**Document S1 - GC analysis**

The gas chromatograph is equipped with a split/splitless inlet, fitted with a 4 mm id glass inlet liner with a deactivated glass wool plug. The inlet is set to 250 C and is operated in constant pressure mode. The carrier gas is hydrogen; nitrogen and air are needed as detector support gases.

An Agilent Ultra-2 column is used. The column is 25 meters long with a 0.2 mm inside diameter and a 0.33 um stationary phase film thickness. The stationary phase in this column is 5% phenyl, 95% methyl polysiloxane, also known as a DB-5 type column. To analyze the lipid extracts, a 2 ul aliquot is injected at a 100:1 split ratio, with the oven temperature at 170 degrees C. Post injection, the oven is programmed to increase at 5 degrees per minute up to 300 C and then hold for 12 minutes. When the system is initially set up, the parameters of column head pressure and oven offset must be adjusted to achieve accurate peak identification. A series of injections of the Midi standard are made and the results used to make adjustments according to instructions in the MIDI manual. Once calibrated in this way, the system may need minor adjustments on occasion but should generally achieve good results using these parameters.

The software schedules injection of the MIDI standard twice at the start of an analytical sequence, and then again after every 11 sample injections. The software monitors the results and may reinject the standard sooner if retention time drift is detected. If no internal standard was added to the samples, a solution of a FAME with a known concentration should also be analyzed and the data used to establish an external calibration of the samples. If the analytes in the samples are too dilute, the samples may be concentrated to a smaller volume and then reanalyzed. Alternatively, they may be reanalyzed using a lower split ratio but the standard must then be diluted in a way to match the increased amount of analyte introduced into the column.

The MIDI system produces a report for each sample containing a table with one line per realized peak. The software reports the peak retention time, peak area, peak identification, along with ECL or estimated chain length, a parameter used for peak identification—and response factor, a parameter used to normalize variations in detector response with respect to retention time. The ECL expresses where among a series of straight chain FAMEs each unknown FAME elutes. So for example, if the retention time of an unknown elutes exactly halfway between those of 12:0 and 13:0 carbon chain, the ECL is reported as 12:5 carbon chain. The software compares the ECL of each peak to those of FAMEs in a database, and where matches occur assigns the corresponding name to the unknown. For cases where two FAMEs in the database have ECLs that are very close, the software reports both names, listing the closest one first.