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Supplemental Information

**Basal Mitophagy Occurs Independently of PINK1
in Mouse Tissues of High Metabolic Demand**

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Supplemental Figures

Figure S1: Monitoring mitophagy/autophagy using *mito-QC*/mCherry-GFP-LC3 and mass spectrometry sequence coverage. Related to Figure 1.

(A) DFP triggers mitophagy in *Pink1* WT and KO *mito-QC* MEFs. MEFs were treated with DMSO (Control) and DFP for 24 hours. Scale bar, 5 μ m. (B) Quantitation of mitophagy induced by iron-chelation in S1A (Two-way ANOVA, ****= $P < 0.0001$). (C) Endogenous activation of the PINK1-Parkin pathway. Adult fibroblasts were established from *Pink1* WT and KO mice and stimulated \pm CCCP for 18 hours. Enriched mitochondrial fractions were processed for ubiquitin capture by TUBE^{UBA2} as previously described. Denatured protein extracts were subjected to SDS-PAGE and immunoblotting for the Parkin substrate, CISD1. Membranes were stripped and re-probed with antibodies to the PINK1 substrate, phospho-S65 Ubiquitin. (D) Targeting strategy for mCherry-GFP-LC3 mice used in the study, generated by Taconic Artemis GmbH. (E) Mouse PINK1 sequence coverage from WT cortex and cerebellum. Unique peptides highlighted in red exhibited a Mascot ion score >22 (indicating identity or extensive homology).

Figure S2: *mito-QC* reveals mitophagy in the dopaminergic system *in vivo*. Related to Figure 2.

(A) Immunoblot showing no differences in levels of GFP, and the OMM Protein Tom20 in total brain extracts from *Pink1* WT and KO *mito-QC* mice. (B) Isosurface volume render of midbrain dopaminergic neurons with high levels of mitochondrial turnover in cell bodies. Inset shows a representative image from the original raw stack used to generate the isosurface render. (C) Additional quantitative parameters measured using *mito-QC*. No differences were observed between genotypes in the

mean size or shape of mitolysosomes in midbrain dopaminergic axons or OB PGNs (n.s.= $P>0.05$; *Student's t-test*). (D) Mitophagy in A16 DA periglomerular neurons of the olfactory bulb (OB); G denotes a glomerulus. Arrows indicate mitophagy within PGNs (E) Analyses of mitophagy in all PGN DA neurons from *Pink1* WT and KO animals reveal no differences between genotypes (*Student's t-test*; n.s.= $P>0.05$). All scale bars, 5 μm . (F) *mito-QC* illuminates the mitochondrial rich nature of olfactory glomeruli. Airysan imaging and isosurface rendering revealed an unexpected complex and dense mitochondrial meshwork in adult olfactory glomeruli, and the intimate associations with TH-positive A16 PGNs. (G) Maximum projection z-stack showing representative example of mitophagy in a GFAP-positive astrocyte *in vivo*. Scale bar, 5 μm .

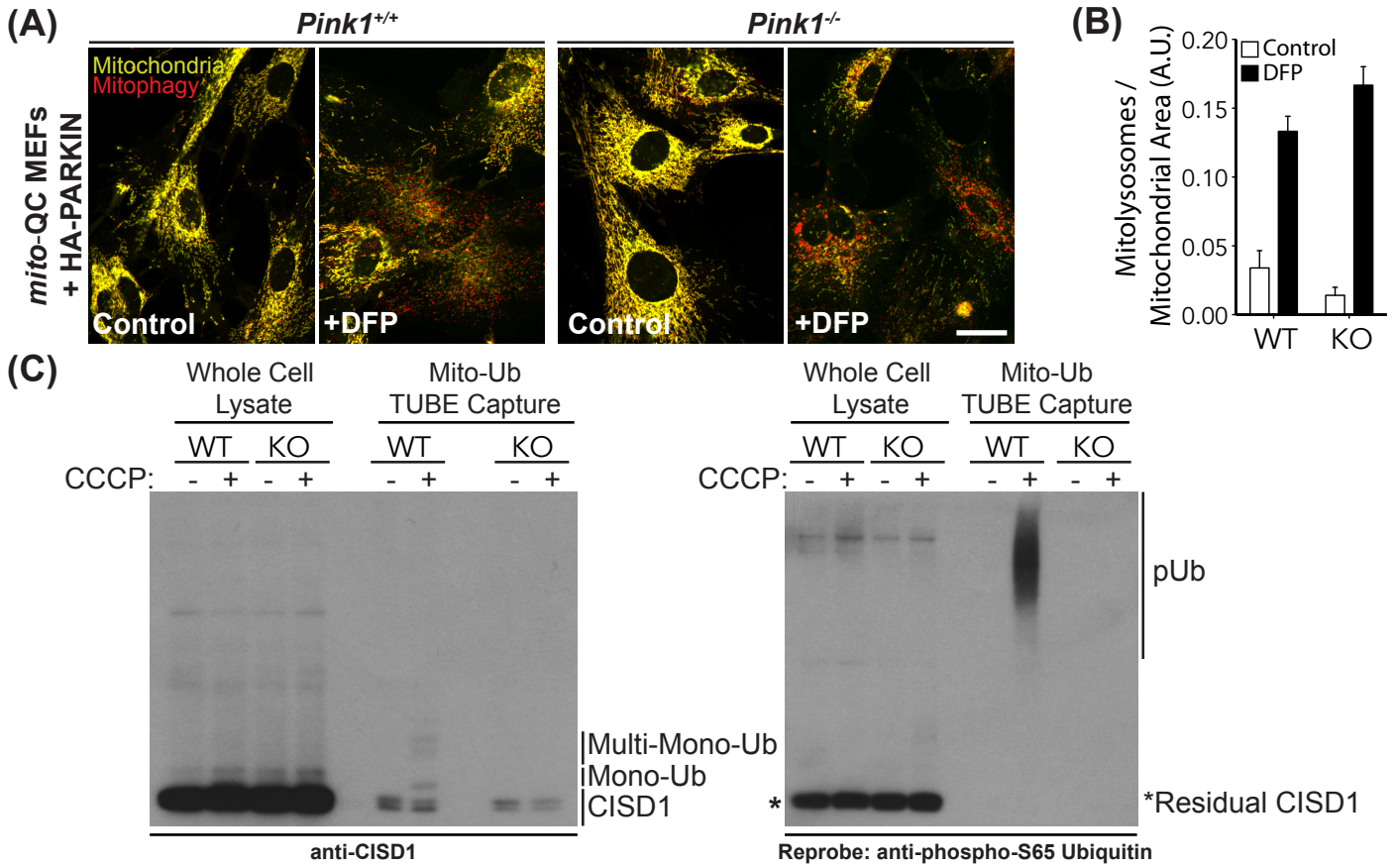
Figure S3: *mito-QC* reveals mitophagy in highly metabolic tissues. Related to Figures 3 and 4.

(A) Section of adult retina with associated extra-ocular muscle. Mitophagy is visible in the ONL, and in muscle shown in transverse and longitudinal orientations. (B) Mitophagy proceeds independently of the visual cycle. Representative images of ONL showing no differences in retinal mitophagy in animals during light or dark cycles. (C) Additional quantitative parameters of mitolysosomes and mitochondrial cell biology: no differences were observed (n.s.= $P>0.05$; *Student's t-test*), apart from a modest decrease in mitolysosome size in KO microglia ($*=P<0.05$; *Student's t-test*). (D) Airyscan image of adult pancreas from a *mito-QC* animal, showing distinct pools of mitochondria previously reported by Petersen and colleagues. PG-M: perigranular mitochondria; PN-M: perinuclear mitochondria; SP-M: subplasmalemmal mitochondria.

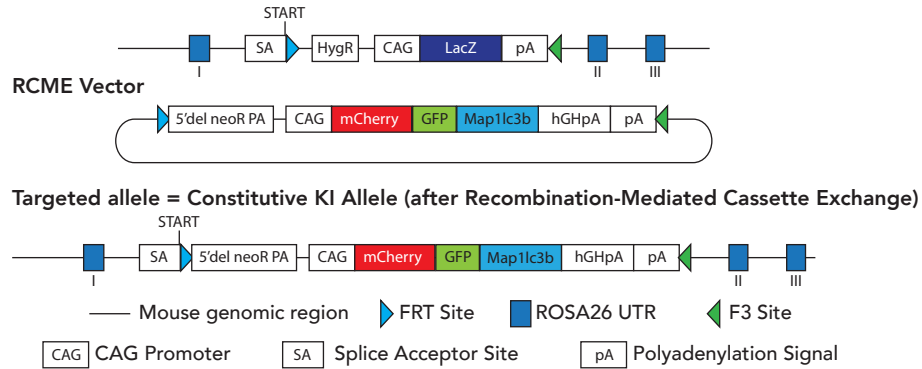
Figure S4: Loss of PINK1 does not influence 3-NPA mitotoxicity *in vivo*. Related to Figure 4.

(A) Analysis of mitophagy reveals no differences in the striata, striatal vasculature and hearts of *Pink1* WT and KO mice treated systemically with the brain-penetrant mitotoxin 3-NPA for 7 days (n.s.= $P>0.05$; One-Way ANOVA with *Bonferroni post-hoc* test). (B) 3-NPA does not activate the endogenous PINK1-Parkin pathway. IP shows stabilization of endogenous PINK1 protein with CCCP, but not 3-NPA treatment. (C) Composite tile-scan micrograph showing a transverse section of hindlimb skeletal

muscle. The highly oxidative fibers of the soleus (S) and highly glycolytic fibers of the white gastrocnemius (GC) are easily distinguished by mitochondrial content using GFP expression of *mito-QC*. Dashed lines delineate different anatomical boundaries of the GC-white (Gw), GC-mixed (Gm) and GC-red (Gr) zones. In this anatomical orientation, *mito-QC* reveals the lateral-medial gradient of glycolytic to oxidative muscle fibers. Shown are representative examples of GC/S muscles treated with 3-NPA from *Pink1* WT and KO *mito-QC* mice. Close-up images reveal the striking detail of the mitochondrial reticulum in different sub-regions. Scale bars = 500, 200 and 10 μm , respectively. (D) Quantitation of mitochondrial content as a function of GFP intensity. A non-significant, yet observable elevation is evident in the skeletal muscles of *Pink1* KO animals treated with 3-NPA. (E) Quantitation of mitophagy as a function of increasing mitochondrial content in 3-NPA treated *Pink1* WT and KO mice (*= $P < 0.05$; 3-NPA treated *Pink1* WT vs. KO using One-Way ANOVA, and *Bonferroni's* post-hoc test to compare all conditions within regions).

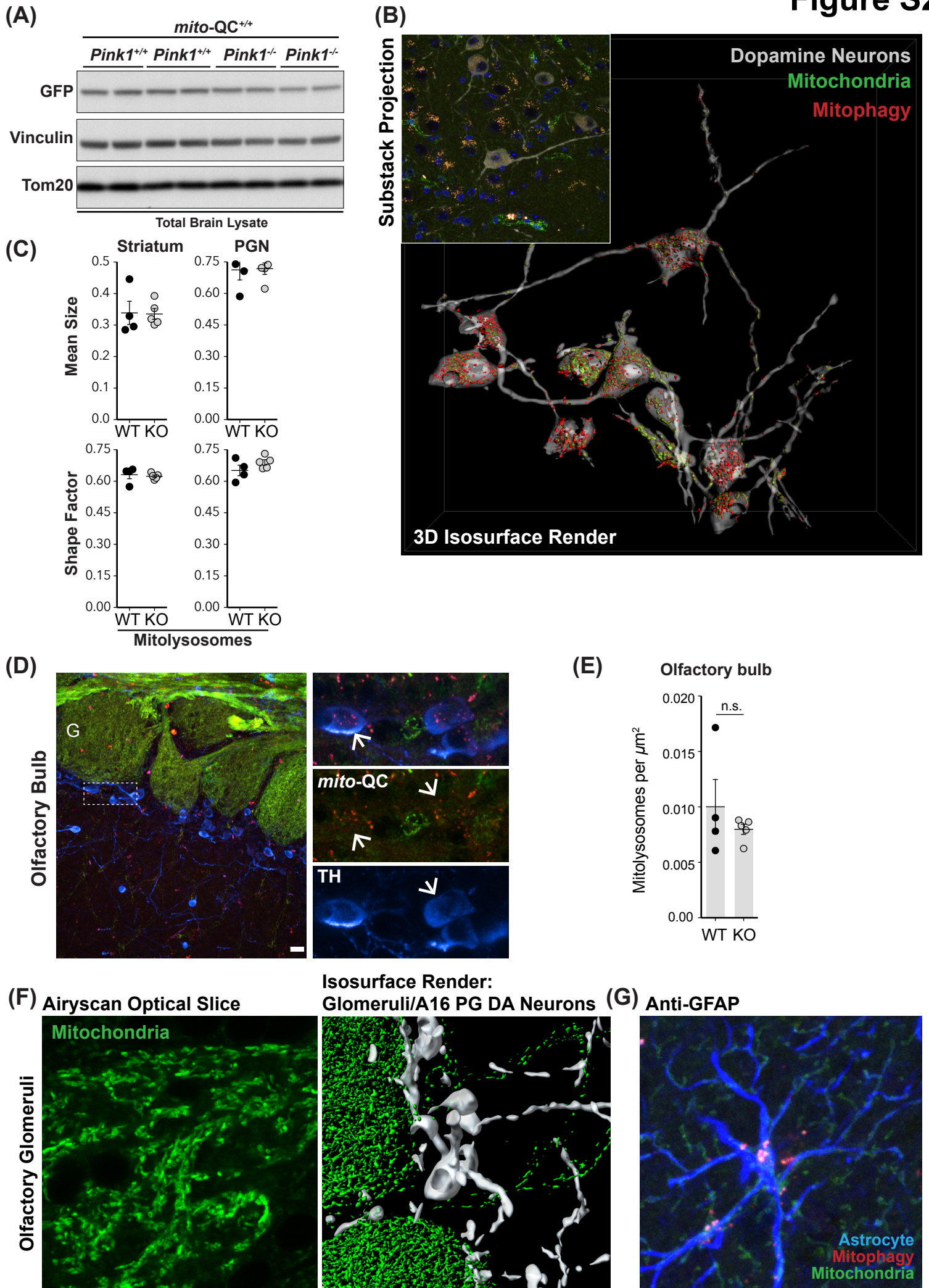


(D) **Generation of Autophagy mCherry-GFP-LC3 Reporter Mice**
 Mouse ROSA26 locus equipped with RCME docking sites (on C57BL/6 background)

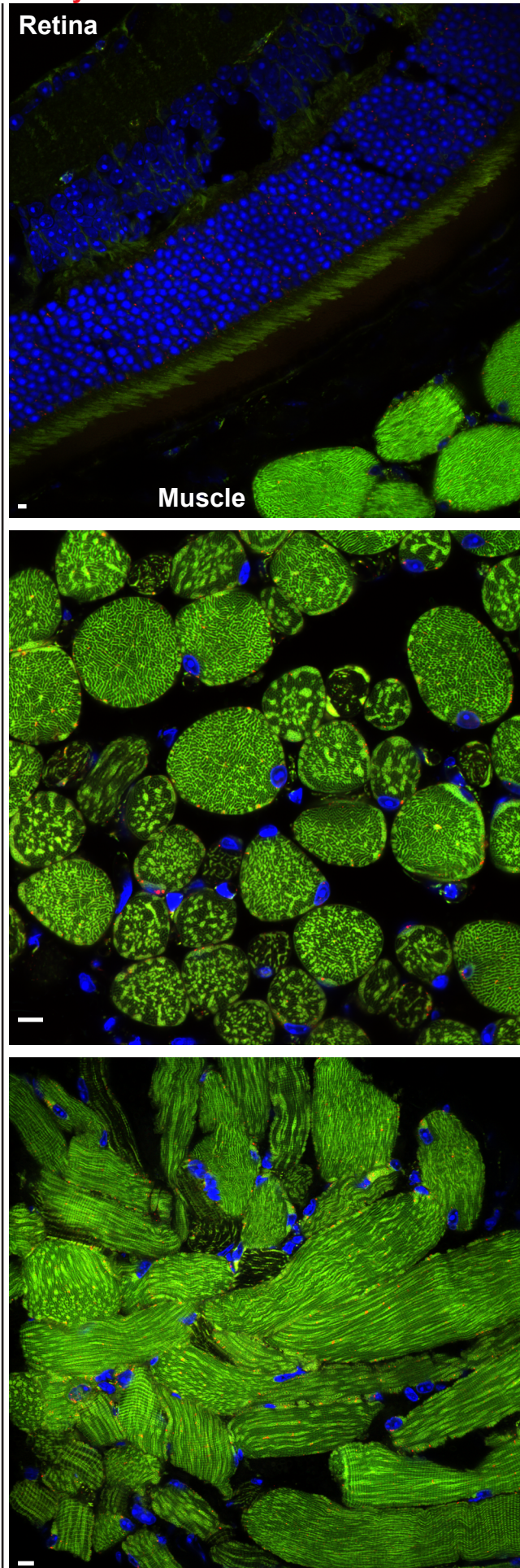


(E) PINK1 peptides identified from PINK1 IP by mass spectrometry

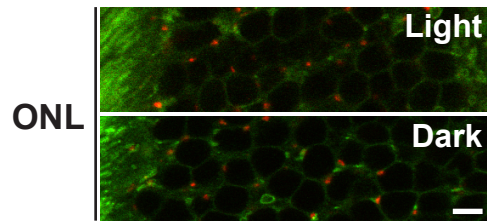
Cortex (CTX) WT - 21% Sequence Coverage					Cerebellum (CB) WT - 18% Sequence Coverage				
1	MAVRQALGRG	LQLGRALLLR	FAPKPGPLFG	WGKPGPAAAW GRGERPGQVV	1	MAVRQALGRG	LQLGRALLLR	FAPKPGPLFG	WGKPGPAAAW GRGERPGQVV
51	SPGAQPRPVG	LPLPDRYRFF	RQSVAGLAAR	IQRQFMVRAR GGAGPCGRAV	51	SPGAQPRPVG	LPLPDRYRFF	RQSVAGLAAR	IQRQFMVRAR GGAGPCGRAV
101	FLAFGLGLGL	IEEKQAEGRR	AASACQEIQA	IFTQKTKRVS DPLDTRCWQG	101	FLAFGLGLGL	IEEKQAEGRR	AASACQEIQA	IFTQKTKRVS DPLDTRCWQG
151	FRLEDYLIQ	AIGKGCNAAV	YEATMPTLPQ	HLEKAKHLGL IGKGPDVVLK	151	FRLEDYLIQ	AIGKGCNAAV	YEATMPTLPQ	HLEKAKHLGL IGKGPDVVLK
201	GADGEQAPGT	PTFPFAIKMM	WNISAGSSSE	AILSKMSQEL VPASRVALAG	201	GADGEQAPGT	PTFPFAIKMM	WNISAGSSSE	AILSKMSQEL VPASRVALAG
251	EYGAVTYRRS	RDGPKQLAPH	PNIIIRVFRF	TSSVPLPGA LADYDMLPP	251	EYGAVTYRRS	RDGPKQLAPH	PNIIIRVFRF	TSSVPLPGA LADYDMLPP
301	HYYPEGLGHG	RTLFLVMKNY	PCTLRQYLEE	QTPSSRLATM MTLQLLEGVD	301	HYYPEGLGHG	RTLFLVMKNY	PCTLRQYLEE	QTPSSRLATM MTLQLLEGVD
351	HLVQQGIAHR	DLKSDNILVE	WSDGCPWLW	ISDFGCCLAD QHVGLRLPFN	351	HLVQQGIAHR	DLKSDNILVE	WSDGCPWLW	ISDFGCCLAD QHVGLRLPFN
401	SSSVERGGNG	SLMAPEVSTA	HSGPSAVIDY	SKADTWAVGA IAYEIFGLAN	401	SSSVERGGNG	SLMAPEVSTA	HSGPSAVIDY	SKADTWAVGA IAYEIFGLAN
451	PFYQGQSAHL	ESRSYQEAQL	PEMPESVPPE	ARRLVRSLLQ REASKRPSAR	451	PFYQGQSAHL	ESRSYQEAQL	PEMPESVPPE	ARRLVRSLLQ REASKRPSAR
501	LAANVLHLSL	WGEHLLALKN	LKLDKMIAWL	LQQAATLLA DRLREKSCVE	501	LAANVLHLSL	WGEHLLALKN	LKLDKMIAWL	LQQAATLLA DRLREKSCVE
551	TKLQMLFLAN	LECEALCQAA	LLSSWRAAP		551	TKLQMLFLAN	LECEALCQAA	LLSSWRAAP	



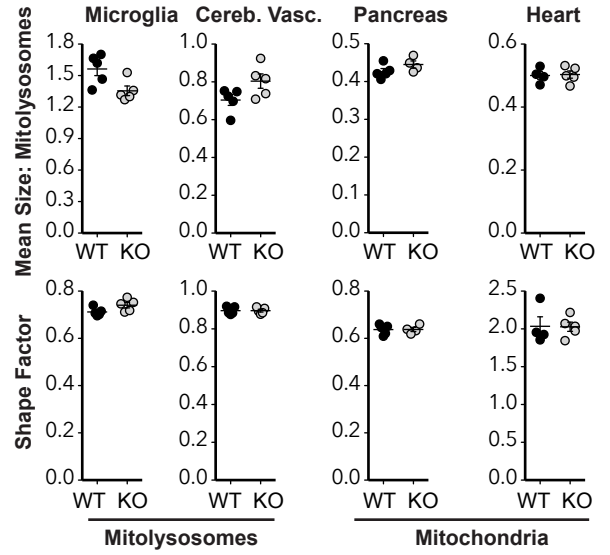
(A) **Mitlysosomes** **Mitochondria** **Nuclei**



(B)

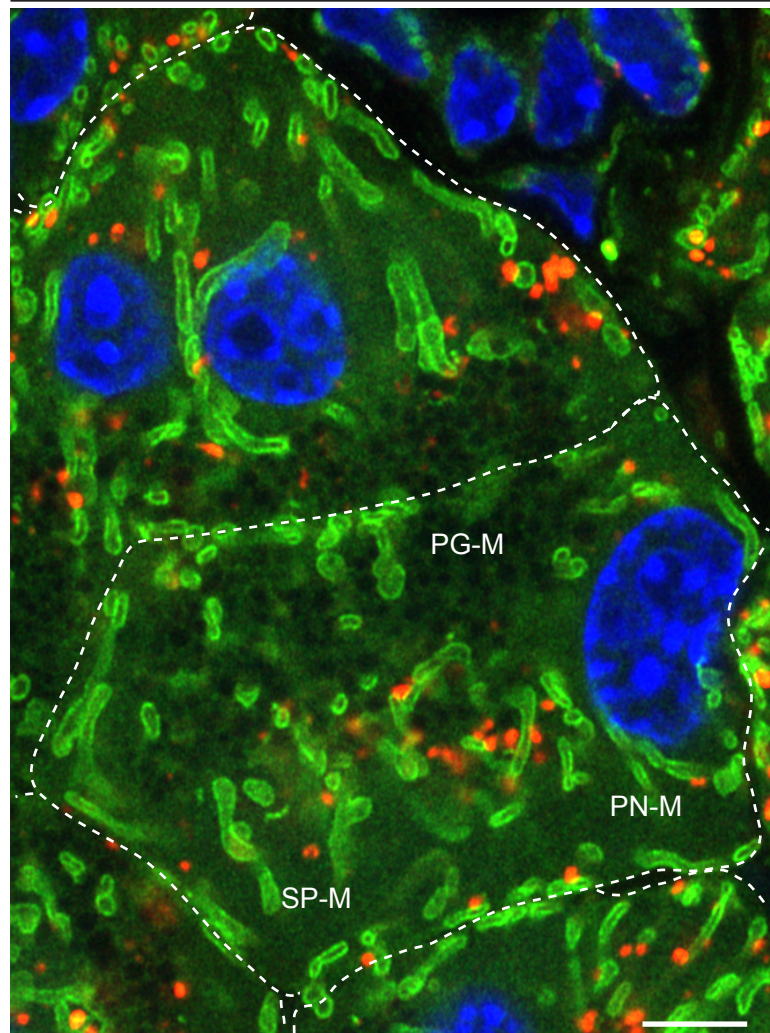


(C)

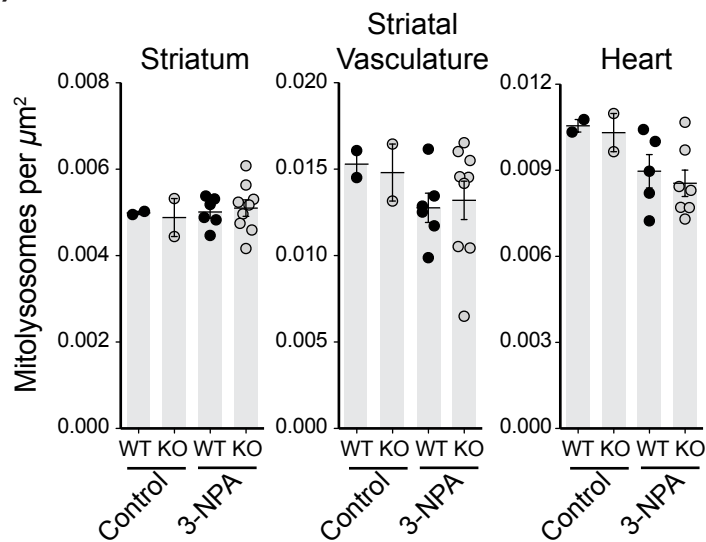


(D)

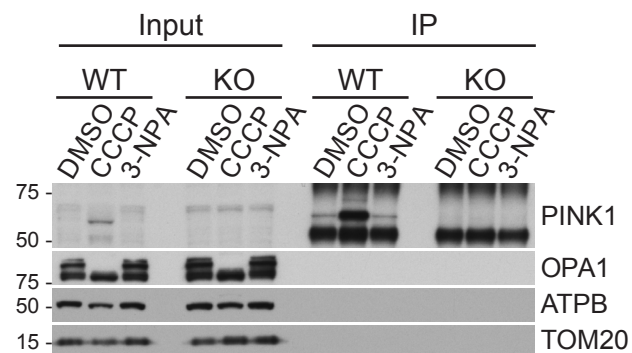
Pancreas



(A)

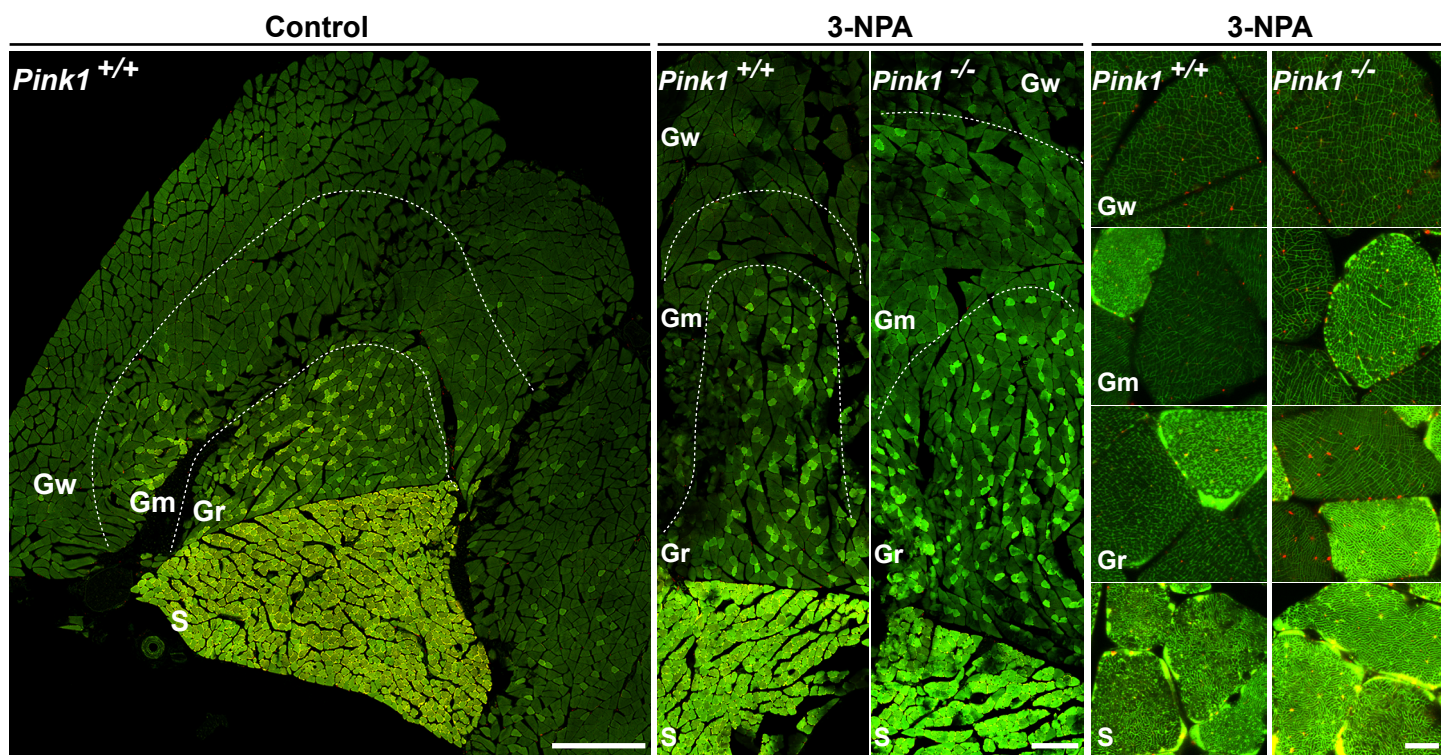


(B)

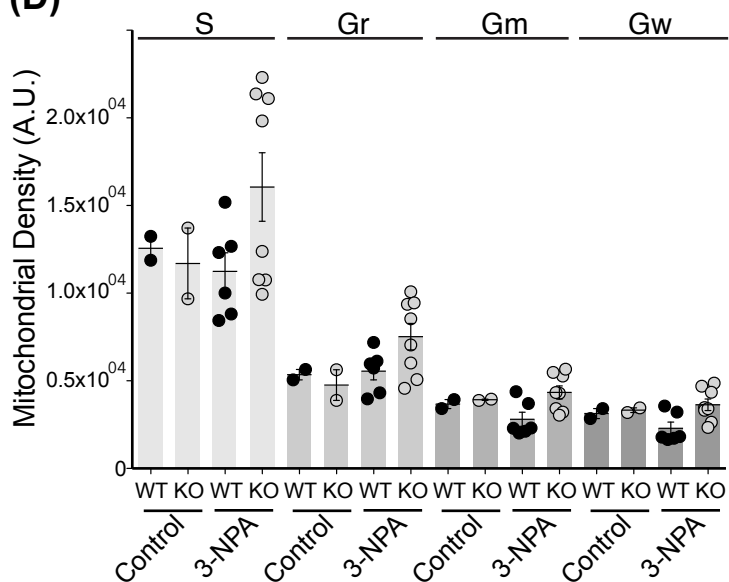


(C)

Hindlimb skeletal muscle



(D)



(E)

