



Supplementary Materials

Effect of Pd₂Spermine on Mice Brain-Liver Axis Metabolism Assessed by NMR Metabolomics

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Figure S1. Average 500 MHz ¹H NMR spectra of lipophilic extracts of (a) brain, and (b) liver from the control (untreated) group of a CDX mouse model of TNBC.

Figure S2. Average 500 MHz ¹H NMR spectra of aqueous extracts of liver, from a CDX mouse model of TNBC, exposed to (a) vehicle solution (control group), (b) cDDP (2 mg/kg/day), and (c) Pd₂Spm (5 mg/kg/day).

Figure S3. (a) Spectral expansions (δ 8.2–9.6 ppm) of ¹H NMR spectra of aqueous extracts of CDX mice brain of controls, cDDP- and Pd₂Spm-treated mice and (b) NAD⁺/NADH ratios for the same three animal groups.

Figure S4. Pairwise score scatter plots of PCA and PLS-DA models for ¹H NMR spectra of (a) aqueous and (b) lipophilic extracts of liver of CDX mice.

Table S1. Statistically significant ($|ES| > ES$ Error and p -value < 0.05) metabolite variations observed in the polar metabolomes of CDX mice brain and liver, compared to controls.

Table S2. Statistically significant ($|ES| > ES$ Error and p -value < 0.05) metabolite variations observed in the lipophilic metabolomes of CDX mice brain and liver, compared to controls.

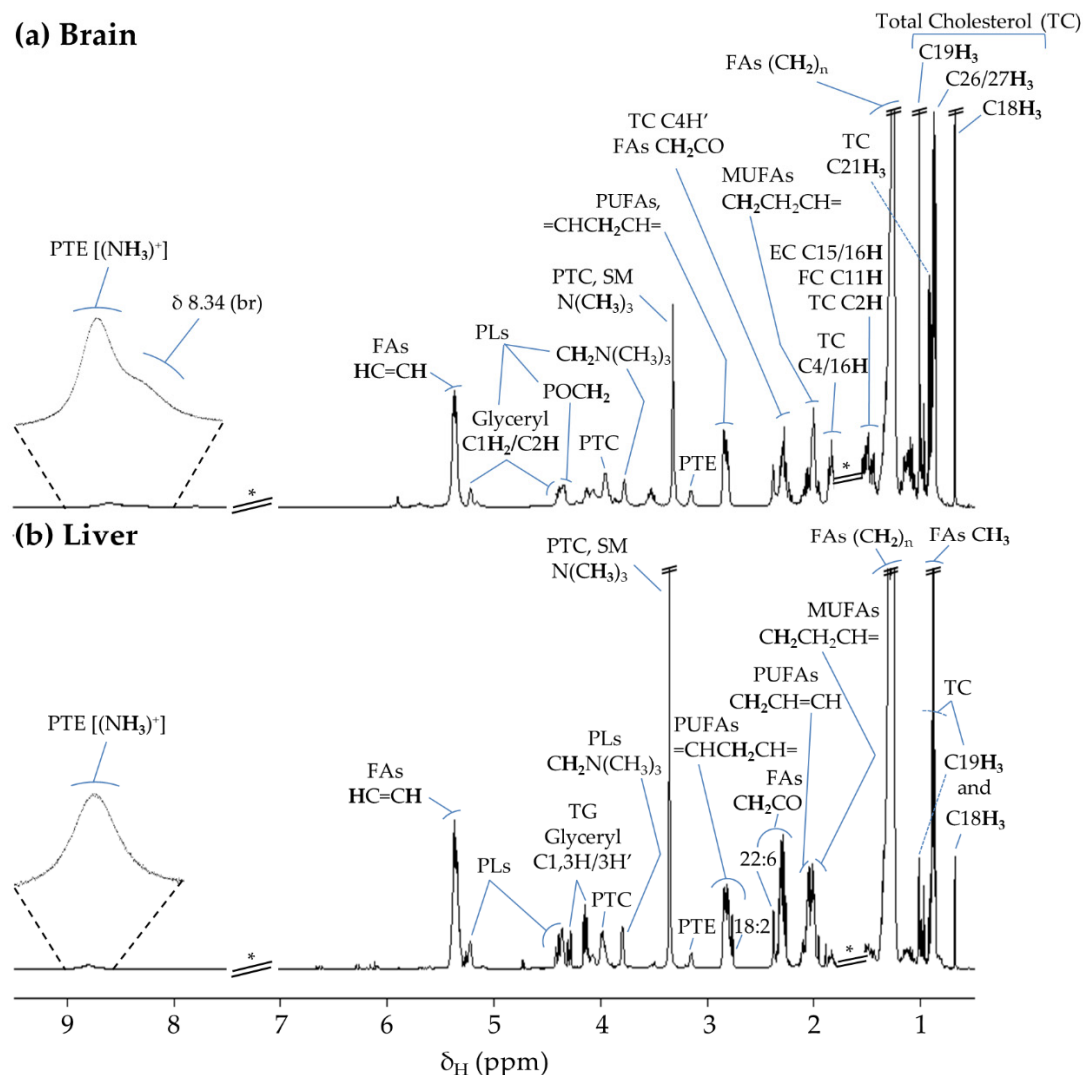


Figure S1. Average 500 MHz ¹H NMR spectra of lipophilic extracts of (a) brain, and (b) liver from the control (untreated) group of a CDX mouse model of TNBC. * Cut-off of residual water signal (δ 1.5–1.8 ppm) and CDCl₃ and corresponding satellites (δ 7.0–7.5 ppm), not considered for multivariate analysis. Abbreviations: EC, esterified cholesterol; FAs, fatty acids; FC, free cholesterol; MUFAs, monounsaturated fatty acids; PLs, phospholipids; PTC, phosphatidylcholine; PTE, phosphatidylethanolamine; PUFAs, polyunsaturated fatty acids; SM, sphingomyelin; TC, total cholesterol; TG, triacylglycerols; br, broad signal.

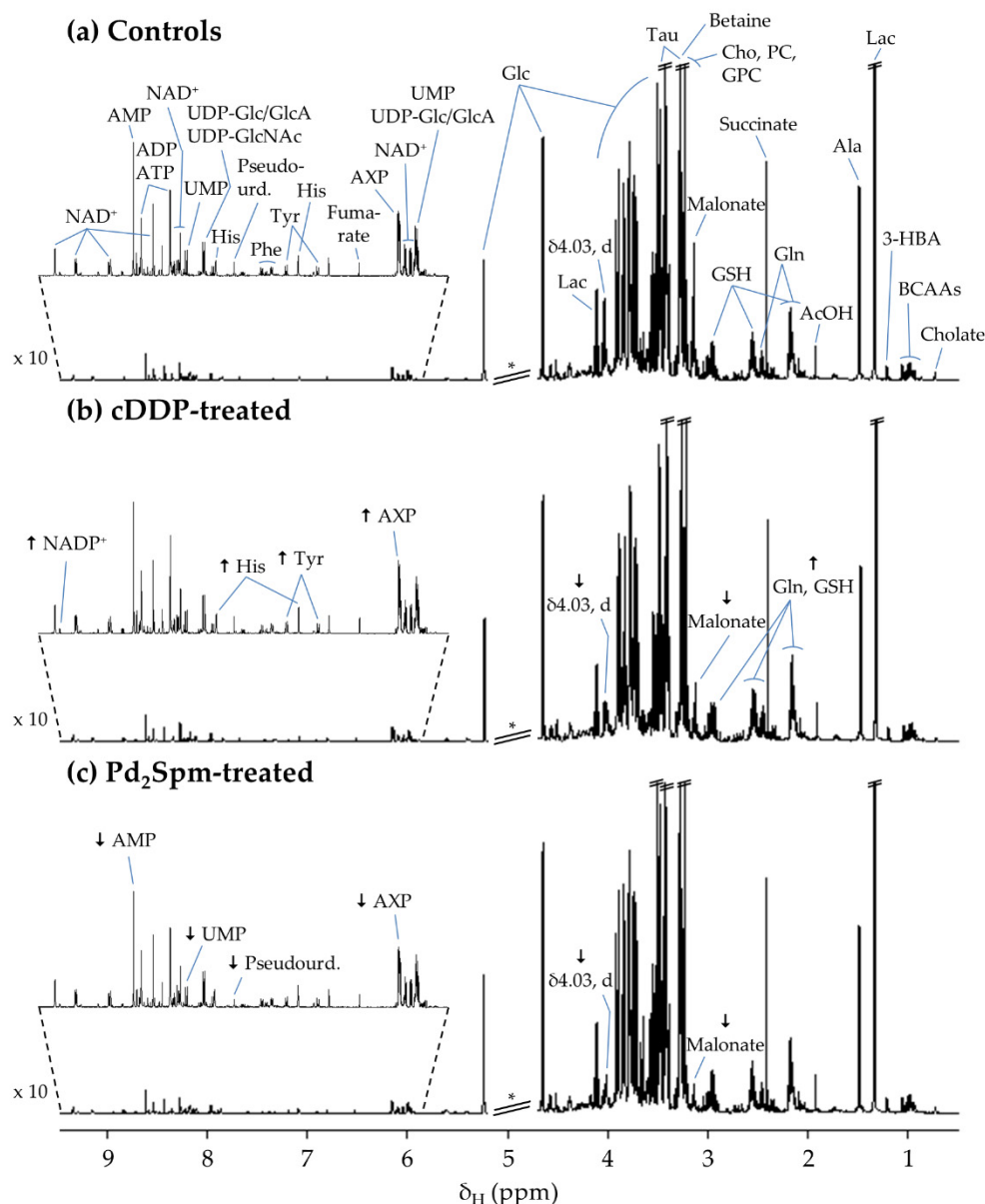


Figure S2. Average 500 MHz ¹H NMR spectra of aqueous extracts of liver, from a CDX mouse model of TNBC, exposed to (a) vehicle solution (control group), (b) cDDP (2 mg/kg/day), and (c) Pd₂Spm (5 mg/kg/day). * Cut-off of water suppression region (δ 4.6–5.1 ppm), not considered for multivariate analysis. The arrows in (b) and (c) identify visual metabolic variations found with qualitative inspection of spectra from each treated group compared to controls. Abbreviations: 3-letter code for amino acids; 3-HBA, 3-hydroxybutyrate; AcOH, acetate; ADP, adenosine diphosphate; AMP, adenosine monophosphate; ATP, adenosine triphosphate; AXP, adenosine nucleotides AMP, ADP and ATP; BCAAs, branched-chain amino acids (ile, leu and val); Cho, choline; Glc, glucose; GPC, glycerophosphocholine; GSH, glutathione (reduced); Lac, lactate; NAD⁺, nicotinamide adenine dinucleotide (oxidized); NADP⁺, nicotinamide adenine dinucleotide phosphate (oxidized); PC, phosphocholine; Pseudourid., pseudouridine (Ψ, tentative assignment); Tau, taurine; UDP-Glc/GlcA, uridine diphosphate glucose/glucuronate; UDP-GlcNAc, uridine diphosphate N-acetylglucosamine; UMP, uridine monophosphate; d, doublet.

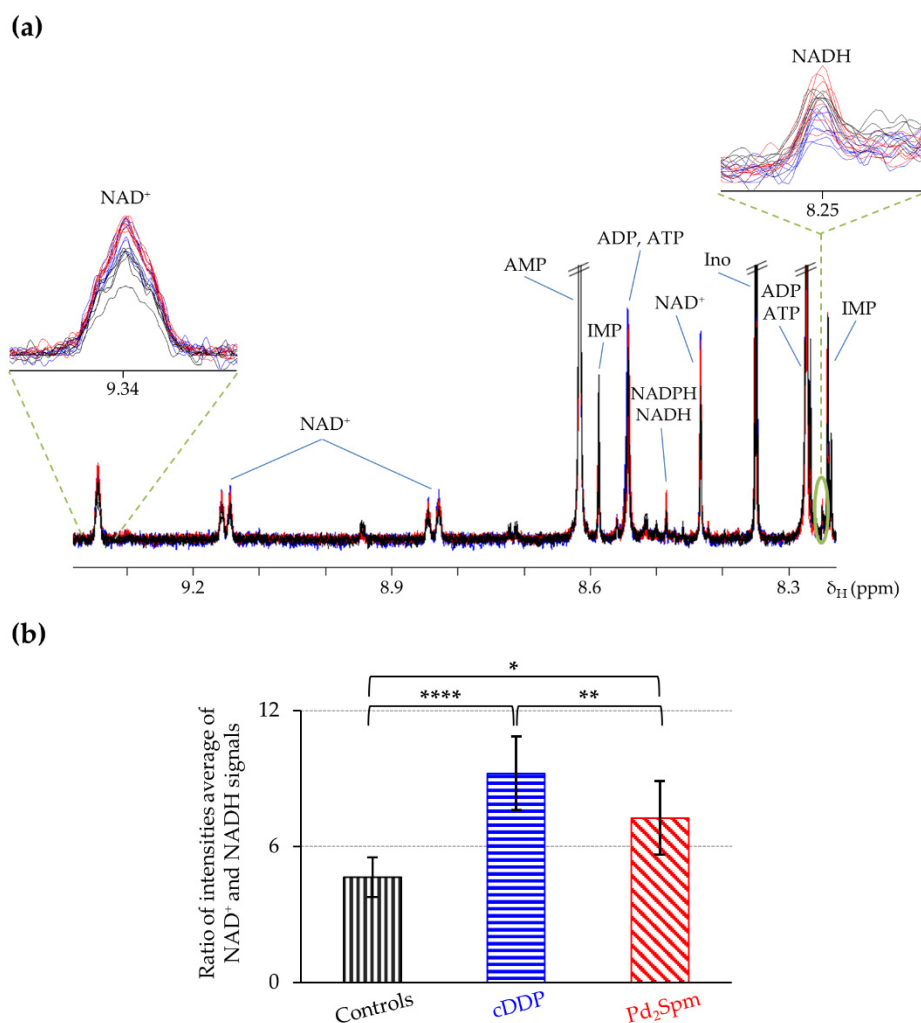


Figure S3. (a) Spectral expansions (δ 8.2–9.6 ppm) of the ^1H NMR spectra of aqueous extracts of CDX mice brain of controls (black trace), cDDP- (blue trace) and Pd₂Spm-treated (red trace) mice and (b) NAD⁺/NADH ratios for the same three animal groups; error bars indicate the respective standard deviation. * p -value $< 5.0 \times 10^{-2}$; ** p -value $< 1.0 \times 10^{-2}$; **** p -value $< 1.0 \times 10^{-4}$.

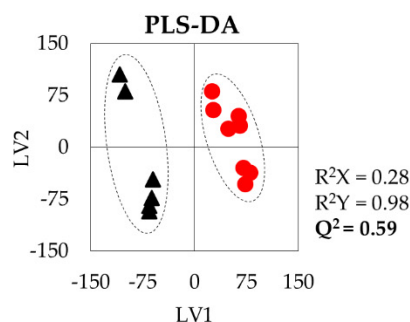
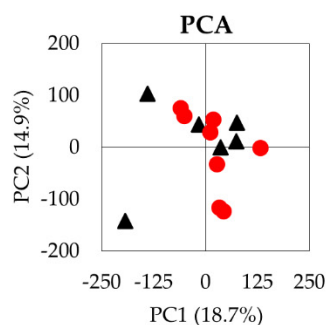
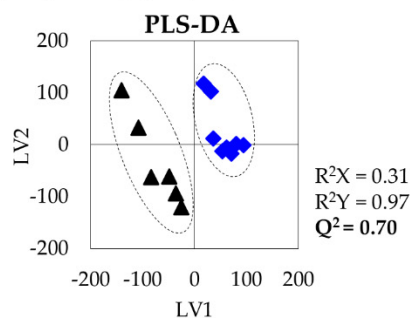
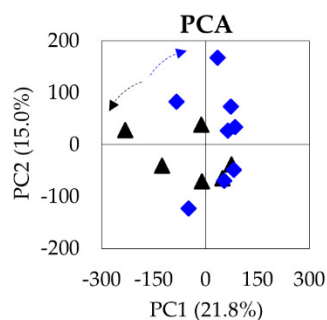
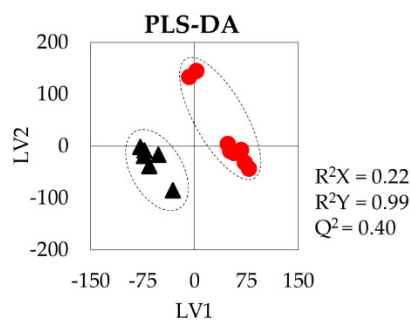
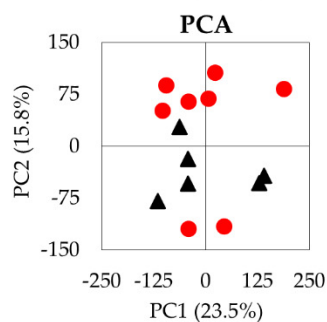
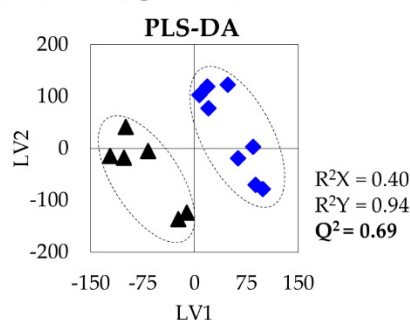
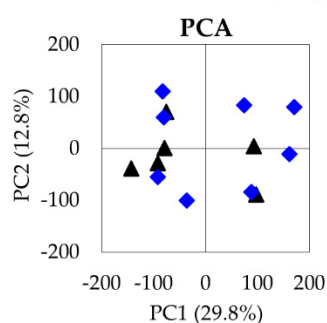
(a) Aqueous extracts▲ Controls ($n=6$); ◆ cDDP ($n=8$); ● Pd₂Spm ($n=8$)**(b) Lipophilic extracts**▲ Controls ($n=6$); ◆ cDDP ($n=8$); ● Pd₂Spm ($n=8$)

Figure S4. Pairwise score scatter plots of PCA and PLS-DA models for ¹H NMR spectra of (a) aqueous and (b) lipophilic extracts of liver of CDX mice (controls, black triangles, $n = 6$; cDDP-treated, blue diamonds, $n = 8$; Pd₂Spm-treated, red circles, $n = 8$). Validation parameters (R^2 and Q^2) are indicated for each PLS-DA model, with Q^2 values > 0.5 highlighted in bold indicating robust classes separation.

Table S1. Statistically significant ($|ES| > ES$ Error and p -value < 0.05) metabolite variations observed in the polar metabolomes of CDX mice brain and liver, compared to controls. [†] Tentative assignment. [‡] Partial integration of resonance peak. ^a Metabolic variation statistically significant after False Discovery Rate (FDR) correction. Abbreviations: 3-letter code used for amino acids; 3-HIBA, 3-hydroxyisobutyrate; Ado, adenosine; AMP, adenosine monophosphate; Cho, choline; GPC, glycerophosphocholine; GSH, glutathione (reduced); IMP, inosine monophosphate; Ino, inosine; NAA, N-acetylaspartate; NAD⁺/NADH, nicotinamide adenine dinucleotide (oxidized/reduced); NADP⁺, nicotinamide adenine dinucleotide phosphate (oxidized); UDP-Glc/GlcA, uridine diphosphate glucose/glucuronate; UDP-GlcNAc, uridine diphosphate N-acetylglucosamine; UMP, uridine monophosphate; TMA, trimethylamine; s, singlet; d, doublet; dd, double doublet; t, triplet; m, multiplet.

		cDDP <i>vs.</i> Controls		PdSpm <i>vs.</i> Controls	
Metabolite	δ/Multiplicity	ES ± Error	<i>p</i> -Value	ES ± Error	<i>p</i> -Value
BRAIN					
3-Aminoisobutyrate	1.18 (d)	1.3 ± 1.2	2.1 × 10 ⁻² ^a	3.5 ± 1.7	5.9 × 10 ⁻⁵ ^a
3-HIBA	1.09 (d)	-	-	4.1 ± 1.8	2.1 × 10 ⁻⁵ ^a
Adenine	8.23 (s)	-	-	-1.5 ± 1.2	3.2 × 10 ⁻²
Ado	8.349 (s)	-	-	-1.9 ± 1.3	6.7 × 10 ⁻⁴ ^a
AMP	8.60 (s)	-	-	-1.6 ± 1.2	1.3 × 10 ⁻² ^a
Cholate [†]	0.73 (s)	1.2 ± 1.1	4.0 × 10 ⁻²	4.7 ± 2.0	3.2 × 10 ⁻⁶ ^a
Creatine	3.04 (s)	-	-	-1.5 ± 1.2	1.3 × 10 ⁻² ^a
Cystathionine [†]	2.74 (d) [‡]	-	-	3.5 ± 1.7	2.1 × 10 ⁻⁵ ^a
Glycerol	3.55 (m)	-1.7 ± 1.2	1.3 × 10 ⁻³ ^a	-	-
GSH	2.96 (m)	1.9 ± 1.3	4.1 × 10 ⁻³ ^a	2.1 ± 1.3	2.9 × 10 ⁻³ ^a
Ile	0.94 (t)	-	-	2.1 ± 1.3	1.6 × 10 ⁻³ ^a
IMP	8.23 (s)	-	-	5.8 ± 2.4	5.4 × 10 ⁻⁶ ^a
Ino	8.35 (s)	-	-	2.1 ± 1.3	1.3 × 10 ⁻³ ^a
Leu	0.96 (t)	-	-	2.4 ± 1.4	6.4 × 10 ⁻⁴ ^a
Lys	1.73 (m)	-	-	6.0 ± 2.5	5.9 × 10 ⁻⁸ ^a
Malate [†]	2.66 (dd)	-1.3 ± 1.2	2.3 × 10 ⁻² ^a	-1.3 ± 1.2	2.5 × 10 ⁻² ^a
NAA	2.02 (s)	-	-	-1.4 ± 1.2	4.8 × 10 ⁻²
NAD ⁺	9.34 (s)	2.1 ± 1.3	1.3 × 10 ⁻³ ^a	3.6 ± 1.7	6.7 × 10 ⁻⁴ ^a
NADH	8.25 (s)	-3.5 ± 1.7	1.9 × 10 ⁻⁵ ^a	-	-
Pantothenate	0.74 (s)	-	-	5.3 ± 2.2	2.6 × 10 ⁻⁷ ^a
Phe	7.33 (m)	-	-	2.9 ± 1.5	1.3 × 10 ⁻⁴ ^a
Pseudouridine [†]	7.68 (s)	-	-	1.3 ± 1.2	2.1 × 10 ⁻² ^a
Succinate	2.41 (s)	-	-	-1.5 ± 1.2	1.2 × 10 ⁻² ^a
UDP-Glc/GlcA	5.97 (m)	-	-	1.6 ± 1.2	7.8 × 10 ⁻³ ^a
UMP	8.12 (d)	-1.6 ± 1.2	6.9 × 10 ⁻³ ^a	-1.5 ± 1.2	9.9 × 10 ⁻³ ^a
Val	1.05 (d)	-	-	3.3 ± 1.6	3.9 × 10 ⁻⁵ ^a
U1	1.46 (d)	1.4 ± 1.2	1.4 × 10 ⁻² ^a	5.4 ± 2.3	2.7 × 10 ⁻⁷ ^a

U2	2.87 (s)	-	-	7.7 ± 3.0	$4.3 \times 10^{-9}^a$
U3	2.98 (d)	-	-	-1.9 ± 1.3	$3.3 \times 10^{-3}^a$
U4	3.33 (s)	-	-	-1.4 ± 1.2	$2.0 \times 10^{-2}^a$
LIVER					
O-Acetylcarnitine [†]	3.18 (s)	-1.8 ± 1.2	$4.8 \times 10^{-3}^a$	-4.0 ± 1.8	$7.3 \times 10^{-6}^a$
AMP	8.60 (s)	-	-	-2.2 ± 1.3	$2.7 \times 10^{-3}^a$
Ado	6.08 (d)	-2.3 ± 1.4	$1.4 \times 10^{-3}^a$	-3.1 ± 1.6	$3.3 \times 10^{-4}^a$
Cho	3.20 (s)	-2.3 ± 1.4	$8.7 \times 10^{-4}^a$	-3.8 ± 1.8	$8.0 \times 10^{-6}^a$
GPC	3.23 (s)	-1.4 ± 1.2	$1.8 \times 10^{-2}^a$	-	-
GSH	2.17 (m)	1.9 ± 1.3	$4.4 \times 10^{-3}^a$	-	-
His	7.08 (s)	2.3 ± 1.4	$7.9 \times 10^{-4}^a$	-	-
Malonate	3.13 (s)	-1.9 ± 1.3	$3.1 \times 10^{-3}^a$	-4.2 ± 1.9	$6.7 \times 10^{-4}^a$
NADP ⁺	9.30 (s)	1.3 ± 1.2	2.5×10^{-2}	-	-
Pseudouridine [†]	7.68 (s)	-	-	-1.8 ± 1.3	$1.4 \times 10^{-2}^a$
TMA	2.89 (s)	1.8 ± 1.3	$8.0 \times 10^{-3}^a$	-	-
Tyr	6.90 (d)	1.2 ± 1.2	5.0×10^{-2}	-	-
UDP-GlcNAc	5.52 (dd)	1.5 ± 1.2	$3.2 \times 10^{-2}^a$	-	-
UMP	8.12 (d)	-	-	-1.6 ± 1.2	$1.3 \times 10^{-2}^a$
U5	3.13 (s)	-1.7 ± 1.2	$5.9 \times 10^{-3}^a$	-4.6 ± 2.0	$5.1 \times 10^{-6}^a$
U6	3.33 (s) [‡]	1.2 ± 1.2	$3.2 \times 10^{-2}^a$	-	-
U7	4.03 (d)	-1.6 ± 1.2	$8.5 \times 10^{-3}^a$	-3.7 ± 1.7	$3.4 \times 10^{-5}^a$

Table S2. Statistically significant ($|ES| > ES$ Error and p -value < 0.05) metabolite variations observed in the lipophilic metabolomes of CDX mice brain and liver, compared to controls. [†] Tentative assignment. [‡] Partial integration of resonance peak. ^a Metabolic variation statistically significant after False Discovery Rate (FDR) correction. Abbreviations: FAs, fatty acids; PLs, phospholipids; PTC, phosphatidylcholine; PTE, phosphatidylethanolamine; PUFAs, polyunsaturated fatty acids; TG, triacylglycerols; s, singlet; d, doublet; t, triplet; q, quartet; br, broad signal.

Metabolite	δ /Multiplicity	cDDP <i>vs.</i> Controls		Pd2Spm <i>vs.</i> Controls	
		ES \pm Error	<i>p</i> -Value	ES \pm Error	<i>p</i> -Value
BRAIN					
Lathosterol C18H3 [†]	0.54 (d)	-	-	-2.3 \pm 1.4	1.4 $\times 10^{-2}$ ^a
FA (CH2) _n	1.25 (br)	-	-	3.2 \pm 1.7	8.5 $\times 10^{-3}$ ^a
PUFAs (ω 3) CH3	0.98 (t)	-	-	-2.2 \pm 1.4	2.4 $\times 10^{-3}$ ^a
18:2 =CHCH2CH=	2.77 (t)	-1.4 \pm 1.2	4.6 $\times 10^{-2}$	-3.0 \pm 1.6	2.5 $\times 10^{-3}$ ^a
TG Glyceryl C2H [†]	5.29 (t)	-	-	-2.4 \pm 1.4	1.1 $\times 10^{-2}$ ^a
PL CH2N(CH3)3	3.75 (br)	-	-	3.1 \pm 1.6	7.1 $\times 10^{-3}$ ^a
PL [†]	8.36 (br)	-	-	1.8 \pm 1.3	3.1 $\times 10^{-3}$ ^a
PTC Glyceryl C3H2 [†]	3.90 (br)	-	-	2.1 \pm 1.4	1.1 $\times 10^{-2}$ ^a
PTE (NH3) ⁺	8.80 (br)	-	-	-2.3 \pm 1.4	1.3 $\times 10^{-3}$ ^a
U1	2.20 (q)	-1.4 \pm 1.2	4.4 $\times 10^{-2}$	-1.9 \pm 1.3	2.5 $\times 10^{-2}$ ^a
U2	3.84 (d) [‡]	-1.6 \pm 2.3	1.3 $\times 10^{-2}$ ^a	-4.1 \pm 1.9	1.6 $\times 10^{-4}$ ^a
LIVER					
PUFAs CH2CH=	2.04 (q)	-1.3 \pm 1.2	2.9 $\times 10^{-2}$	-	-
PTE (NH3) ⁺	8.80 (br)	-1.7 \pm 1.2	6.7 $\times 10^{-3}$ ^a	-	-
U3	1.015 (s)	-	-	-1.5 \pm 1.2	3.1 $\times 10^{-2}$
U4	2.34 (br)	-	-	-1.3 \pm 1.2	4.3 $\times 10^{-2}$
U5	3.64 (s)	1.5 \pm 1.2	1.3 $\times 10^{-2}$	-	-
U6	3.88 (s)	-	-	2.0 \pm 1.3	2.1 $\times 10^{-3}$ ^a