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Supplemental Table 1. Antibody lists

Supplemental Table 2. The primer list for RT-PCR.

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Supplemental Figure legends:

Supplemental Figure 1. NO66 is expressing in muscle nuclei. Co-immunostaining of NO66 and laminin revealed that NO66 is expressed in muscle nuclei. NO66=red color, laminin=green color, nuclei=DAPI (blue). Bar=50 μ m.

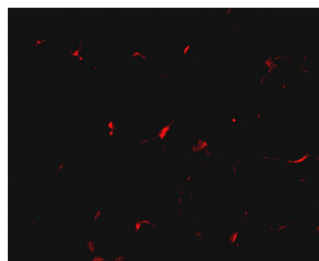
Supplemental Figure 2. CKD decreases mixed fiber muscle weights. Compared to values of sham operated control mice, CKD mice have lower weights in gastrocnemius (A) and tibialis anterior (B) (n = 9 mice in each group, * p<0.05 vs. sham-operated control).

Supplemental Figure 3. MCK-NO66 mice are resistant to CKD-induced muscle wasting. A&B. In the presence of CKD, comparing MCK-NO66 and NO66^{flox/flox} mice, there is an increase in muscle weights of gastrocnemius (A) and tibialis anterior (TA) (B) (n = 8 mice in each group, *, p<0.05 vs. Sham- NO66^{flox/flox} mice. #, p<0.05 vs. CKD- NO66^{flox/flox} mice). C. Immunostaining of muscle cross sections of TA muscles with anti-laminin outlines areas of myofibers (left panel, Bar=25 μ m). The average myofiber area in muscles of MCK-NO66 mice was significantly larger than that of NO66^{flox/flox} mice that were in the presence of CKD (right panel).

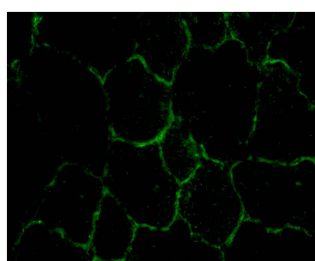
Supplemental Figure 4. NO66 and myostatin independently regulate muscle mass. A. KO NO66 from muscle does not change myostatin mRNAs (n=5 mice in each group). B. overexpress NO66 in muscle cell does not affect levels of myostatin protein.

Supplemental Figure 5. The Gene ontology classification analysis is based on differential expression of genes identified by RNA-seq from soleus muscle of NO66^{flox/flox} and NO66^{-/-} mice.

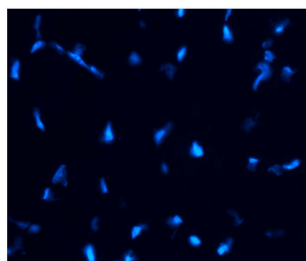
NO66



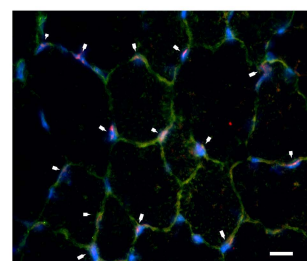
Laminin



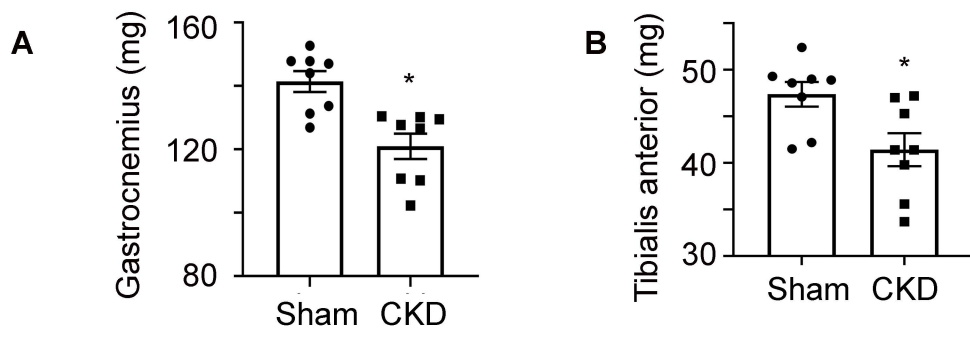
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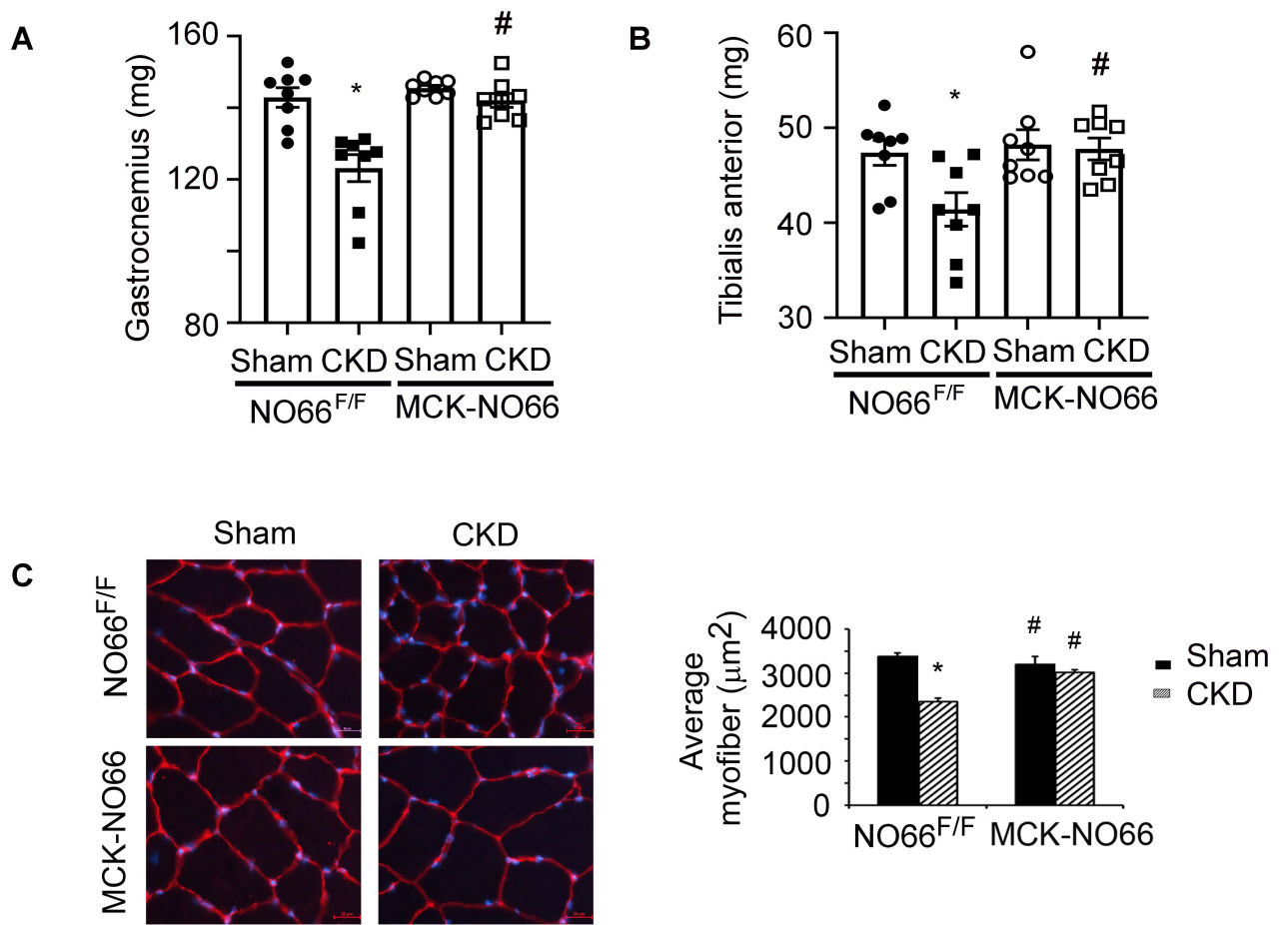
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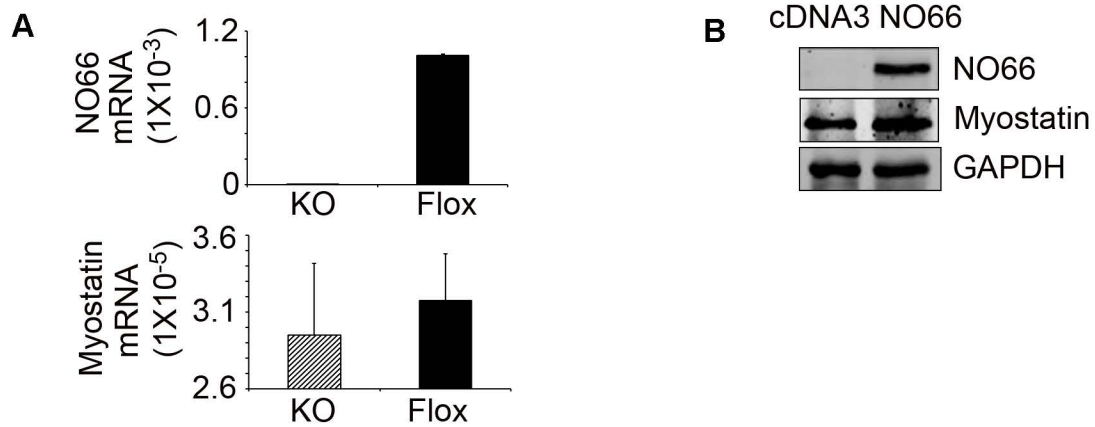
Supplemental Figure 1



Supplemental Figure 2



Supplemental Figure 3



Supplemental Figure 4

Gene Ontology Classification Analysis (NO66 KO vs. CTRL)

Molecular Function

GO:0097159 organic cyclic compound binding
GO:1901363 heterocyclic compound binding
GO:0003676 nucleic acid binding
GO:0044822 poly(A) RNA binding
GO:0003723 RNA binding

Cellular Component

GO:0032991 macromolecular complex
GO:0044430 cytoskeletal part
GO:0043232 intracellular non-membrane-bounded organelle
GO:0043228 non-membrane-bounded organelle
GO:0005654 nucleoplasm
GO:0070013 intracellular organelle lumen
GO:0043233 organelle lumen
GO:0031974 membrane-enclosed lumen
GO:0044422 organelle part
GO:0031981 nuclear lumen
GO:0044446 intracellular organelle part
GO:0044428 nuclear part

Biological Process

GO:0019538 protein metabolic process
GO:0043933 macromolecular complex subunit organization
GO:0009059 macromolecule biosynthetic process
GO:0034645 cellular macromolecule biosynthetic process
GO:0006725 cellular aromatic compound metabolic process
GO:0046483 heterocycle metabolic process
GO:0044267 cellular protein metabolic process
GO:0006996 organelle organization
GO:0010467 gene expression
GO:0034641 cellular nitrogen compound metabolic process
GO:0006139 nucleobase-containing compound metabolic process
GO:0016070 RNA metabolic process
GO:0090304 nucleic acid metabolic process
GO:0007049 cell cycle



Supplemental Figure 5. The Gene ontology classification analysis based on differential expression genes identified by RNA-seq between soleus muscle from NO66^{Flox/Flox} and NO66^{-/-} mice