### Supplemental Methods

### 2.2.4 Sugar quantification

Pooled samples were homogenized in 100 µL ice-cold acetate buffer (pH 5.6). Immediately following each homogenization, samples were incubated at 95º C for 20 minutes to inactivate enzymatic activity and prevent degradation. Samples were then centrifuged at 12,000 rpm for 2 minutes and the resulting supernatant was collected for glucose, trehalose, and glycogen analysis. Trehalose and glycogen samples were treated with trehalase (0.25 units/mL) and amyloglucosidase (5 units/mL), and incubated for 12 hours at 37ºC and 60ºC, respectively. These enzymes hydrolyze each sugar into glucose. Resulting glucose levels for three sugars were analyzed using Glucose Assay Reagent (Sigma GAHK20). For each sugar, 1 µL of sample was incubated with 99 µL Glucose Assay Reagent in 96-well UV plates (Corning 3635) for 20 minutes, and absorbance was measured at 340 nm using a Multiskan GO Microplate Spectrophotometer. To calculate trehalose and glycogen concentrations, absorbance values for those two sugars were first doubled in order to correct for enzyme dilution. Then, the amount of free glucose in the corresponding glucose sugar sample was subtracted from the doubled amount of trehalose or glycogen. Each sugar’s absorbance was then compared to a sugar-specific standard curve. Samples were normalized to weight using a regression-based approach.

### Lipid Analysis

#### Extraction

Pooled samples were homogenized in 200 µL ice-cold methanol containing internal standards using a Physcotron Handy Micro Homogenizer. Internal standards contained triheptadecanoin, a heavy triglyceride compound not found in nature (Larodin Fine Chemcials). Following homogenization, 400 µL methyl-tert-butyl ether (MTBE) was added to each sample and samples were shaken for seven minutes at 1100 rpm. Next, 100 µL HPLC-grade H2O was added and samples were shaken at 4º C for 30 seconds at 1000 rpm. Samples were then centrifuged at 2000 rpm for five minutes. Finally, 200 µL of the top layer (MTBE containing lipids) was transferred to a new glass insert, speed vacuumed to dryness, and stored at -20º C until analysis.

#### Analysis and quantification of Lipids using UHPLC-MS

For analysis, dried samples were resuspended in 150 µl of toluene, sonicated 10 minutes, take 10 µL into 90 µL methanol to make a ten times dilution and again sonicated 10 min. This resuspension procedure was automated using a PAL Combi-xt autosampler. The autosampler syringe was washed with 400 µl toluene and 200 µl methanol between samples. For each sample, 3 µl of ten times dilution was injected in a Waters ACQUITY UPLC Class-I in tandem with a Waters SYNAPT G2-S High Definition Mass Spectrometer equipped with Ion Mobility. Lipids were separated in a ACQUITY UPLC CSH C18 1.7 µm 2.1  x 100 mm  analytical column at 400 µL/min, 60º C. A separation gradient, using two solvents (A and B), starts with 85% solvent A and 15% solvent B, then solvent ratio is shifted (in terms of solvent B) from 15% to 60% in 3 minute, 60% to 72% in 0.5 minute, 72% to 80% in 4.5 minutes, 80% to 100% in 1 minute, hold at 99% for 2 minutes and finally column equilibration for 1 minutes at 15%; a post-separation washing gradient of 99% for 2 minutes and equilibration at 15% for 2 minutes, for a total of 17 minutes. The solvent composition for this gradient was Solvent A 60:40 Acetonitrile:Distilled water (10 mM Ammonium Formate + 0.1% Formic Acid) and 90:10 2-Isopropanol:Acetonitrile (10 mM Ammonium Formate + 0.1% Formic Acid) for Solvent B. Autosampler solvents were 60:40 Acetonitrile:Distilled water for aspirating and loading sample into sample loop and 90:10 2-Isopropanol:Acetonitrile (0.1% Formic Acid) for washing needle to avoid carryover between samples. Mass spectrometer used a LockMass solution of Leucine/Enkephalin 2 pmol/ml in 50% Acetonitrile (0.1% Formic Acid), infused every 30 seconds, for automatic mass correction during acquisition time.

Mass spectrometer settings were as follow, 2.0 kV spray voltage, cone voltage 30 V, desolvation temperature 400ºC, desolvation gas 900 L/Hr, source temperature 120 ºC, acquisition range from 50 to 1700 m/z, scan rate 10 hz, acquisition mode MSe (Independent Data Acquisition), high resolution 35,000 FWHM, continuum mode, quad profile automatic, collision energy was 6 V for low energy (Collision Trap), and ramped from 20 to 40 V in high energy mode. Mass spectrometer was calibrated with Sodium Formate 500 mM in water.

Acquisition of mass spectrometric data was done using Waters MassLynx v4.1. Chromatographic data was processed using MzMine2 open-source software, for mass correction (using acquired lock mass data), alignment, normalization, deconvolution of high energy data (MSe), isotope grouping, peak picking and peaks identification based on high energy fragmentation, using Lipid Maps database (18Mar2014 version). Following peak identification, possible metabolic species were listed and individual compounds were manually assigned from this list based on isotope similarity, compound score (as provided by software), and expected retention times.

The total sum of all identified triglycerides were then divided into an internal standard, which was added to the sample prior to processing and provided relative lipid concentrations for each sample.