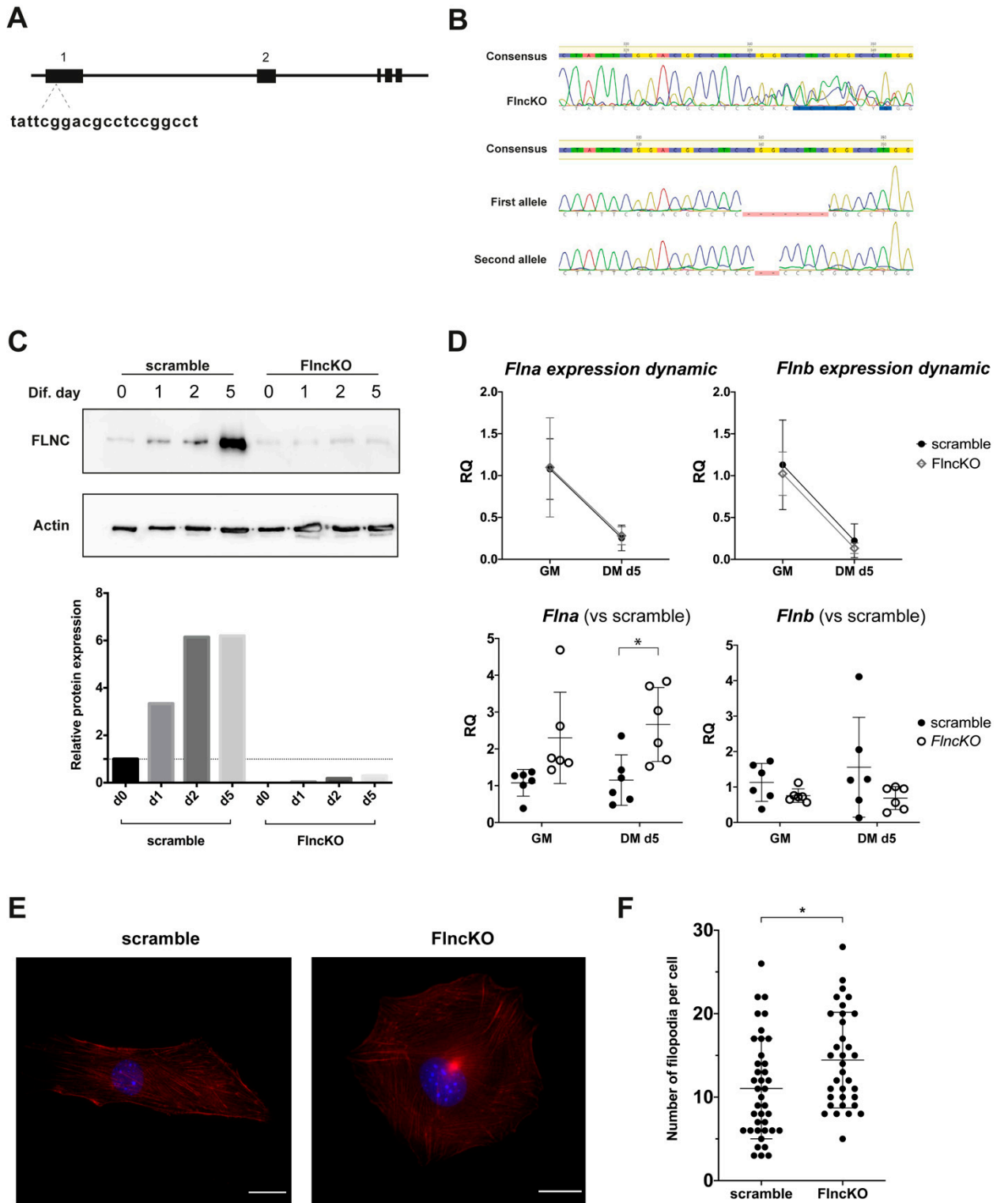


**Supplementary table S1.** Oligonucleotide sequences used for CRISPR/Cas9 plasmid cloning, qPCR and sequencing.

Gene	Oligonucleotide sequence (5'-3')	Application
<i>Myh1</i> (Forw)	GCTGAGAGAAGCTACCACATT	qPCR
<i>Myh1</i> (Rev)	ACAAAGGCGTAGTCGTATGG	qPCR
<i>Myh4</i> (Forw)	CAACAGTGCAGAGCAGGGAAG	qPCR
<i>Myh4</i> (Rev)	GGCCATGTCCTCAATCTTGTCGTAC	qPCR
<i>Mymk</i> (Forw).	CCTGTGATGGGCCTGGTTTGTC	qPCR
<i>Mymk</i> (Rev)	GGTTCATCAAAGTCGGCCAGTGC	qPCR
<i>Myog</i> (Forw)	GAGACATCCCCCTATTTCTACCA	qPCR
<i>Myog</i> (Rev)	GCTCAGTCCGCTCATAGCC	qPCR
<i>Ctgf</i> (Forw)	CCCTAGCTGCCTACCGACT	qPCR
<i>Ctgf</i> (Rev)	GTA ACTCGGGTGGAGATGCC	qPCR
<i>Cyr61</i> (Forw)	CTGAAGAGGCTTCTGTCTTT	qPCR
<i>Cyr61</i> (Rev)	GTGGTCTGAACGATGCATTTTC	qPCR
<i>Flna</i> (Forw)	GCTAAAGGTCACTGTAAAGGGT	qPCR
<i>Flna</i> (Rev)	TTCACCTCAAACGGACTTCGAC	qPCR
<i>Flnb</i> (Forw)	GGGGAAAGTAACCTGCGTGA	qPCR
<i>Flnb</i> (Rev)	CATGGCTGTGACTTCCCCAT	qPCR
<i>Gapdh</i> (Forw)	GGATCTGACGTGCCGCCTG	qPCR
<i>Gapdh</i> (Rev)	GAAGGTGGAAGAGTGGGAGTTGC	qPCR
<i>Flnc</i> <i>_</i> guide sense	CACCGTATTTCGGACGCCTCCGGCCT	CRISPR plasmid cloning
<i>Flnc</i> <i>_</i> guide antisense	AAACAGGCCGGAGGCGTCCGAATAC	CRISPR plasmid cloning
<i>Scramble</i> <i>_</i> guide sense	CACCGGTGCGAATACGCCACGCGAT	CRISPR plasmid cloning
<i>Scramble</i> <i>_</i> guide antisense	AAACATCGCGTGGCGTATTCGCACC	CRISPR plasmid cloning
<i>U6</i>	GAGGGCCTATTTCCCATGATTC	Sequencing
<i>Flnc</i> <i>_</i> exon1 (Forw)	GCGCTAACGAAGTCTCCGA	Sequencing, allele cloning
<i>Flnc</i> <i>_</i> exon1 (Rev)	TTGAGATGCTCGTTGCACCA	Sequencing, allele cloning

Supplementary Figure S1



**Figure S1. Generation of FLNC-deficient C2C12 cell line using CRISPR/Cas9 technique.**

(A) GuideRNA-driven CRISPR/Cas9 genome editing performed within the first exon of mouse *Fln*. (B) Sanger sequencing of total cell DNA represents introduction of deletions 3 nucleotides upstream to PAM-site. TA-allele cloning revealed the presence of two different deletions in each allele (2 nt and 7 nt), no WT alleles was observed after screening of at least 20 TA-clones. (C) Western Blotting of *Fln*KO cells showed loss of FLNC in undifferentiated myoblasts with slight increase of FLNC during myogenic differentiation compared to a scramble cell line (control). (D) Expression dynamics of *Flna* and *Flnb* during myogenic differentiation in scramble control and *Fln*KO cells(upper panel), and changes of *Flna* and *Flnb* expression in *Fln*KO cells comparing to scramble control (lower panel). (E) Representative images of scramble control and *Fln*KO undifferentiated myoblasts stained with Phalloidin Rhodamine. (D) Quantification of filopodia sites per cell in undifferentiated *Fln*KO and scramble control myoblasts. GM – growth media, DM d5 – 5 days in differentiation media.\* $p < 0.05$ . Scale bar 20  $\mu\text{m}$ .