. Experimentally proven interactions are highlighted by thick lines. Although α -actinin 2 (ACTN2) and F-actin (represented in grey) were not among the identified proteins, they were included in the protein association network, since they are known to associate with many of the identified proteins.

Table SI: Gene expression microarray analysis on tibialis anterior muscle from NebΔSH3 mice compared to WT.

Gene Name	Gene symbol	Gene identifier	Fold upreg.	Fold downreg.	<i>P</i> value	Adj. <i>P</i> value*
Lipoprotein lipase	LPL	NM_008509		1.46	0.0019	0.9945
Elongation factor 1-alpha 1	EEF1A1	XM_134967	1.44		0.0095	0.9945
Ubiquitin B	UBB	NM_011664	1.42		0.0419	0.9945
Uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	NM_028283	1.40		0.0055	0.9945
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit	ATP5J	NM_016755		1.39	0.0029	0.9945
Translocase of inner mitochondrial membrane 8 homolog b (yeast)	TIMM8B	NM_013897		1.34	0.0464	0.9945
Cytochrome c oxidase, subunit VIIIb	COX8B	NM_007751		1.34	0.0479	0.9945
Y box protein 1	YBX1	NM_011732		1.32	0.0142	0.9945
Dystrophia myotonica-protein kinase	DMPK	NM_032418	1.27		0.0099	0.9945
Milk fat globule-EGF factor 8 protein	MFGE8	NM_001045489	1.27		0.0241	0.9945
Capping protein (actin filament) muscle Z-line, beta	CAPZB	NM_001037761		1.25	0.0366	0.9945
Collagen, type VI, alpha 1	COL6A1	NM_009933	1.24		0.0088	0.9945
G1 to S phase transition 1, transcript variant 1	GSPT1	NM_146066		1.24	0.0146	0.9945
Prion protein	PRNP	NM_011170	1.23		0.0220	0.9945
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	NDUFB6	XM_131359		1.21	0.0158	0.9945
Aspartyl-tRNA synthetase, transcript variant 2	DARS	NM_145507		1.21	0.0196	0.9945
Polymerase (RNA) II (DNA Directed) Polypeptide L, 7.6kDa	POLR2L	ILMN_2503728	1.21		0.0366	0.9945
Cullin 3	CUL3	NM_016716		1.21	0.0289	0.9945
Transmembrane protein 147	TMEM147	NM_027215	1.20		0.0081	0.9945
Prefoldin 2	PFDN2	NM_011070	1.20		0.0127	0.9945
Ornithine decarboxylase antizyme 1	OAZ1	NM_008753	1.20		0.0485	0.9945

P < 0.05, fold change > 1.2. *Adjusted *P* value is calculated using the Benjamini and Hochberg method.