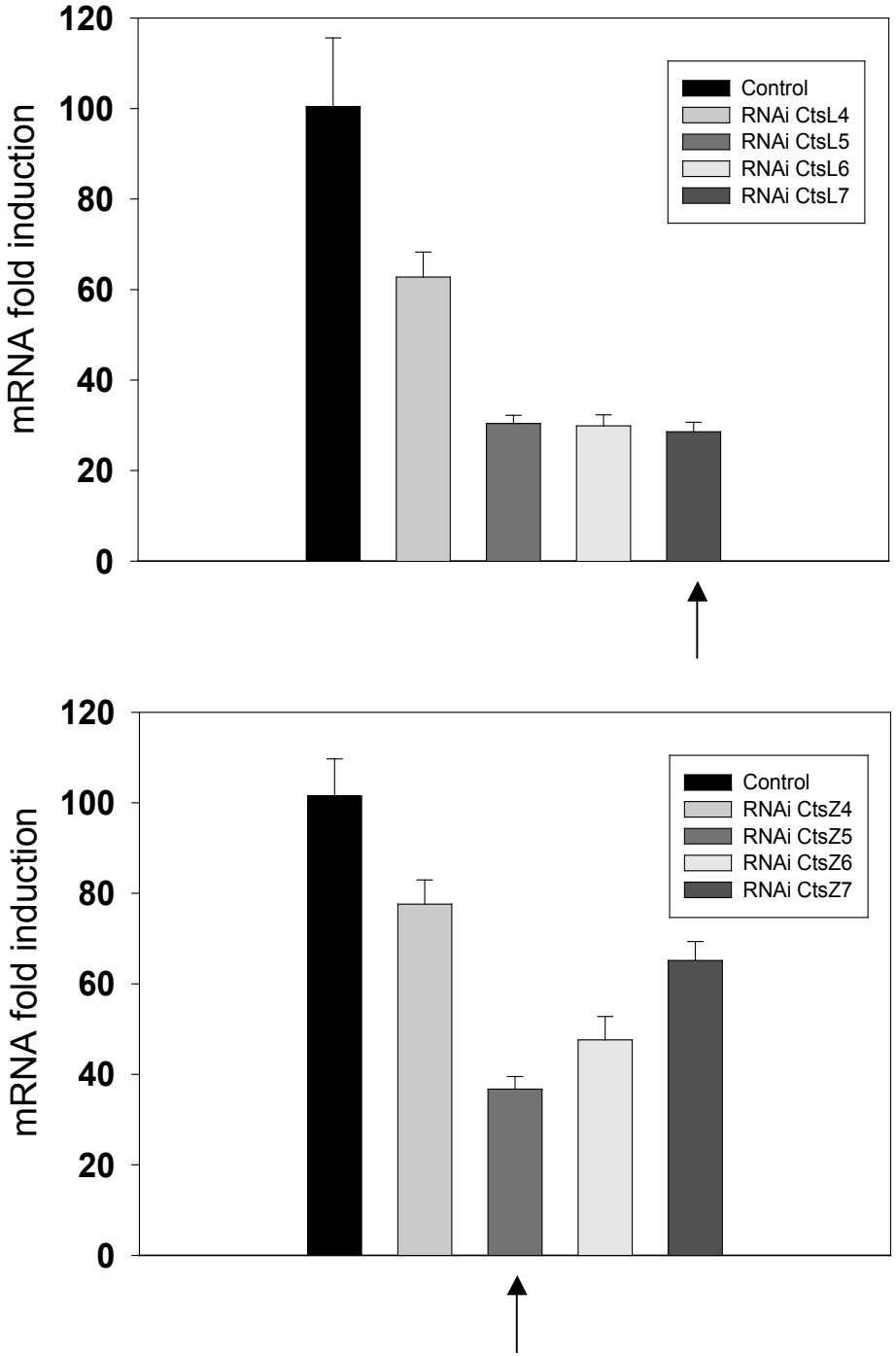
Fig. S1


120
100
80
60
40
20
0
mRNA fold induction
Control
RNAi CtsL4
RNAi CtsL5
RNAi CtsL6
RNAi CtsL7
120
100
80
60
40
20
0
mRNA fold induction
Control
RNAi CtsZ4
RNAi CtsZ5
RNAi CtsZ6
RNAi CtsZ7

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. The RNAi constructs used reduce the expression of Cathepsin L or Z by 65-70% in N1-E115 cells.
N1-E115 cells were transfected for 48h with RNAi constructs against Cathepsin L or Z. The expression levels of these genes was tested by Q-PCR and normalized against an housekeeping gene (*tripeptidyl peptidase II*).

SUPPLEMENTARY MATERIALS AND METHODS

RNA isolation, Reverse Transcription and Quantitative Real-Time PCR.

Total RNA was isolated from muscles with TRIzol (Invitrogen). RNA concentration, purity and integrity were measured in a spectrophotometer (Ultrospec 2000, Pharmacia Biotech) and by running a denaturing agarose gel. Analysis of mRNA / mg in muscle was performed using TaqMan reverse transcription reagents (Applied Biosystems). Real-Time PCR reactions were carried out with DyNAmo HS SYBR Green qPCR kit (Finnzymes) and the appropriate primer pairs in an ABI 7900HT fast Real-Time PCR system (Applied Biosystems). We used the following primers:

- for murine Cathepsin L
TCGAGGTTCTTGCTGCTACA, CtslF1
TTCTGTTGCTATGGACGCAA, CtslR1

- for murine Cathepsin Z
TCTGTACGGACAGCAGGATG, CtszF1
TCACCAGGAACCAGCACAT, CtszR1

As housekeeping gene stable in all tissues tested, tripeptidyl peptidase II (Tpp2) gene was used to normalize:
CCTTGAGAGCCTTTGGATAGAA, Tpp2F1
TGGTCTTTCTGGAAGAGTGC, Tpp2R1.