

## Supplementary Tables

**Table S1: Non-linear gradient settings for the separation of central carbon metabolites by reversed-phase chromatography.**

<i>Time [min]</i>	<i>Solvent B [%]</i>	<i>Flow rate [mL/min]</i>
0	0	0.4
5.0	0	0.4
9.0	2	0.4
9.5	6	0.4
11.5	6	0.4
12.0	11	0.4
13.5	11	0.4
15.5	28	0.4
16.5	53	0.15
22.5	53	0.15
23.0	0	0.15
27.0	0	0.4
33.0	0	0.4

**Table S2: LOD and LOQ values for the quantification of DINCH and its metabolites.**

<i>Analyte</i>	<i>LOD supernatant [nM]</i>	<i>LOQ supernatant [nM]</i>	<i>LOD intracellular [nmol/cellx10<sup>6</sup>]</i>	<i>LOQ intracellular [nmol/cellx10<sup>6</sup>]</i>
<i>DINCH</i>	6.9	8.5	0.003	0.007
<i>MINCH</i>	0.23	0.64	0.0002	0.0008
<i>cx-MINCH</i>	0.01	0.16	0.0002	0.001
<i>OH-MINCH</i>	0.03	0.10	0.00003	0.0003
<i>oxo-MINCH</i>	0.04	0.14	0.00004	0.0002

**Table S3: Sequences of forward and reverse primers of the genes used for qPCR.**

<i>Name</i>	<i>Forward</i>	<i>Reverse</i>
<i>hUBC</i>	GTGTCTAAGTTTCCCCTTTTAAGG	TTGGGAATGCAACAACCTTTAT TG
<i>hUCP1</i>	GTG TGC CCA ACT GTG CAA TG	CCA GGA TCC AAG TCG CAA GA
<i>hADIPOQ</i>	GGC CGT GAT GGC AGA	CCT TCA GCC CCG GGT
<i>hPPARG</i>	AGC CTC ATG AAG AGC CTT CCA	TCC GGA AGA AAC CCT TGC A
<i>hPGC1<math>\alpha</math></i>	CTG TGT CAC CAC CCA AAT CCT TAT	TGT GTC GAG AAA AGG ACC TTG A
<i>hFABP3</i>	GTCACTCGGTGTGGGTTTTG	CTCTTGCCCGTCCCATTCT
<i>hPRDM16</i>	CGA GGC CCC TGT CTA CAT TC	GCT CCC ATC CGA AGT CTG TC
<i>hFASN</i>	GTGGGTCTGCGCTTGGTCTTTCT	ACAGGCCTGGGGGTCTCTAC