

Figure S1. (A) Tibialis Anterior sections (6 µm) were stained with anti-FLAG antibody to determine the localization of SNARK transgenes in SDN and SWT animals (green). Control animals do not have FLAG expression and are included as a negative control. Nuclei are visualized by DAPI (blue) staining. Magnification is 400x. (B) Hearts were collected from SNARK transgenic mice and wild-type littermate controls, sectioned and stained with Hematoxylin & Eosin. Magnification is 400x. Images for panels A & B are representative of 4 animals/group. (C) Heart rate and blood pressure were measured from 52-week old SNARK transgenic mice and littermate controls using a tail-cuff plethysmography system. N=4/group.

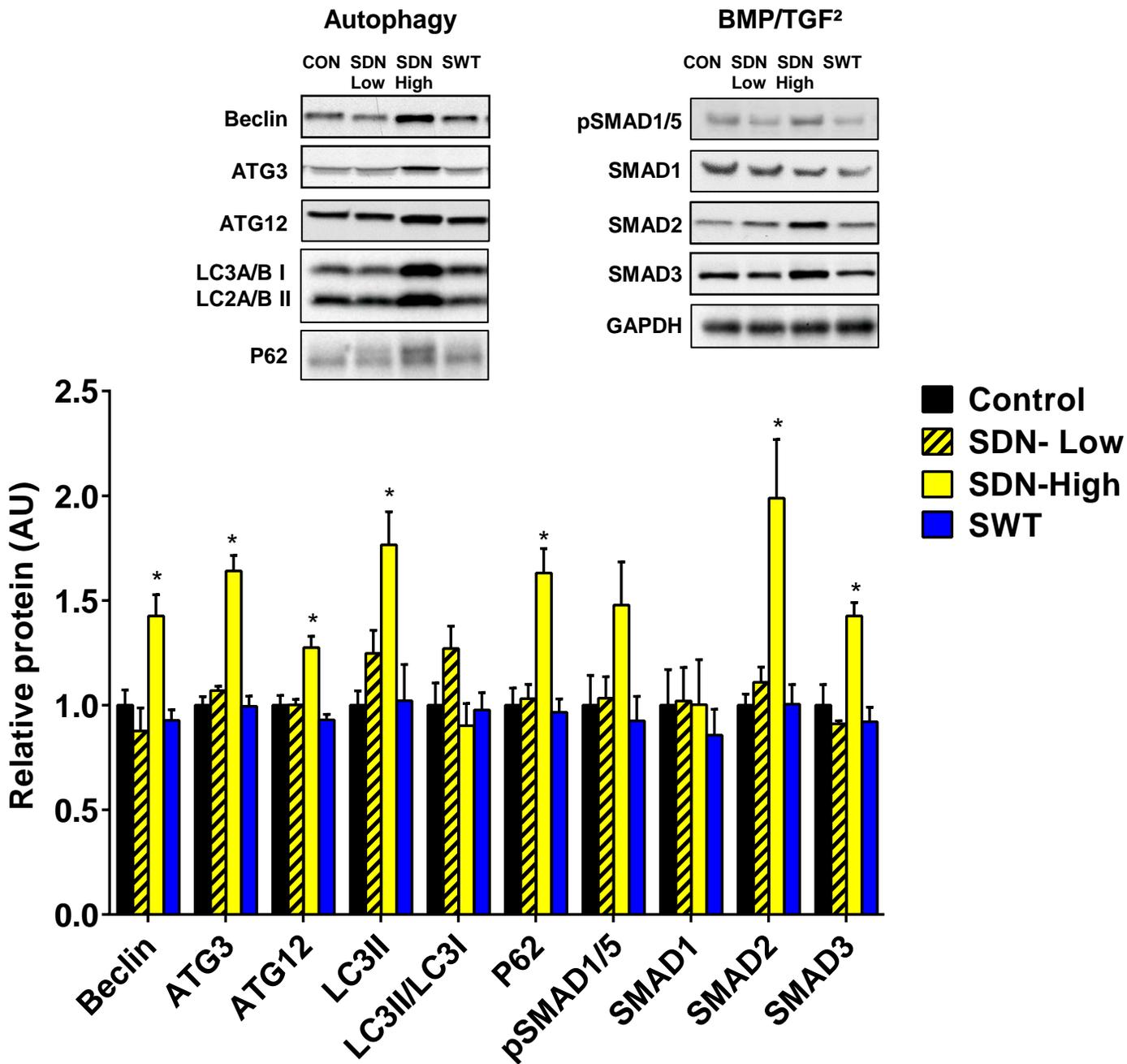
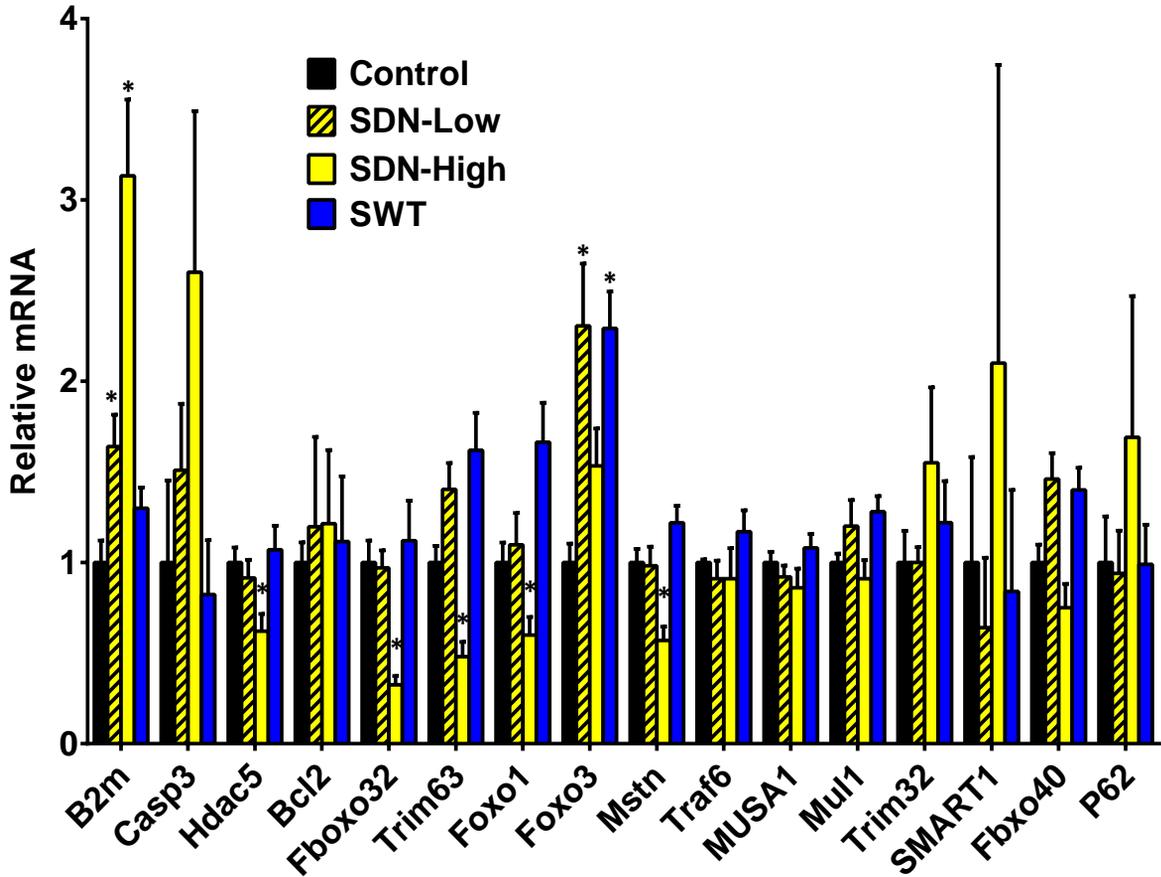


Figure S2. Protein levels of key mediators of muscle autophagy, BMP/TGF² signaling and protein synthesis were measured in the skeletal muscle of SNARK transgenic mice and littermate controls at 58 wks. ATG, Autophagocytosis-associated protein; LC3, Microtubule-associated protein 1A/1B-light chain 3; P62, sequestosome 1; SMAD, SMA/MAD homolog. GAPDH is included as a loading control. n=5-6/group; *P<0.05 vs WT. One-way ANOVA with Bonferroni posthoc test was used to determine statistical significance.

Apoptosis, Autophagy & Muscle Atrophy



Muscle Hypertrophy & Myogenesis

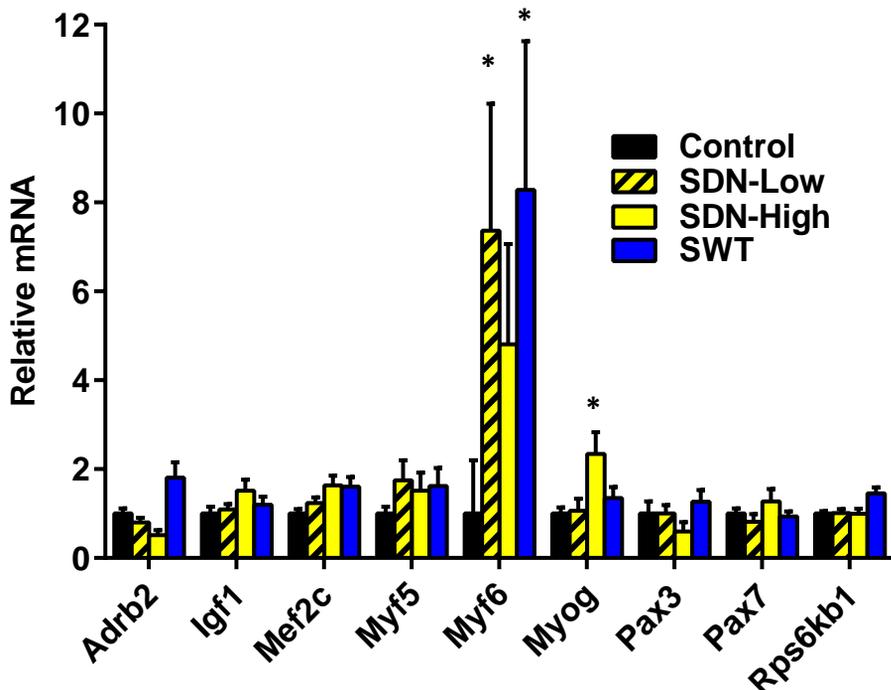


Figure S3. Real-time PCR was used to measure skeletal muscle mRNA levels of key regulators of apoptosis, autophagy and muscle atrophy, as well as regulators of muscle hypertrophy and myogenesis in SNARK transgenic animals and littermate controls. N=5 samples/group. *P<0.05 vs Control. One-way ANOVA with Bonferroni posthoc test was used to determine significance.

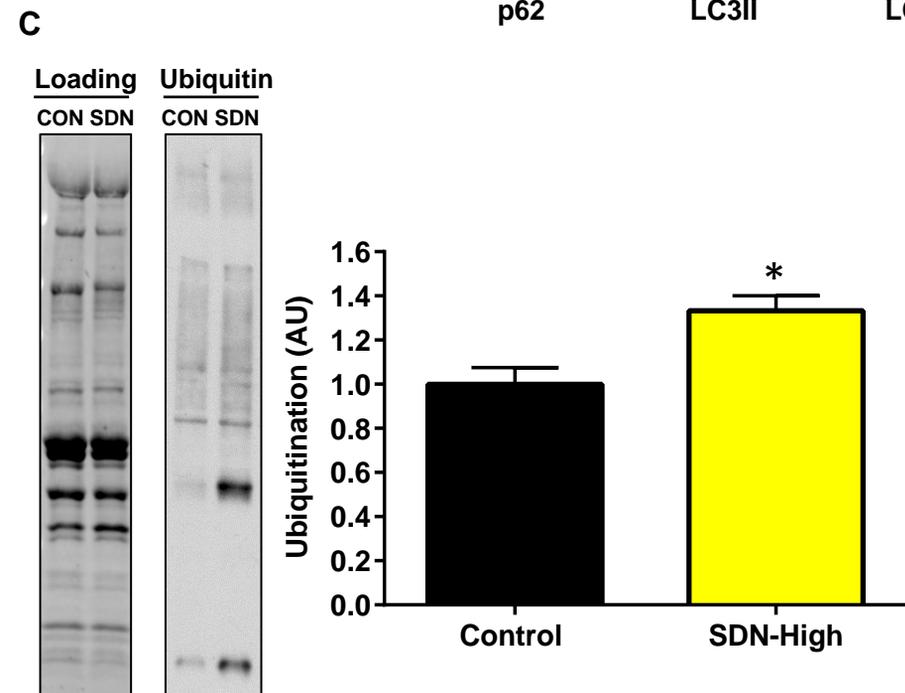
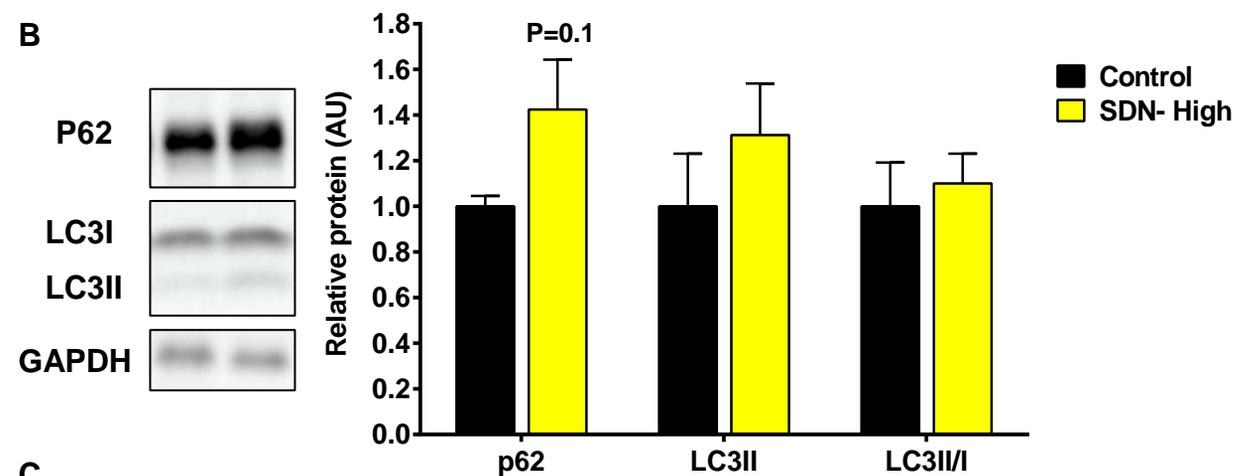
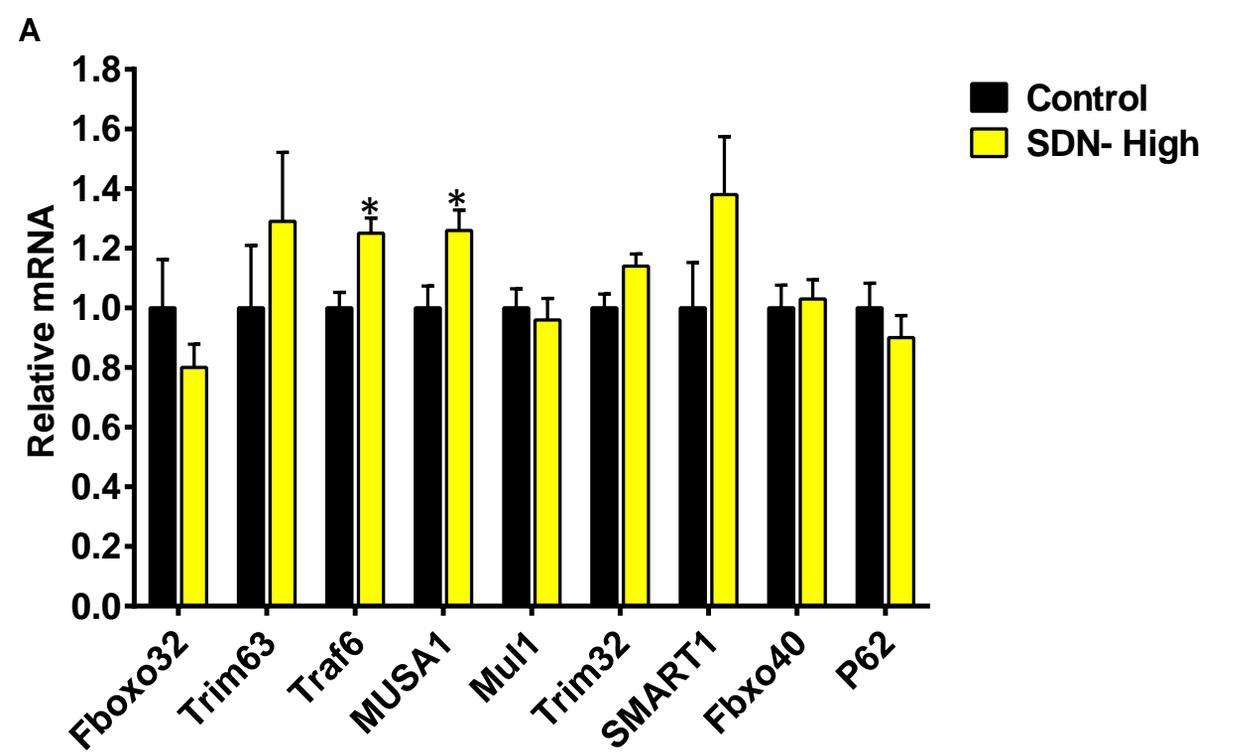


Figure S4: Skeletal muscle was collected from SDN-High SNARK transgenic mice and littermate controls at 8 wks of age; prior to the onset of severe muscle atrophy. (A) mRNA expression of genes associated with muscle atrophy were measured using ARBP as a reference gene. (B) Protein lysates were analyzed for P62 levels, LC3II lipidation, and (C) global ubiquitination. GAPDH (B) and stain-free imaging (C; BioRad) were used as loading controls. N=4/group; *P<0.05 by unpaired t-test.