

Supplementary information

Table S1 Taxon comparison of treatment groups at the genus level

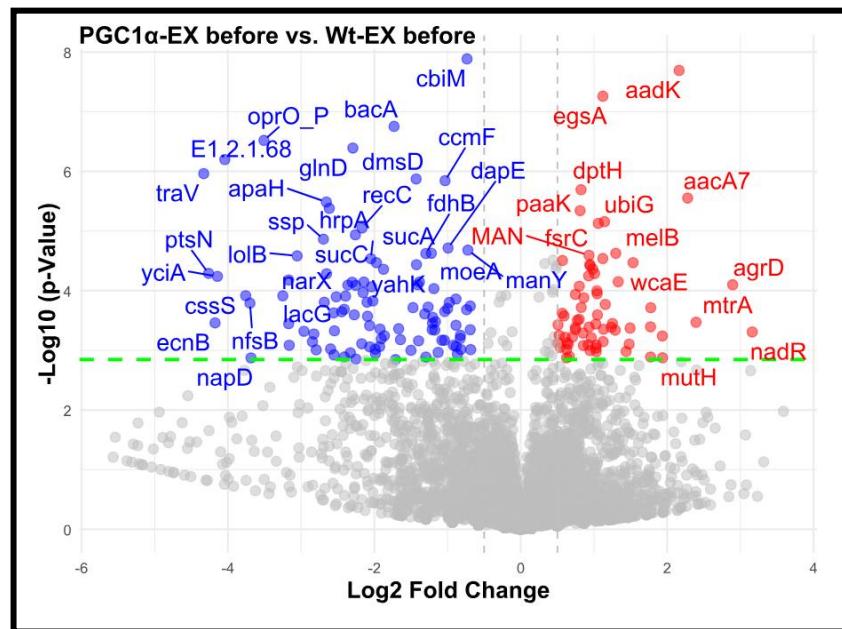
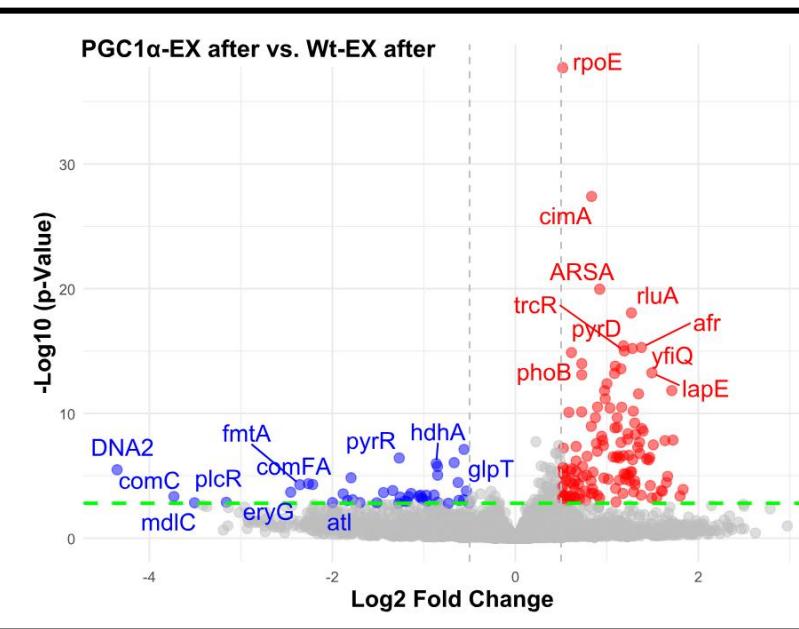
Columns depict taxon name, log 2 fold changes, the unmodified p value of group comparison, and Benjamini-Hochberg corrected p values

Table S2 Biological pathway comparison of treatment groups at the genus level

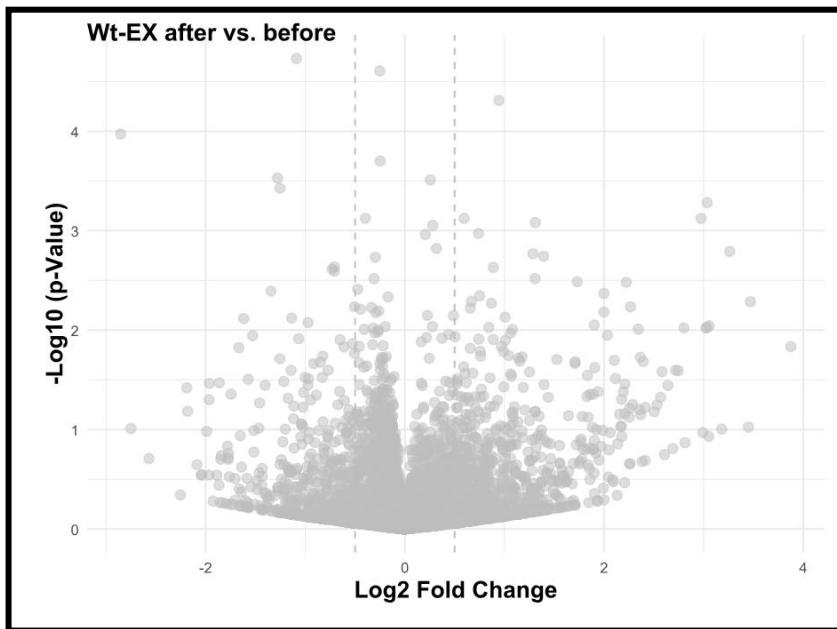
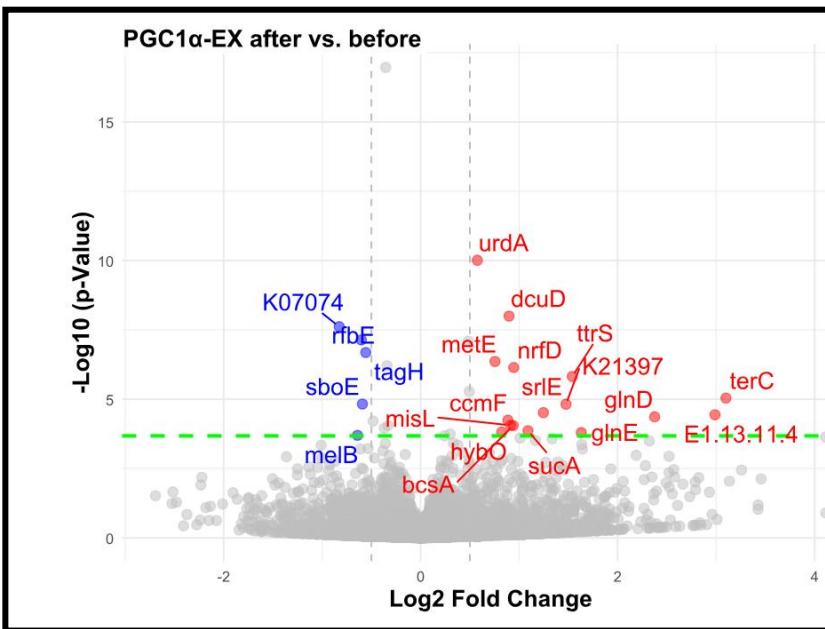
Columns depict biological pathway name, log 2 fold changes, the unmodified p value of group comparison, and Benjamini-Hochberg corrected p values

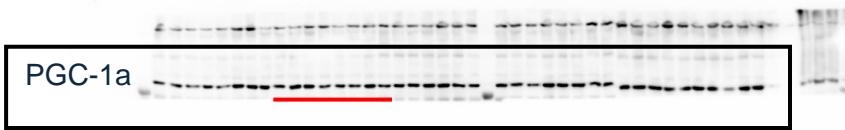
Figure S1 Effects of muscle specific PGC-1 α over expression and exercise on gut microbiological biological pathways. a-d panels show the changes in the abundance of bacterial pathways in the gut microbiome at the genus level. Red dots represent significantly increased abundance, while blue dots indicate significantly decreased abundance between the groups depicted in the upper right corner of each panel. The green dashed line marks the Benjamini-Hochberg (BH) correction threshold, and gray lines indicate ± 0.5 Log2 fold change.

Original western blot images. Red underlines indicate the bands selected and shown in Figure 3 a-j and Figure 1 b.

a**b**

- Relative Ab. increased
- Relative Ab. decreased
- Not significant
- BH threshold

c**d**

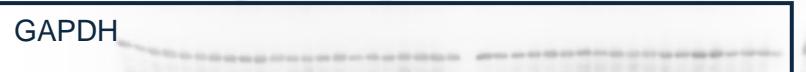


PGC-1 α (figure 3 h)



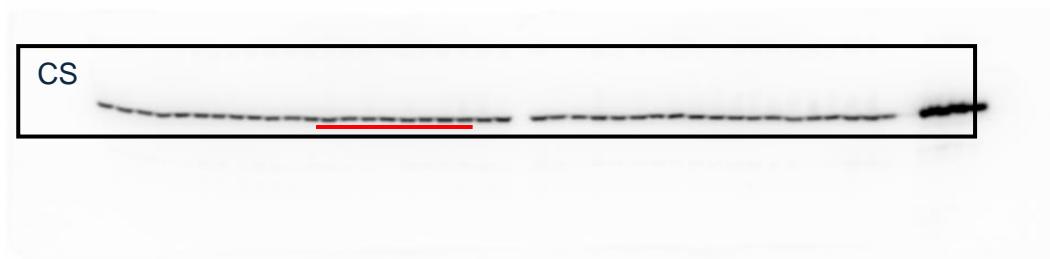


Mfn1

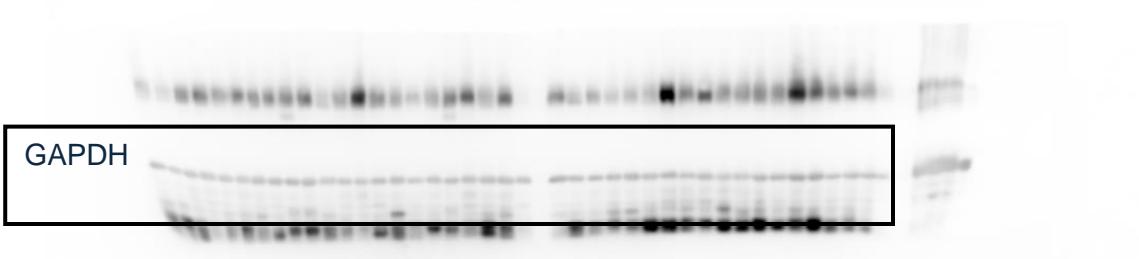


GAPDH

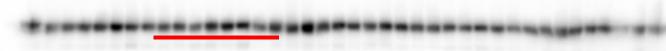
MFN1(figure 3 j)



CS (figure 3 i)



pAMPK

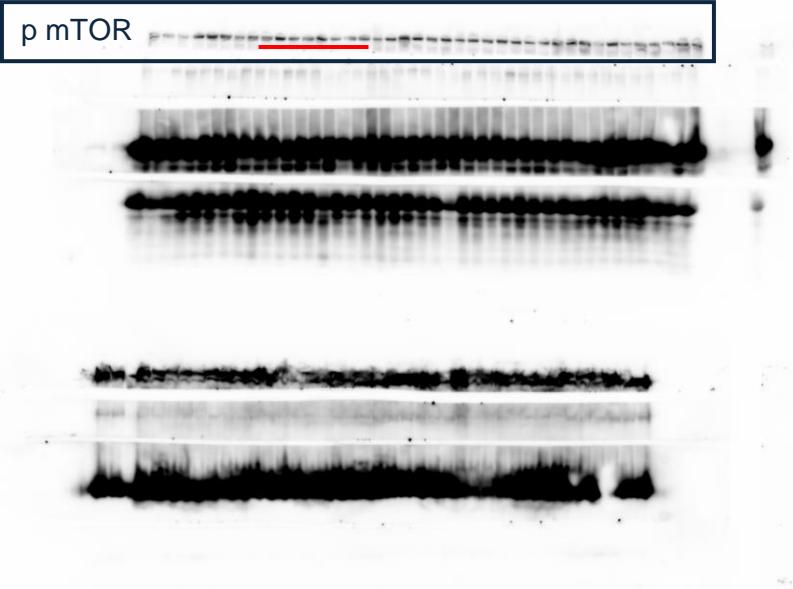


p/t AMPK (figure 3 a)

total AMPK

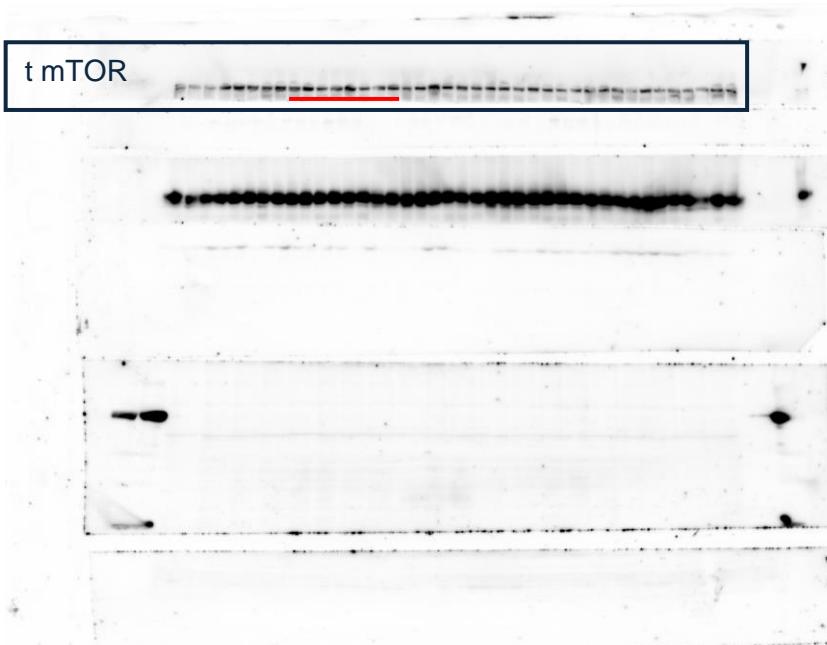


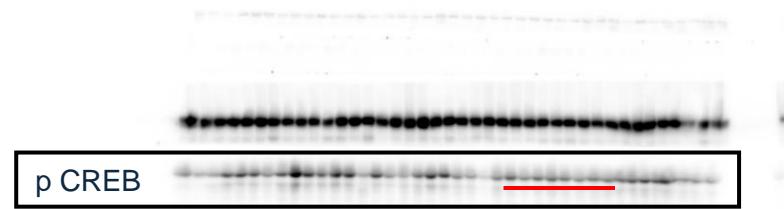
p mTOR



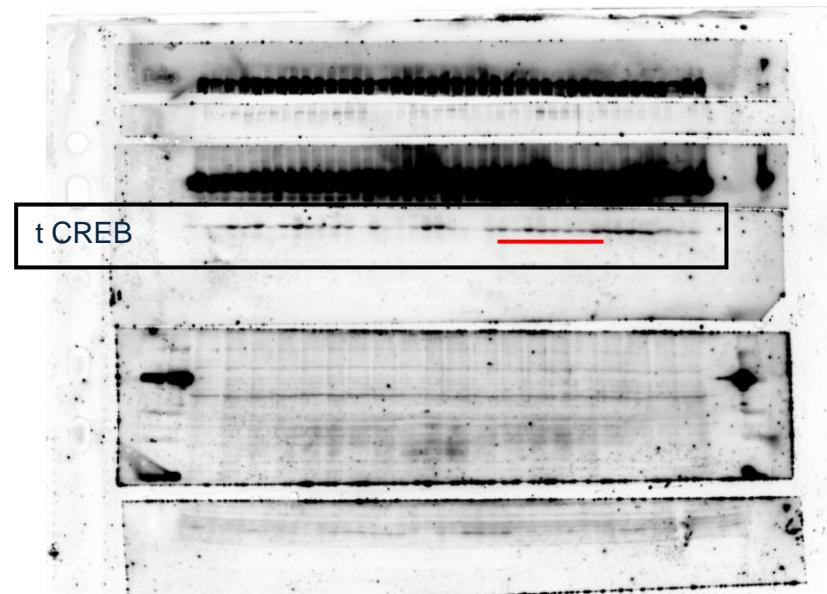
p/t mTOR (figure 3 c)

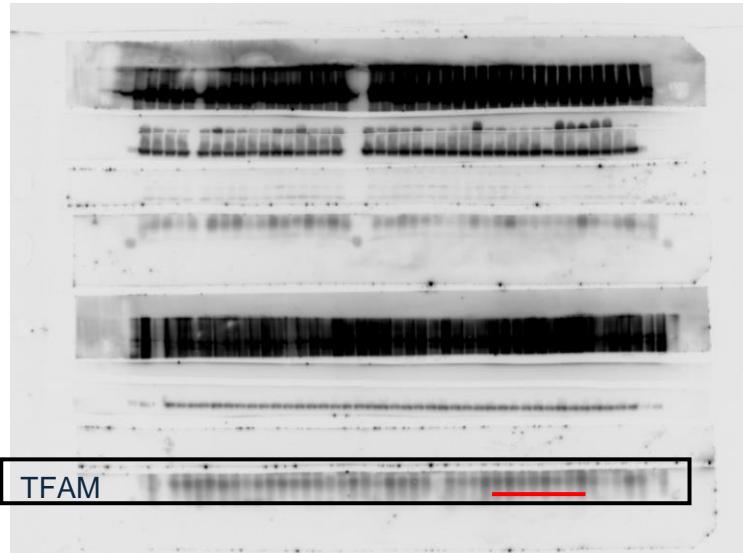
t mTOR



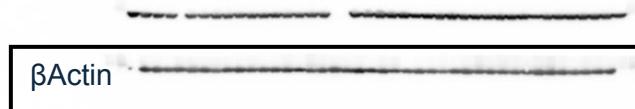


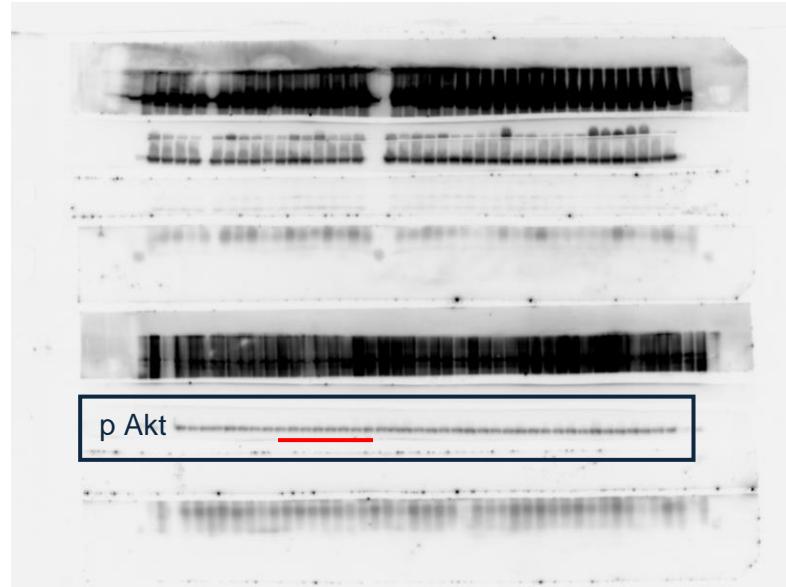
p/t CREB (figure 3 b)



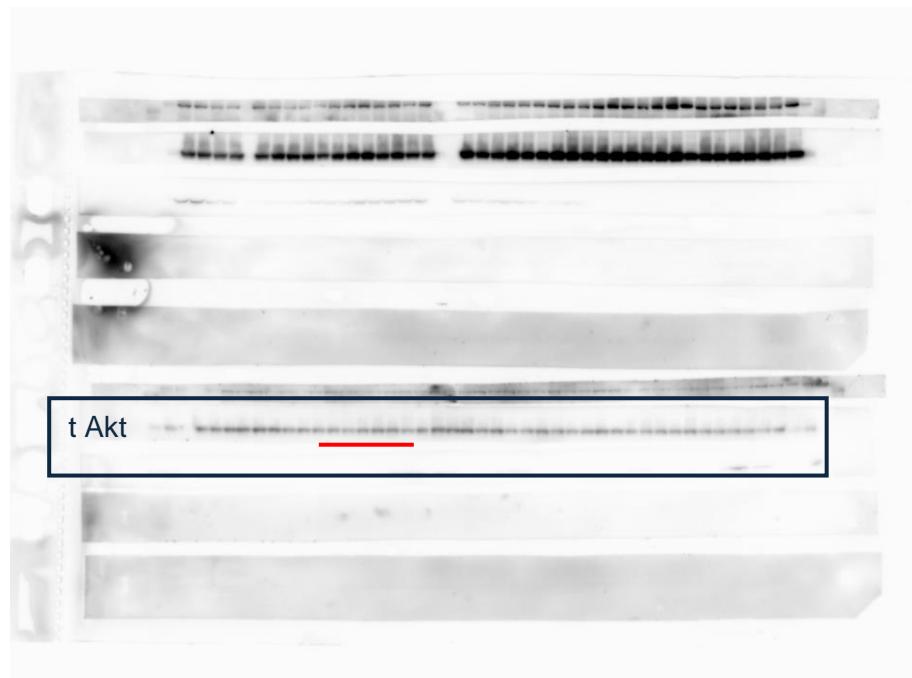


TFAM (figure 3 e)

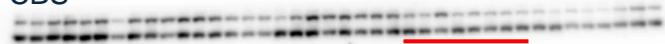




p/t AKT(figure 3 d)

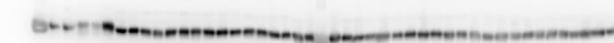


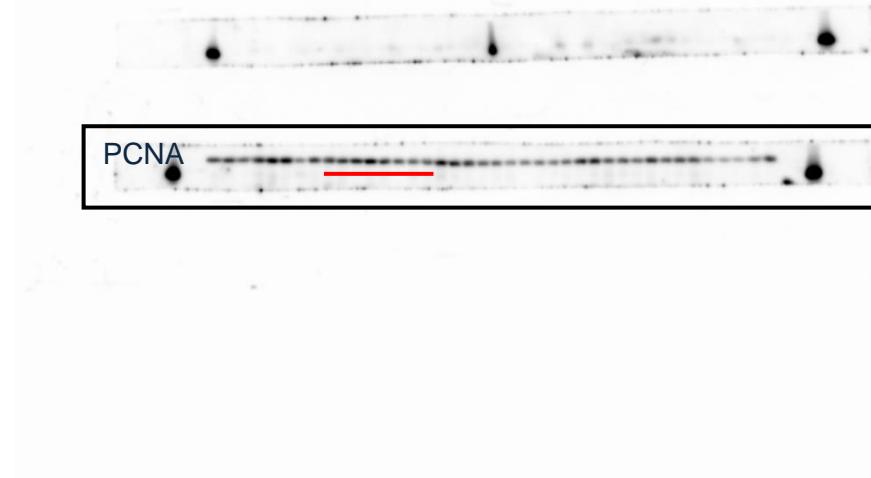
CBS



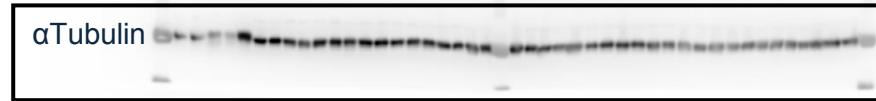
CBS (figure 3 f)

α Tubulin





PCNA (figure 3 g)



PGC-1a

α Tubulin

PGC-1 α in skeletal
muscle