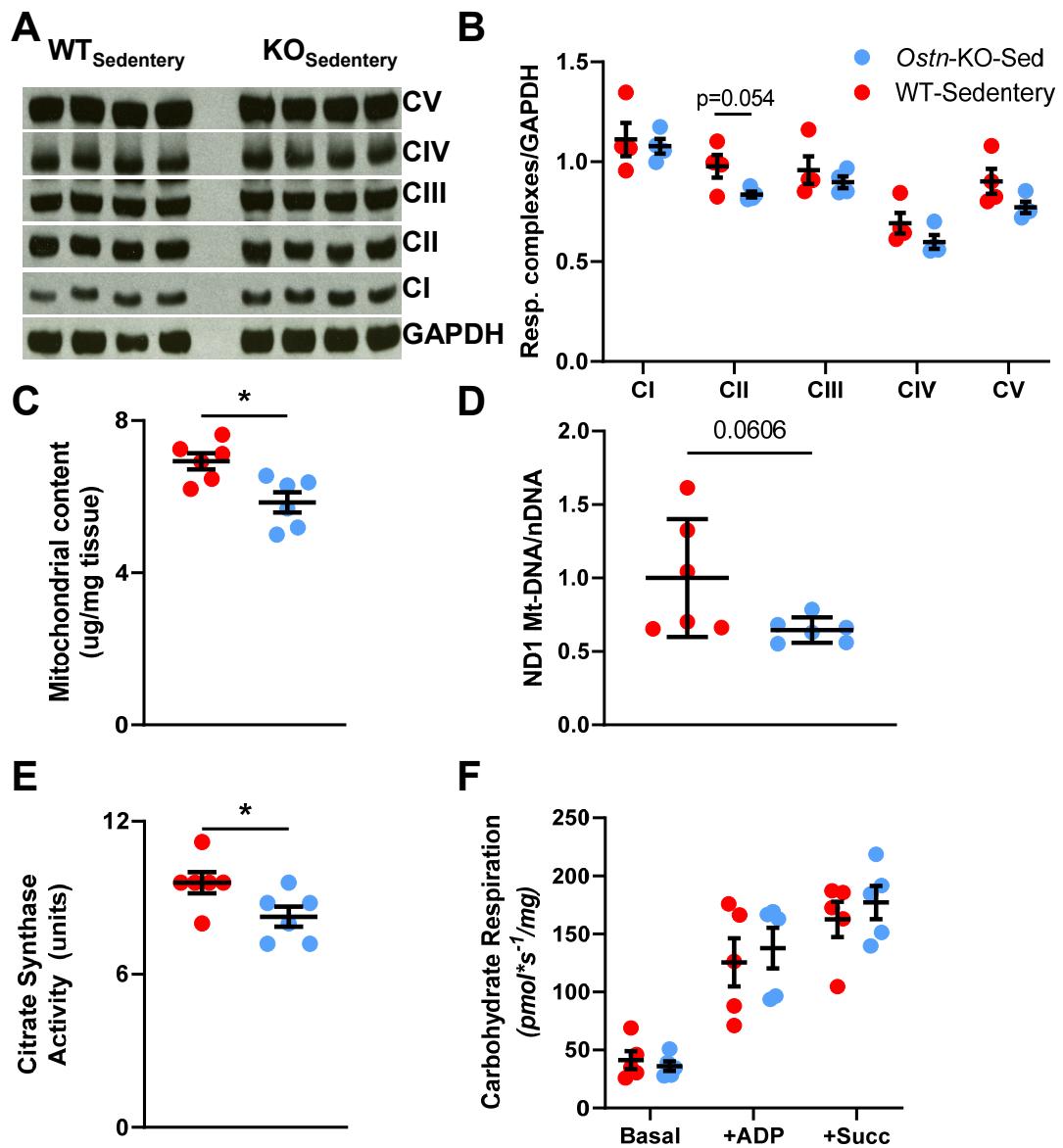
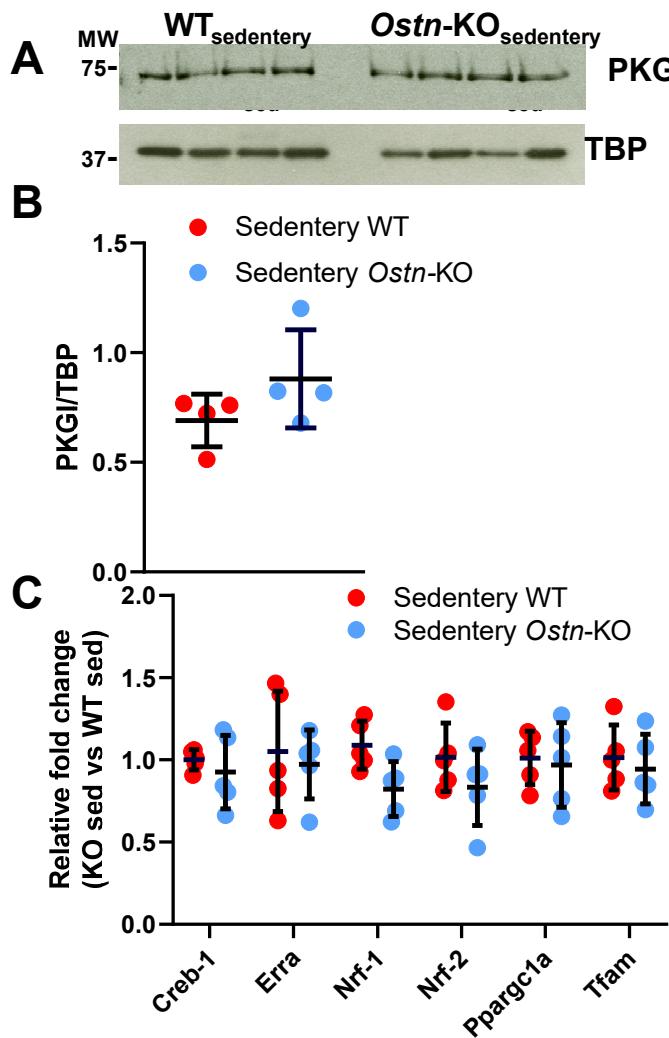


## Supplemental materials

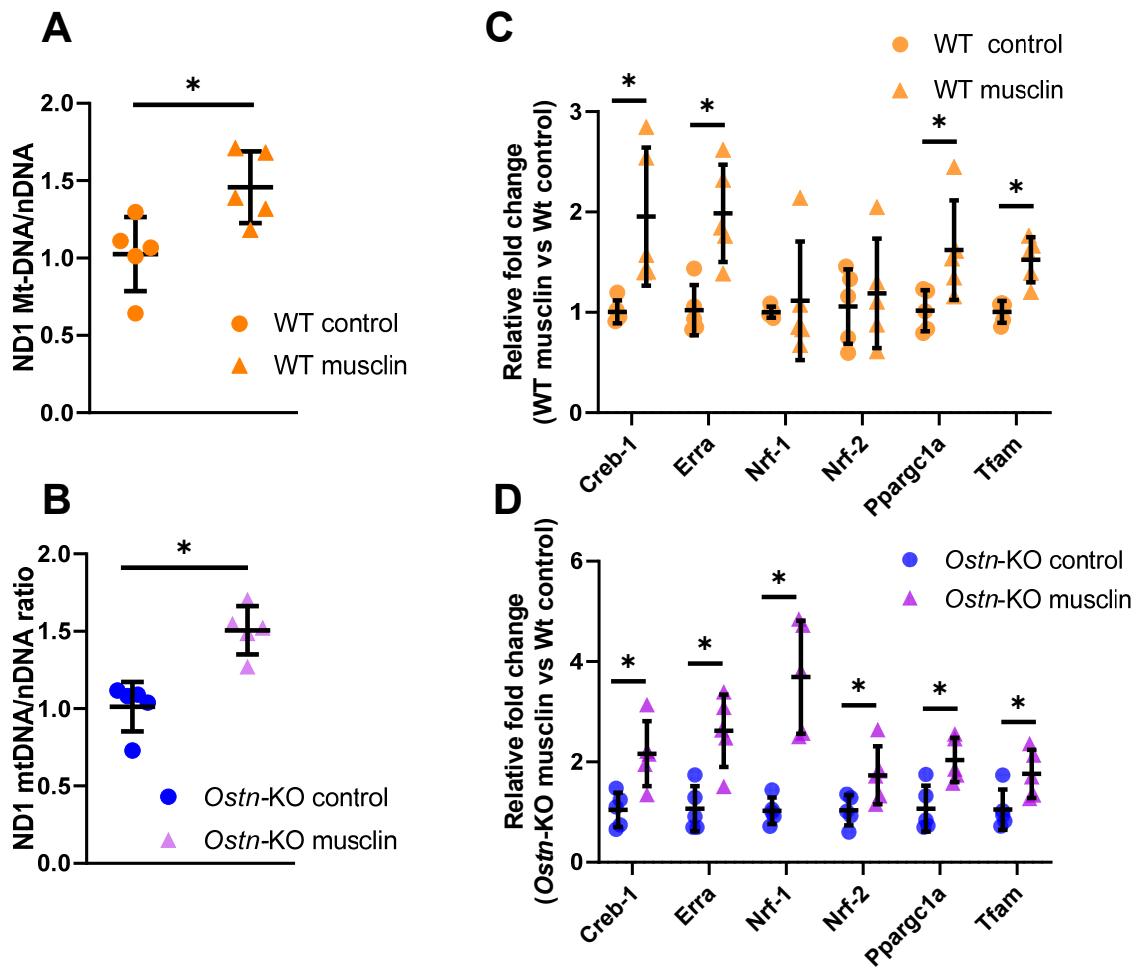


**Figure S1. Mitochondrial biogenesis and respiratory capacity in hearts of *Osn*-KO and WT control mice under “sedentary” (regular housing) conditions. (A)**  
 Representative western blots of respiratory chain enzymes and GAPDH and (B)  
 summary statistics for respiratory complex expression normalized to GAPDH in hearts  
 of sedentary WT and *Osn*-KO mice (n=4 each): Complex I expression (1.08±0.08 vs.

$1.11 \pm 0.17$  AU,  $p=0.7$ ), complex II expression ( $0.83 \pm 0.03$  vs.  $0.98 \pm 0.11$  AU,  $p=0.054$ ), complex III expression ( $0.89 \pm 0.06$  vs.  $0.96 \pm 0.14$  AU,  $p=0.45$ ), complex IV expression ( $0.6 \pm 0.07$  vs.  $0.69 \pm 0.1$  AU,  $p=0.18$ ), complex V expression ( $0.77 \pm 0.06$  vs.  $0.9 \pm 0.13$  AU,  $p=0.11$ ) (C) Summary statistics for mitochondrial content by tissue weight in hearts from sedentary WT and *Ostn*-KO mice ( $n=6$  each,  $6.67 \pm 0.60$  vs.  $5.85 \pm 0.66$   $\mu\text{g}/\text{mg}$  tissue,  $p=0.01$ ). (D) Summary statistics for expression of ND-1 normalized to hexokinase 2 in hearts from sedentary WT and *Ostn*-KO mice ( $n=6$  each,  $1.00 \pm 0.40$  vs.  $0.65 \pm 0.09$  AU,  $p=0.06$ ). (E) Summary statistics for citrate synthase activity in mitochondrial extracts from hearts of sedentary WT and *Ostn*-KO mice ( $n=6$  each,  $9.59 \pm 1.01$  vs.  $8.26 \pm 0.97$  AU,  $p=0.04$ ). (F) Summary statistics for carbohydrate driven mitochondrial respiration in semi-permeabilized fibers normalized to tissue weight in hearts from sedentary WT and *Ostn*-KO mice ( $n=5$  each): Under carbohydrate-supported conditions respiration in myofibers isolated from hearts of sedentary WT and *Ostn*-KO mice were comparable (basal:  $41.39 \pm 17.18$  vs.  $36.21 \pm 9.41$   $\text{pmol}^*\text{s}^{-1}/\text{mg}$ ,  $p=0.57$ , with ADP stimulation:  $125.56 \pm 46.32$  vs.  $137.88 \pm 39.05$   $\text{pmol}^*\text{s}^{-1}/\text{mg}$ ,  $p=0.66$ , and with addition of succinate:  $162.63 \pm 33.89$  vs.  $177.17 \pm 31.87$   $\text{pmol}^*\text{s}^{-1}/\text{mg}$ ,  $p=0.5$ ). Data are means  $\pm$  SD; \* $P<0.05$ .



**Figure S2. Nuclear protein kinase G1 expression and mRNA expression of mitochondrial biogenesis-related genes in *Ostn*-KO and WT mice under “sedentary” (regular housing) conditions.** (A) Representative western blots of PKG1 and TATA binding protein in nuclear extracts from hearts of sedentary WT and *Ostn*-KO mice, (B) Summary statistics for PKG1 normalized TBP in nuclear extracts from hearts of sedentary WT and *Ostn*-KO mice ( $0.51 \pm 0.76$  vs.  $0.68 \pm 1.2$ , n=4, p=0.19). (C) Summary statistics for mRNA expression of *Creb1*, *Erra*, *Nrf1*, *Nrf2*, *Ppargc1a*, and *Tfam* in hearts from sedentary WT and *Ostn*-KO mice (n=6). Data are means  $\pm$  SD.



**Figure S3.** Synthetic musclin infusion promotes mitochondrial biogenesis. (A) Summary statistics for expression of ND-1 normalized to hexokinase 2 in hearts from sedentary WT mice infused with control peptide or synthetic musclin for 14 days ( $1.09 \pm 0.24$  vs.  $1.46 \pm 0.23$ , n=5 each, p=0.02). (B) Summary statistics for expression of ND-1 normalized to hexokinase 2 in hearts from sedentary Osn-KO mice infused with control peptide or synthetic musclin for 28 days ( $1.01 \pm 0.16$  vs.  $1.51 \pm 0.16$ , n=5 each, p=0.001). (C) Summary statistics for mRNA expression of *Creb1*, *Erra*, *Nrf1*, *Nrf2*, *Ppargc1a*, and *Tfam* in hearts from sedentary WT mice infused with control peptide or synthetic musclin for 14 days (all n=5 each, *Creb1*:  $1.01 \pm 0.11$  vs.  $1.95 \pm 0.69$  fold change, p=0.02, *Erra*:  $1.02 \pm 0.25$  vs.  $1.99 \pm 0.49$  fold change, p=0.004, *Nrf1*:  $1.0 \pm 0.06$  vs.  $1.12 \pm 0.59$  fold change, p=0.02, *Nrf2*:  $0.85 \pm 0.15$  vs.  $1.25 \pm 0.35$  fold change, p=0.02, *Ppargc1a*:  $0.95 \pm 0.15$  vs.  $1.45 \pm 0.45$  fold change, p=0.02, *Tfam*:  $0.95 \pm 0.15$  vs.  $1.45 \pm 0.45$  fold change, p=0.02). (D) Summary statistics for mRNA expression of the same genes in Osn-KO mice (all n=5 each, *Creb1*:  $1.0 \pm 0.1$  vs.  $3.5 \pm 1.0$  fold change, p=0.02, *Erra*:  $1.0 \pm 0.1$  vs.  $3.5 \pm 1.0$  fold change, p=0.02, *Nrf1*:  $0.85 \pm 0.15$  vs.  $5.0 \pm 1.5$  fold change, p<0.001, *Nrf2*:  $0.85 \pm 0.15$  vs.  $2.5 \pm 0.5$  fold change, p=0.02, *Ppargc1a*:  $1.0 \pm 0.1$  vs.  $2.5 \pm 0.5$  fold change, p=0.02, *Tfam*:  $0.85 \pm 0.15$  vs.  $2.5 \pm 0.5$  fold change, p=0.02).

change, p=0.68, *Nrf2*:  $1.06 \pm 0.37$  vs.  $1.19 \pm 0.55$  fold change, p=0.67, *Ppargc1a*:  $1.02 \pm 0.2$  vs.  $1.62 \pm 0.49$  fold change, p=0.04), and *Tfam*:  $1.01 \pm 0.11$  vs.  $1.52 \pm 0.22$  fold change, p=0.002). (D) Summary statistics for mRNA expression of *Creb1*, *Erra*, *Nrf1*, *Nrf2*, *Ppargc1a*, and *Tfam* in hearts from sedentary *Ostn*-KO mice infused with control peptide or synthetic musclin for 28 days, n=5 each (*Creb1*:  $1.05 \pm 0.34$  vs.  $2.16 \pm 0.65$  fold change, p=0.009, *Erra*:  $1.07 \pm 0.45$  vs.  $2.62 \pm 0.72$  fold change, p=0.003, *Nrf1*:  $1.03 \pm 0.27$  vs.  $3.695 \pm 1.12$  fold change, p=0.001, *Nrf2*:  $1.04 \pm 0.3$  vs.  $1.73 \pm 0.58$  fold change, p=0.04, *Ppargc1a*:  $1.07 \pm 0.46$  vs.  $2.04 \pm 0.44$  fold change, p=0.009, and *Tfam*:  $1.05 \pm 0.4$  vs.  $1.76 \pm 0.48$  fold change, p=0.03). Data are means  $\pm$  SD; \*P<0.05.,