

CLINICAL LIPIDOMICS AND METABOLISM UNIT (UCA-CCM)

**LIPID METABOLISM
RESEARCH**

Principal investigador: Oscar Pastor Rojo, PhD

V0.5 – 02/2023

VALIDATED METHODOLOGY

- ✓ Reverse phase LC-MS/MS (SCIEX)
- ✓ Targeted approach: more than 200 lipid species from 19 classes
- ✓ Modified Folch extraction for better reproducibility
- ✓ 3 levels of quality control samples
- ✓ Concentration quantitation combining internal standard and matrix calibration.

Abbreviation	Full Name	Lipid Class	Lipid Subclass
ACer	Acylceramide	Sphingolipids	Ceramides
PHCer	Phytoceramide	Sphingolipids	Ceramides
Cer	Ceramide	Sphingolipids	Ceramides
HexCer	Hexosylceramide (Gluco/Galacto)	Sphingolipids	Glycosphingolipids
SM	Sphingomyelin	Sphingolipids	Phosphosphingolipids
DHCer	Dihydroceramide	Sphingolipids	Ceramides
dhHexCer	Dihydrohexosylceramide	Sphingolipids	Glycosphingolipids
dhSM	Dihydrosphingomyelin	Sphingolipids	Phosphosphingolipids
LPC	Lysophosphatidylcholine	Glycerophospholipids	Lysophospholipids
LPE	Lysophosphatidylethanolamine	Glycerophospholipids	Lysophospholipids
PC	Phosphatidylcholine	Glycerophospholipids	Phospholipids
PC_O	Alkyl/Vinyl phosphatidylcholine	Glycerophospholipids	Plasmalogens
PE	Phosphatidylethanolamine	Glycerophospholipids	Phospholipids
PE_O	Alkyl/Vinyl phosphatidylethanolamine	Glycerophospholipids	Plasmalogens
PI	Phosphatidylinositol	Glycerophospholipids	Phospholipids
SE	Sterol ester	Sterol lipids	Sterol esters
FC	Free cholesterol	Sterol lipids	Free sterols
TAG	Triacylglycerol	Glycerolipids	Neutral glycerolipids
DAG	Diacylglycerol	Glycerolipids	Neutral glycerolipids

QC EVALUATION

QC EVALUATION

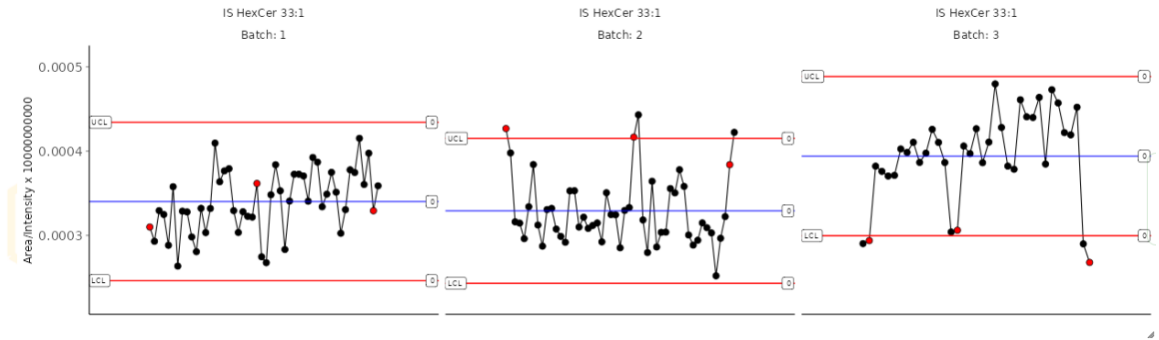
✓ Extraction evaluation:

✓ Internal standard variability



Internal Standard between batch stability

On this tab you can see IS average signal mean plot for each lipid class. The QC samples are marked in red.



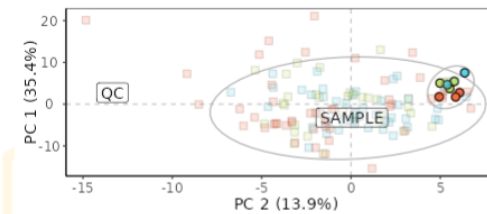
QualityControl sample global evaluation

On this tab you can see a global evaluation of the select QC sample group by species and class, between and within batches:

Internal Standard Calibration (IS-calibration)

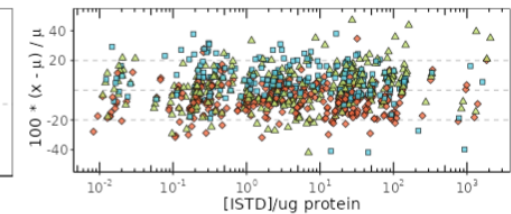
A PCA QC vs SAMPLES

1 2 3



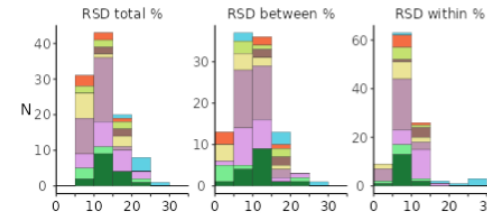
B Residual plot all species (CAL_PL_)

1 2 3

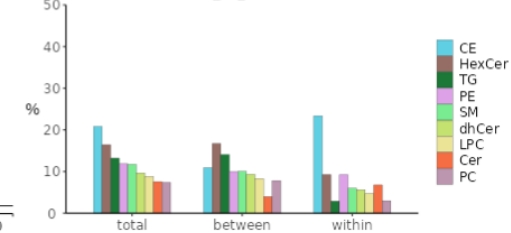


C Histogram species (CAL_PL_)

104 species in 9 classes



D RSD class sum (CAL_PL_)



✓ QC intra batch variability



QC EVALUATION

✓ Robustness evaluation:

✓ Long term quantitation accuracy

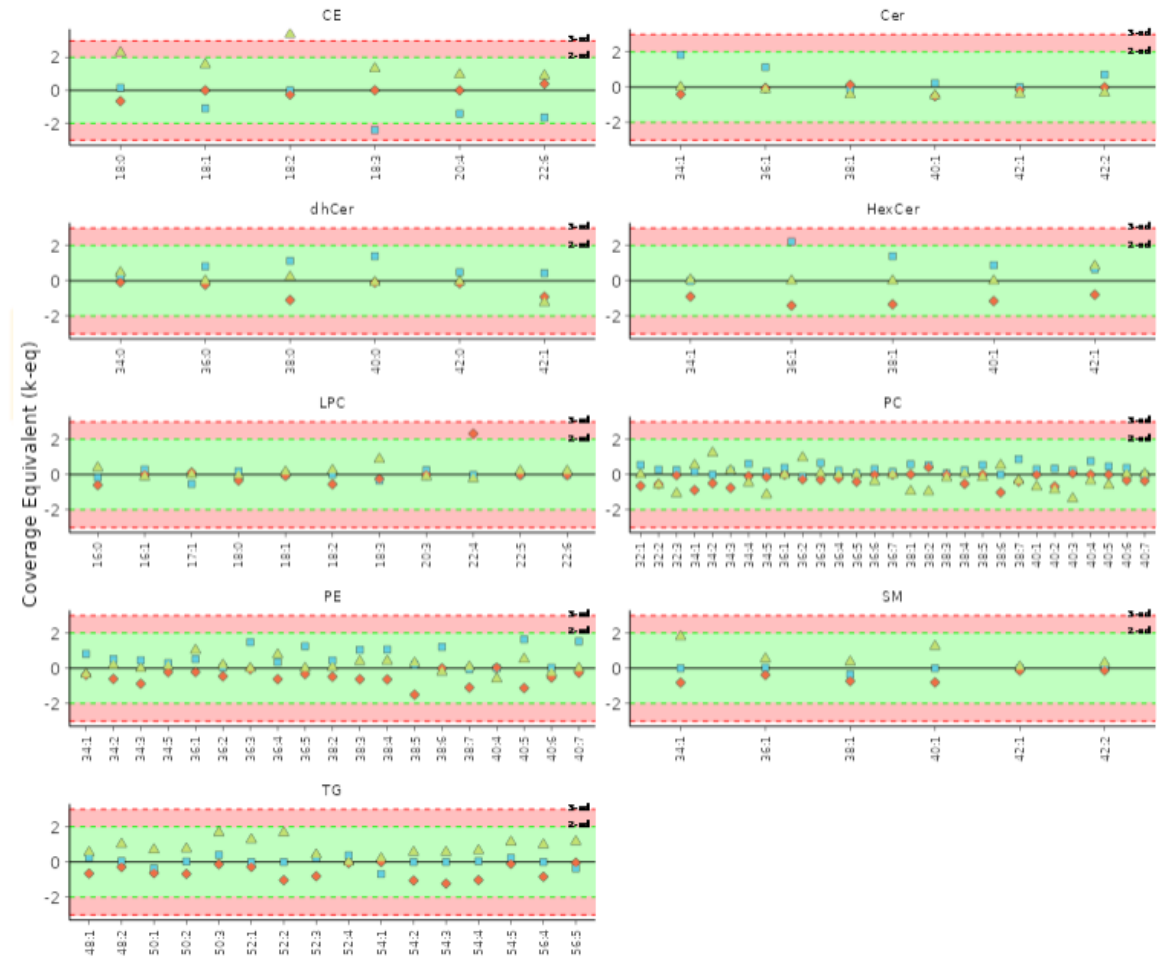


QualityControl sample between batch monitoring

On this tab you can see coverage equivalent of every species of QC sample.

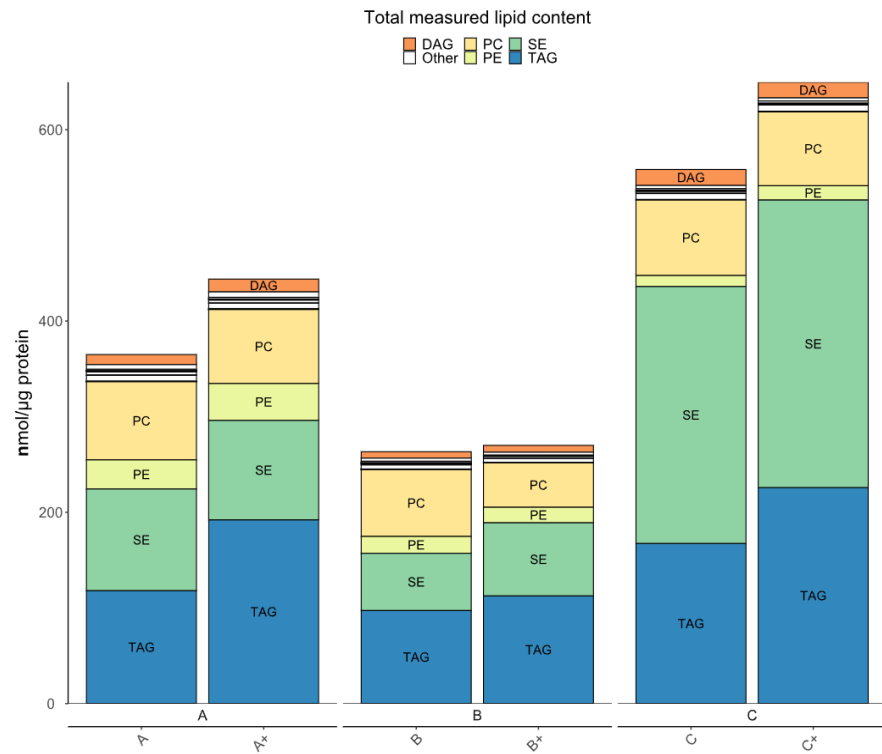
Between batch monitoring (QC_PL_)

1 2 3

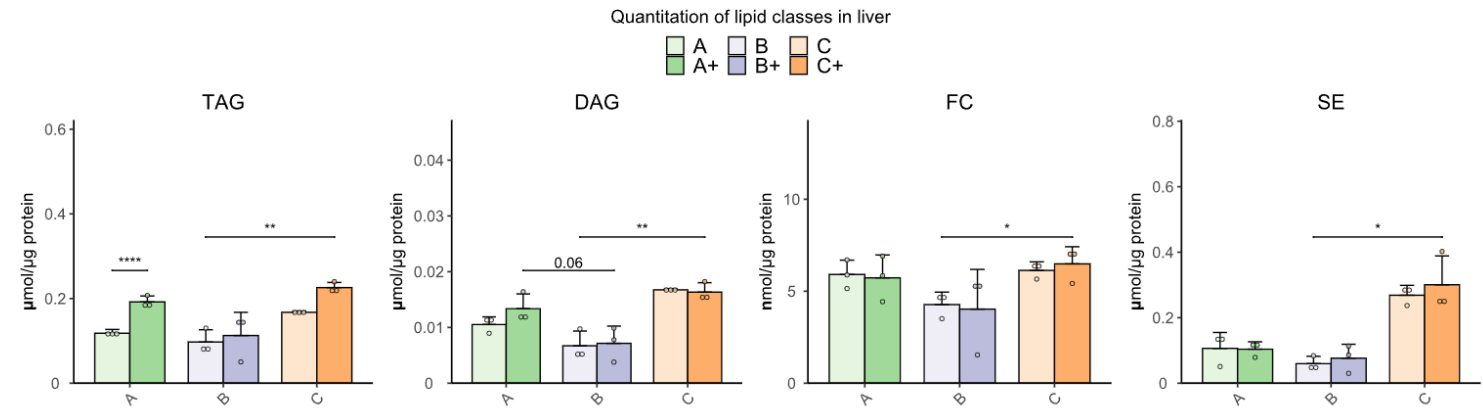


REPORT FORMAT

✓ Total lipid content

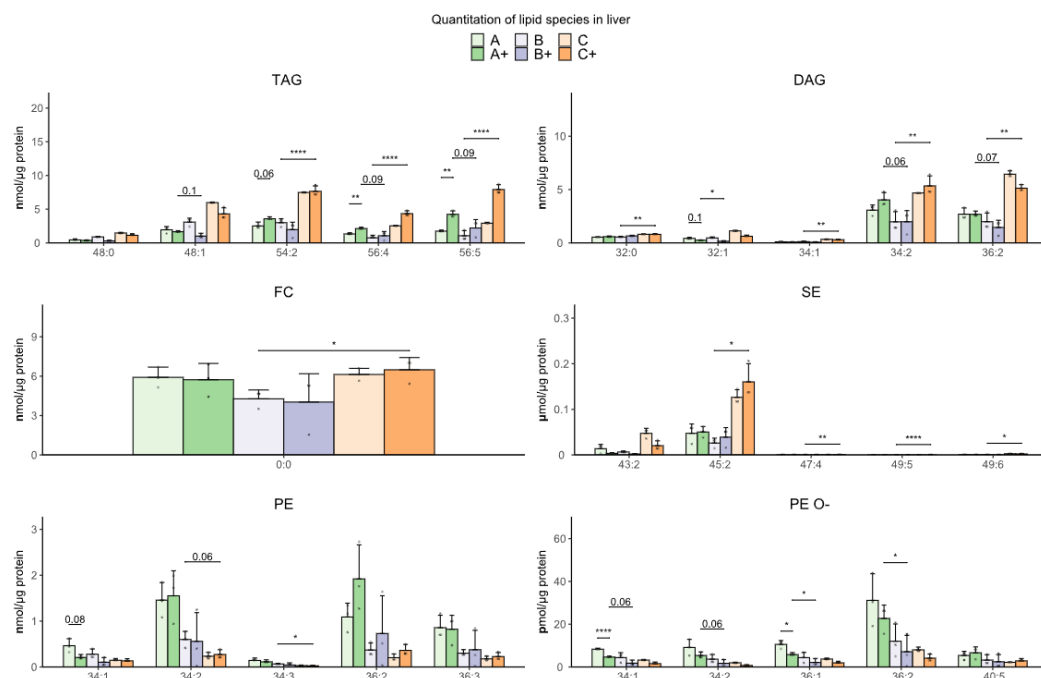


✓ Class sum barplot

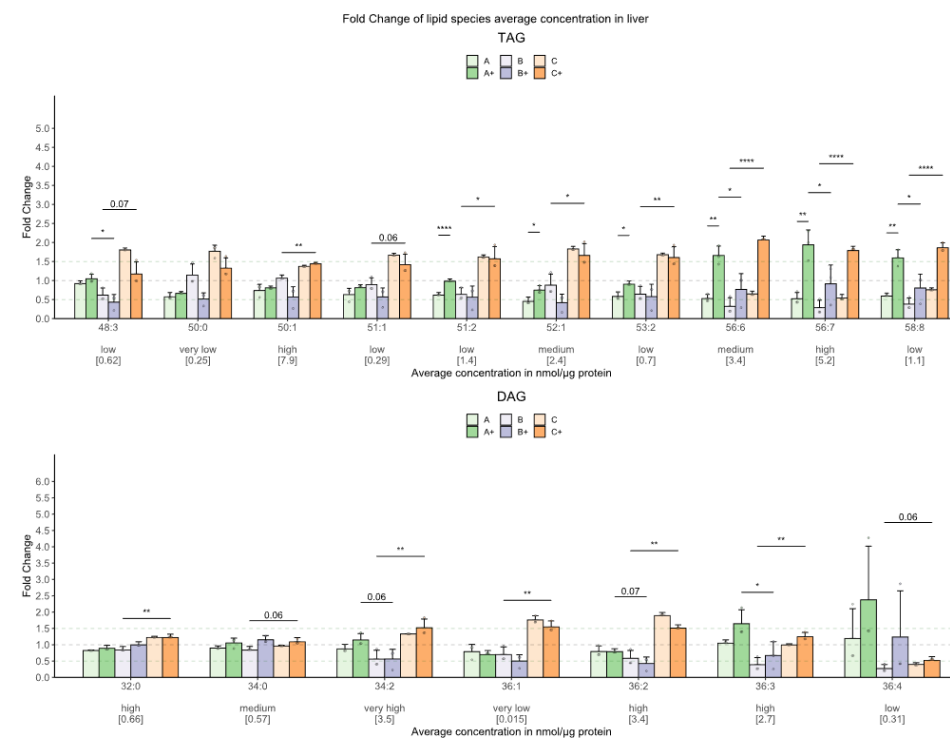


REPORT FORMAT

✓ Most abundant species barplot



✓ Most variable species barplot



- ✓ Report in Excel format with quantitation data and basic statistics like ANOVA

Sample.Name	GRUPO	ID	Batch.number	ACer 52:1	ACer 52:2	ACer 54:2	ACer 60:2	ACer 60:3	Cer 32:1	Cer 34:1	Cer 36:1
A_1	A	A_1	1	0.00016307	0.00019991	8.2013E-05	0.00180266	0.0019372	0.00037938	0.03117402	0.00319646
A_2	A	A_2	1	0.00020158	0.00031084	0.00014775	0.00316138	0.0031085	0.00064981	0.05350234	0.00440434
A_3	A	A_3	1	0.00016036	0.00025142	0.00012732	0.00263424	0.00281768	0.00051549	0.0387854	0.00392809
A+_1	A+	A+_1	1	0.00037494	0.0003616	0.00017607	0.00366583	0.0036946	0.00053642	0.0561035	0.00669985
A+_2	A+	A+_2	1	0.00052449	0.0003915	0.00026374	0.00364553	0.00281404	0.00058012	0.05473476	0.00989767
A+_3	A+	A+_3	1	0.00040225	0.00031536	0.00021986	0.00271558	0.00264128	0.00040502	0.03624037	0.00846845
B_4	B	B_4	1	0.00011404	0.00016507	0.00010329	0.00152275	0.00159181	0.00042472	0.02220737	0.00244705
B_5	B	B_5	1	0.00048811	0.00037204	0.00021925	0.00224716	0.00292582	0.00067522	0.04252782	0.00773245
B_6	B	B_6	1	0.0001228	0.00014918	8.9215E-05	0.00143785	0.00156493	0.00031242	0.01644429	0.00208587
B+_1	B+	B+_1	1	0.0001641	0.00012267	6.7286E-05	0.00061915	0.00087533	0.00011951	0.00747638	0.00217802
B+_2	B+	B+_2	1	0.00029169	0.00027173	0.00014943	0.00226404	0.00270684	0.00034609	0.02081971	0.00536616
B+_3	B+	B+_3	1	0.00039475	0.00035448	0.00016784	0.00288894	0.00312693	0.00042206	0.04026197	0.00633812
C_7	C	C_7	1	0.00084823	0.0013544	0.0006334	0.00642536	0.00907621	0.00077867	0.03208803	0.0079718
C_8	C	C_8	1	0.00125571	0.00159601	0.00077704	0.00805499	0.00986397	0.00094341	0.04974311	0.00994151
C_9	C	C_9	1	0.00119996	0.00154768	0.00078864	0.00773286	0.00927252	0.00082468	0.03815688	0.00957301
C+_1	C+	C+_1	1	0.00170772	0.00178997	0.00079277	0.00852271	0.00985984	0.00100162	0.06568597	0.01655013
C+_2	C+	C+_2	1	0.00144748	0.00141866	0.00062508	0.00680298	0.00827886	0.00084462	0.06033298	0.01392937
C+_3	C+	C+_3	1	0.00128673	0.00132886	0.00056014	0.00630602	0.00772406	0.00073918	0.04167854	0.01189657

Lipid.Name	A	A+	B	B+	C	C+	p.signif	A_vs_A+	A_vs_B	A_vs_B+	A_vs_C	A_vs_C+
ACer 52:1	0.00018 ± 0.0	0.00043 ± 0.0	0.00024 ± 0.0	0.00028 ± 0.0	0.00011 ± 0.0	0.00148 ± 0.0	<0.0001	<0.05	ns	ns	<0.05	<0.05
ACer 52:2	0.00025 ± 0.0	0.00036 ± 0.0	0.00023 ± 0.0	0.00025 ± 0.0	0.00015 ± 0.0	0.00151 ± 0.0	<0.0001	ns	ns	ns	<0.001	<0.05
ACer 54:2	0.00012 ± 0.0	0.00022 ± 0.0	0.00014 ± 0.0	0.00013 ± 0.0	0.00007 ± 0.0	0.00066 ± 0.0	<0.0001	<0.05	ns	ns	<0.01	<0.05
ACer 60:2	0.00253 ± 0.0	0.00334 ± 0.0	0.00174 ± 0.0	0.00192 ± 0.0	0.00074 ± 0.0	0.00721 ± 0.0	<0.0001	ns	ns	ns	<0.01	<0.05
ACer 60:3	0.00262 ± 0.0	0.00305 ± 0.0	0.00203 ± 0.0	0.00224 ± 0.0	0.00094 ± 0.0	0.00862 ± 0.0	<0.0001	ns	ns	ns	<0.001	<0.05
Cer 32:1	0.00051 ± 0.0	0.00051 ± 0.0	0.00047 ± 0.0	0.00003 ± 0.0	0.00085 ± 0.0	0.00086 ± 0.0	<0.01	ns	ns	ns	<0.05	<0.05
Cer 34:1	0.04115 ± 0.0	0.04903 ± 0.0	0.02706 ± 0.0	0.02285 ± 0.0	0.04 ± 0.0	0.0559 ± 0.0	ns	ns	ns	ns	ns	ns
Cer 36:1	0.00384 ± 0.0	0.00836 ± 0.0	0.00409 ± 0.0	0.00463 ± 0.0	0.00916 ± 0.0	0.01413 ± 0.0	<0.001	<0.05	ns	ns	<0.01	<0.05
Cer 38:1	0.01731 ± 0.0	0.03085 ± 0.0	0.01415 ± 0.0	0.01868 ± 0.0	0.0212 ± 0.0	0.02223 ± 0.0	ns	<0.05	ns	ns	ns	ns
Cer 40:1	0.18002 ± 0.0	0.24983 ± 0.0	0.11712 ± 0.0	0.14804 ± 0.0	0.09426 ± 0.0	0.10252 ± 0.0	<0.05	ns	<0.05	ns	<0.01	<0.05
Cer 41:1	0.0562 ± 0.01	0.05309 ± 0.0	0.03111 ± 0.0	0.03533 ± 0.0	0.04253 ± 0.0	0.05301 ± 0.0	ns	ns	ns	ns	ns	ns
Cer 42:1	0.16117 ± 0.0	0.11147 ± 0.0	0.0862 ± 0.0	0.07949 ± 0.0	0.08377 ± 0.0	0.10092 ± 0.0	<0.05	ns	ns	ns	ns	ns
Cer 42:2	0.19979 ± 0.0	0.1635 ± 0.02	0.12659 ± 0.0	0.10785 ± 0.0	0.18347 ± 0.0	0.22649 ± 0.0	<0.05	ns	ns	ns	ns	ns
Cer 44:1	0.0008 ± 0.0	0.00075 ± 0.0	0.00045 ± 0.0	0.00042 ± 0.0	0.00057 ± 0.0	0.00091 ± 0.0	ns	ns	ns	ns	ns	ns
DAG 32:0	0.54246 ± 0.0	0.58649 ± 0.0	0.5509 ± 0.0	0.65406 ± 0.0	0.80407 ± 0.0	0.80328 ± 0.0	<0.0001	ns	ns	ns	<0.001	<0.05
DAG 32:1	0.42558 ± 0.0	0.25485 ± 0.0	0.46511 ± 0.0	0.15542 ± 0.0	0.12434 ± 0.0	0.62314 ± 0.0	<0.0001	ns	ns	<0.05	<0.01	ns
DAG 34:0	0.50941 ± 0.0	0.59905 ± 0.0	0.47488 ± 0.0	0.65413 ± 0.0	0.54618 ± 0.0	0.62044 ± 0.0	<0.05	ns	ns	ns	ns	ns

GRUPO	Lipid.Name	N	nmol/ug pro	sd	median	suma	cv	se	ci
A	ACer 52:1	3	0.000175	2.3056E-05	0.00016307	0.00052501	13.1745699	1.3311E-05	5.7274E-05
A	ACer 52:2	3	0.00025406	5.5514E-05	0.00025142	0.00076218	21.8507264	3.2051E-05	0.0001379
A	ACer 54:2	3	0.00011903	3.3642E-05	0.00012732	0.00035708	28.2648419	1.9423E-05	8.3573E-05
A	ACer 60:2	3	0.00253276	0.00068502	0.00263424	0.00759829	27.0464774	0.0003955	0.00170169
A	ACer 60:3	3	0.00262113	0.00060989	0.00281768	0.00786338	23.268146	0.00035212	0.00151505
A	Cer 32:1	3	0.00051489	0.00013522	0.00051549	0.00154468	26.2608329	7.8066E-05	0.00033589
A	Cer 34:1	3	0.04115392	0.01135103	0.0387854	0.12346176	27.5818912	0.00655352	0.02819752
A	Cer 36:1	3	0.00384296	0.00060842	0.00392809	0.01152888	15.8321672	0.00035127	0.00151141
A	Cer 38:1	3	0.01730539	0.0034	0.01715119	0.05191618	19.647059	0.00196299	0.00844607
A	Cer 40:1	3	0.18002279	0.01825452	0.17613233	0.54006837	10.1401179	0.01053925	0.04534675
A	Cer 41:1	3	0.05620125	0.01828661	0.06187943	0.16860375	32.537737	0.01055778	0.04542647
A	Cer 42:1	3	0.16116646	0.03940642	0.17079525	0.48349938	24.4507573	0.02275131	0.09789097
A	Cer 42:2	3	0.19978743	0.05125956	0.21049235	0.59936228	25.6570514	0.02959472	0.12733581
A	Cer 44:1	3	0.00079765	0.00031086	0.00066035	0.00239294	38.9724785	0.00017948	0.00077223
A	DAG 32:0	3	0.54246212	0.01032477	0.54536727	1.62738637	1.90331718	0.00596101	0.02564816
A	DAG 32:1	3	0.42557951	0.10099626	0.43723841	1.27673852	23.7314676	0.05831022	0.25088862
A	DAG 34:0	3	0.50941449	0.03769659	0.52126027	1.52824348	7.39998337	0.02176414	0.09364352
A	DAG 34:1	3	0.10031727	0.02823317	0.1113432	0.3009518	28.1438837	0.01630043	0.07013509
A	DAG 34:2	3	0.06940736	0.0486431	0.21576112	0.920822209	15.8477174	0.28084107	1.2083616
A	DAG 36:1	3	0.01162246	0.00326557	0.01281972	0.03486737	28.097028	0.00188537	0.00811211
A	DAG 36:2	3	0.269173776	0.58850726	2.59348551	8.07521329	21.8634692	0.33977482	1.46193307
A	DAG 36:3	3	0.281361065	0.26779957	2.74173343	8.44083194	9.51800384	0.15461415	0.66525101
A	DAG 36:4	3	0.36639411	0.27977618	0.21569763	1.09918234	76.3593541	0.16152885	0.69500255
A	DHCer 34:0	3	0.00152183	0.00044416	0.00142566	0.00456548	29.185691	0.00025643	0.00110334
A	DHCer 36:0	3	0.00055977	0.00018099	0.00052591	0.0016793	32.3336789	0.0001045	0.00044961

Lipid.Name	A	A+	B	B+	C	C+	p.signif	A_vs_A+	A_vs_B	A_vs_B+	A_vs_C	A_vs_C+
DAG 32:1	0.42558 ± 0.0	0.25485 ± 0.0	0.46511 ± 0.0	0.15542 ± 0.0	0.12434 ± 0.0	0.62314 ± 0.0	<0.0001	ns	ns	<0.05	<0.01	ns
DAG 34:0	0.50941 ± 0.0	0.59905 ± 0.0	0.47488 ± 0.0	0.65413 ± 0.0	0.54618 ± 0.0	0.62044 ± 0.0	<0.05	ns	ns	ns	ns	ns

REPORT FORMAT

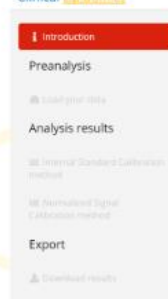
- ✓ Results are compatible with our own QC Tool online tool for lipidomic data mining. Recommended tools can be found here: [Lipidomics tools](#)

Bioinformatics tools for lipidomics data analysis



QC tool

Tool for lipidomic quantification and quality control



Tool for lipidomic quantification and quality control

Lipid nomenclature and others app usage recommendation

To use this tool you will need 5 files (all files have to be in csv format):

1) **Data file** may be in a long format (columns: lipid names, sample names and areas/intensities) or in a wide format with columns for lipid names and rows as samples. Lipid names must follow standardized nomenclature, TG 52:2 or TG 16:0, 18:1, 18:1, always with a separation after the class name. In the case of sample names, it should be named as group name followed by an unique sample number at the end, Tamoxifen_SuM_1 or Tamoxifen SuM 1, using under lines or whitespaces.

Remember! All files must have the same lipid and sample names!

2) **Samples file** must have the following columns: sample names, quantities of the sample and batch of analysis (only if you have different batches in your analysis).

3) **Internal standard file** must have the following columns: lipid name, quantity and number of carbons (if you want to apply type 1 isotopic correction).

4) Optional: **calibrator sample values file** must have the following columns: lipid name and consensus quantity. Calibrator sample must be present in every batch.

5) Optional: **quality control sample values file** must have the following columns: lipid name, consensus quantity and Standard Deviation. After every analysis, you may download the QC history file to compare with in future experiments. QC sample must be present in every batch.

We recommend you to try demonstration mode first in order to see how the app works. Contact us if you have any question.

☐ Demonstration mode

Start

Contact us

Basic batch structure (n samples)

LTR_1 QC_1	Calibrator replicate 1 QC replicate 1
Samples 1,2,3,4...	First half of batch samples
LTR_2 QC_2	Calibrator replicate 2 QC replicate 2
Samples 5,6,7,8	Second half of batch samples
LTR_3 QC_3	Calibrator replicate 3 QC replicate 3

*OUR NEXT STEPS IN QUALITY
IMPROVEMENT*

Interlaboratory Trial on Human Plasma Lipidome – International Lipidomic Society

