Supporting information for:

Optimized Protocol To Analyze Changes in the Lipidome of Xenografts after Treatment with 2-Hydroxyoleic Acid

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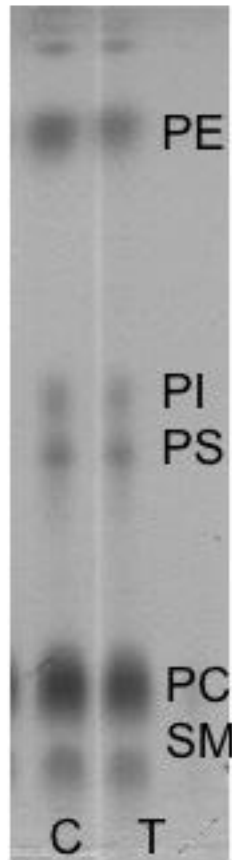

Fig S1. Analysis of xenograft lipid extracts by HPTLC.
Representative HPTLC of lipid extracts of xenografts generated in control (C) and 2-OHOA-treated immunodepressed mice (T, 600 mg · kg^{-1} · d^{-1}, 50 d). Phospholipids were separated using chloroform/methanol/acetic acid/water (55:37.5:3:2 by vol), which separates all major glycerophospholipids. Lipids were identified using commercially available standards (Larodan, Sweden). Plates were air-dried after development, sprayed with 8% (w/v) H_3PO_4 containing 10% (w/v) $CuSO_4$, and charred at 170°C for 10 min. Bands were quantified by photodensitometry using Quantity One software (Bio-Rad, Barcelona, Spain).

PC: phophatidylcholine; PE: phosphatidylethanolamine; PI: phophatidylinositol, PS: phosphatidylserine; SM: sphingomyelin

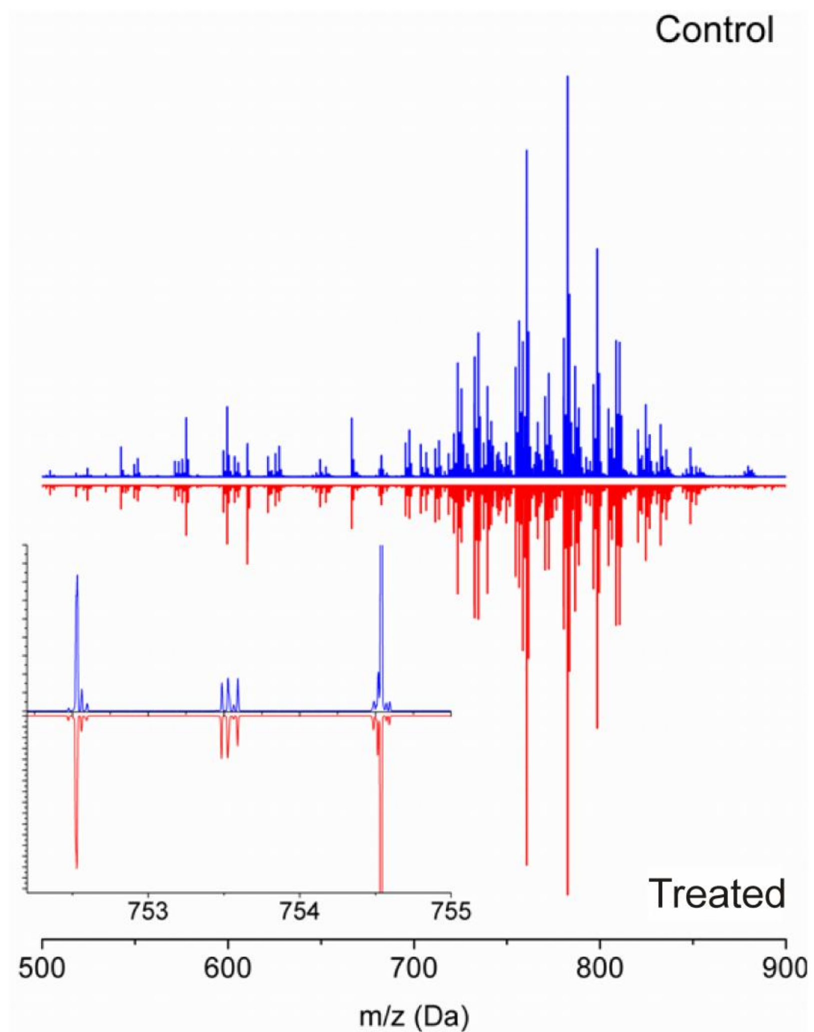

Fig. S2. Representative average spectra over a section of control (blue) and treated (red) xenografts. The insert shows a zoom over a random section of the spectra to demonstrate the similarity between both traces. Such similarity clearly shows why an image technique was required to unravel the changes in the lipid profile due to the treatment.

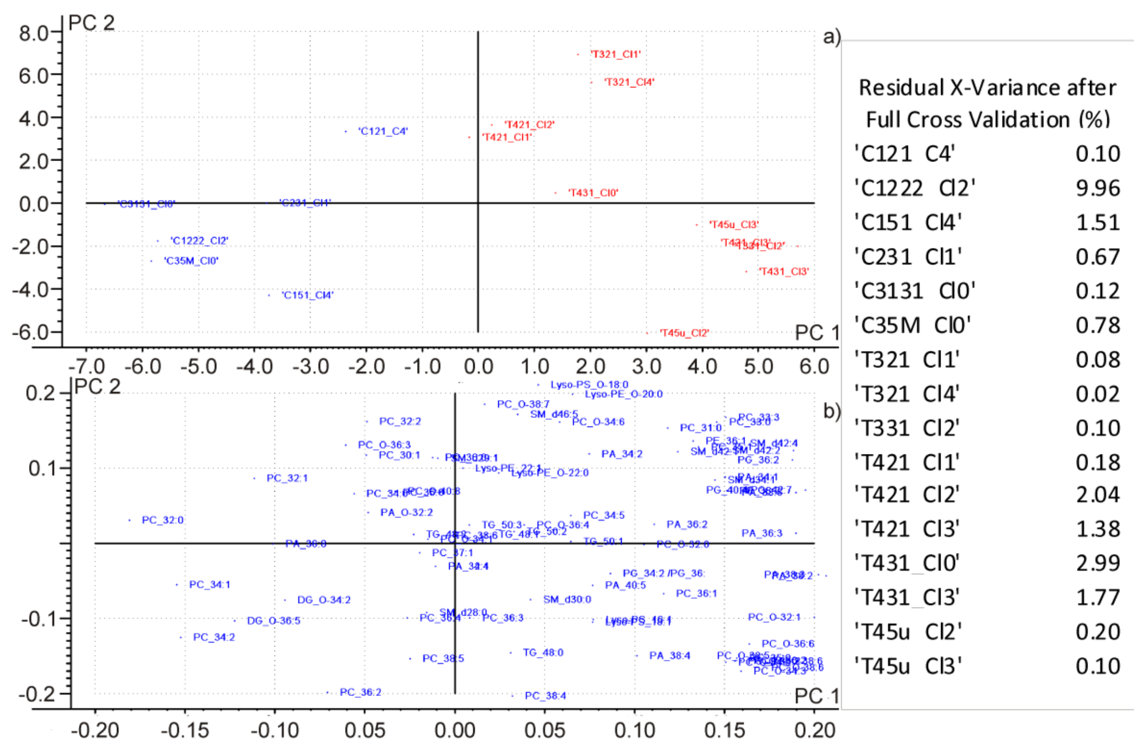

Fig. S3. (a) Scores plot of the ROIs of viable tissue. Control samples (left) and treated samples (right) were well classified along the PC 1. (b) Loadings plot. The residual variance is also included.