# The multifunctional RNA-binding protein hnRNPK is critical for the proliferation and differentiation of myoblasts

Yongjie Xu, Rui Li, Kaili Zhang, Wei Wu, Suying Wang, Pengpeng Zhang<sup>\*</sup>, Haixia Xu<sup>\*</sup>

College of Life Science, Xinyang Normal University, Xinyang 464000, China

\*Corresponding author: Haixia Xu, hxxu214@126.com

Pengpeng Zhang, ppzhang15@163.com

#### SUPPLEMENTARY METHODS

## Cell culture and C2C12 myoblast differentiation

C2C12 myoblasts were cultured in either growth medium (GM) or differentiation medium (DM). All the cells were maintained in the incubator under 37°C, 5% CO<sub>2</sub>. C2C12 myoblasts were grown under the condition of DMEM supplemented with 10% fetal bovine serum (Gibco). To make C2C12 cell undergo myogenic differentiation, the cells at 80% confluence were induced to differentiate by switching to DMEM containing 2% horse serum (Hyclone). To measure fusion index, cells incubated in DM for 5 days were fixed in 4% paraformaldehyde (PFA) and stained with antibody against MHC (sc-376157, Santa Cruz Biotechnology), then pictures were captured randomly at more than 6 different spots. For the obtained images, the number of nuclei within the myotubes and the total number of nuclei were counted using Adobe Photoshop software and the fusion index was calculated as the percentage of nuclei incorporated into myotubes vs. total number of nuclei.

## **RNA isolation and quantitative RT-PCR**

Total cellular RNA was extracted using TRIzol (Invitrogen) according to the manufacturer's protocol and was used for reverse transcription with a PrimeScript RT-PCR kit (TaKaRa). QRT-PCR was conducted using a standard SYBR Green PCR kit (Roche) protocol with a LightCycler 96 Real-Time System. The relative expression was calculated using the comparative cycle threshold  $(2^{-\Delta\Delta Ct})$  method. The transcription level of *Gapdh* was used as the internal control. **Supplementary Table 1** lists the specific primers used.

# Western blotting

Cells were harvested and lysed in RIPA buffer (Beyotime, China). 30 µg proteins were denatured by heating at 100°C, separated by electrophoresis on 12.5% SDS-PAGE, and transferred to PVDF membranes. The primary antibodies were anti-hnRNPK (sc-28380, Santa Cruz Biotechnology), anti-Phospho-hnRNPK (PA5-36811, Pierce Protein Biology), anti-Myog (sc-12732, Santa Cruz Biotechnology) and anti-β-tubulin

(AT819, Beyotime). Incubate the membrane in the primary antibody solution (1:1000) overnight at 4°C with agitation. Anti-mouse IgG was used as secondary antibodies (A0286, Beyotime). Incubate the membrane in the secondary antibody reagent (1:1000) for 2 h at room temperature. Perform the detection of proteins using enhanced chemiluminescence (ECL), and then image the blot using the FluorChem M imaging system.

## SUPPLEMENTARY FIGURE LEGENDS





**Supplementary Fig. 1. HnRNPK single-guide (sg) RNA and target sites.** Top: domain structure of full-length mouse hnRNPK. The locations of the N-terminal bipartite nuclear localization signal (NLS), 3 K homology (KH) domains, K protein interactive (KI) domain, and Nuclear shuttling domain (KNS) are showed. Middle: schematic representation of the *hnRNPK* gene. The two sgRNA target sites are located at the exon 12, which encodes amino acids upstream of the K homology (KH) domain. Bottom: close-up representation of the sgRNA target sites. The two 20-nt guide sequences are shown. This sequence pairs with the DNA target site (indicated on the bottom strand). Immediately 3' to the target sequence is the trinucleotide protospacer adjacent motif (PAM; 5'-NGG).

# Supplementary figure 2



Supplementary fig. 2. Sequences of individually cloned fragments from clone 5 and wild-type genomic DNA of hnRNPK protein.

Supplementary figure 3



Supplementary fig. 3. Myoblast proliferation was impeded in clone 5 cells. (A) Cell growth rate curve showed growth retardation of clone 5 cells compared to WT control detected by MTT conversion assays. Data are presented as mean  $\pm$  s.d., n = 8. \**P* < 0.05, \*\**P* < 0.01 compared to WT. (B) Fluorescence images of Ki67 pulse-labeling at 24 h time point showed less clone 5 Ki67 positive cells compared to the WT control. Scale bar = 100 µm. (C) Quantification and comparison of Ki67 positive clone and WT control C2C12 cells. Data are presented as mean  $\pm$  s.d., n = 3. \**P* < 0.05, \*\**P* < 0.01 compared to WT control. Scale bar = 100 µm. (C) Quantification and comparison of Ki67 positive clone and WT control bar = 100 µm.

Gene	Primer sequences (5'–3')	Primer	Tm	Product	GenBank
		length	Value	size	NO.
Hnrnpk-g	F: CCCTGCCTCTGTTACCTTT	19 bp	56 °C	499 bp	NC_000079.6
	R: GGGTGATTTTAATGTGACCA	20 bp			
Hnrnpk	F: ATCTGCCTCTTCCTCCTCCA	20 bp	60 °C	111 bp	NM_025279.3
	R: CATCAGCACTGAACCCAACC	20 bp			
Myog	F: GTGGAGGATATGTCTGTTGCC	21 bp	60 °C	213 bp	NM_031189.2
	R: GGTGTTAGCCTTATGTGAATGG	22 bp			
Cdkn1a	F: TACCGTGGGTGTCAAAGCA	19 bp	60 °C	126bp	NM_00111109
	R: AGGGAGGGAGCCACAATAC	19 bp			9.2
Cyclin D1	F: TGTGCCACAGATGTGAAGTT	20 bp	60 °C	204 bp	XM_01124197
	R: GAGGGGGGTCCTTGTTTAGCC	20 bp			7.1
Cyclin E2	F: ATTTGGCTTTGCTGAATGAAGT	22 bp	60 °C	231 bp	NM_00103713
	R: TGGCAGTGTAACTCCTTAGACA	22 bp			4.2
Cyclin B1	F: GACAACGGTGAATGGACACC	20 bp	60 °C	232 bp	NM_172301.3
	R: ATGCCTTTGTCACGGCCTTA	20 bp			
Cyclin A2	F: TCTCGCTGCATCAGGAAGAC	20 bp	60 °C	153 bp	XM_01731944
	R: CCTTAAGAGGAGCAACCCGT	20 bp			4.1
Cdk4	F: TGCTACTGGAAATGCTGACCTT	22 bp	60 °C	143 bp	NM_009870.3
	R: CGAGGGTTTCTCCACCAAGA	20 bp			
Cdk2	F: ACGGAGCTTGTTATCGCAAA	20 bp	60 °C	160 bp	NM_183417.3
	R: CAAGTCAGACCACGGGTGAA	20 bp			
Cdk1	F: GACAGAGAGGGGTCCGTCGTA	20 bp	60 °C	168 bp	NM_007659.3
	R: GCACTCCTTCTTCCTCGCTT	20 bp			
Cdc25b	F: AAGAACCTAAGGCCCGTGTC	20 bp	60 °C	138 bp	NM_023117.4
	R: CTTGGTGTTTGCCATCCACG	20 bp			
Cdc25c	F: AGGACCTATCCCACCTGCAA	20 bp	60 °C	197 bp	XM_00652555
	R: ATTTTGGGGGTTCCTCCCGAC	20 bp			1.2
Gapdh	F: GTGAACGGATTTGGCCGTATTG	22 bp	60 °C	142 bp	NM_00128972
	R: TGCCGTGAGTGGAGTCATAC	20 bp			6.1

# Supplementary table 1 Primer sequences for the PCR amplification of specific genes