**Lipid extraction.**  Muscle homogenates/mitochondrial isolates were extracted using a modified single-phase chloroform/methanol extraction as described previously [Weir et al. 2016]. In brief, 20 volumes of chloroform:methanol (2:1) was added to the sample along with a series of internal standards. Samples were vortexed and spun on a rotoary mixer for 10 minutes. After sonication on a sonicator bath for 30 minutes, samples were rested for a further 20 minutes prior to centrifugation at 13,000 x g for 10 minutes. Supernatants were transferred into a 96 well plated, dried down and reconstituted in 50L water saturated butanol and sonicated for 10 minutes. After the addition of 50l of methanol with 10mM ammonium formate, the samples were spun down again at 4000RPM on a plate centrifuge (Heraeus multifuge 1S-R, ThermoFisher) and transferred into glass vials with inserts for mass spectrometry analysis.

**Targeted lipidomics analysis.** Liquid chromatography tandem mass spectrometry (LC-MS/MS) was performed according to previously published methods, with slight modification for tissue samples [Huynh et al. 2019]. Sample extracts were analysed using either (i) a 4000 QTRAP mass spectrometer (Sciex) for cardiolipins as described preciously [Tan et al. 2020] or (ii) an Agilent 6490 QQQ mass spectrometer all other lipid species. Lipids run on the Agilent 6490 were measured using scheduled multiple reaction monitoring with the following conditions: Isolation widths for Q1 and Q3 were set to “unit” resolution (0.7 amu), gas temperature, 150°C, nebulizer 20psi, sheath gas temperature 200°C, gas flow rate 17L/min, capillary voltage 3500V and sheath gas flow 10L/min. The list of MRMs used and chromatographic conditions were extensively described previously [Huynh et al. 2019]

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