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Untargeted MS-based lipidomic analyses

In 1 collection

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We use this protocol and it's working

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Abstract

Untargeted MS-based lipidomic analyses

1 Collect iPSC-derived microglia and prepare cell pellets. Flash-freeze cell pellets to be shipped on dry ice (our pellets were sent to Lipotype Gmbh, Dresden, Germany)

2 Samples were processed using a modified chloroform/methanol extraction protocol with internal standards specific to each lipid class (Ref. main text Surma et al., 2021).

3 Lipid extracts were analyzed on a Q Exactive Orbitrap mass spectrometer (Thermo Fisher Scientific) equipped with a Triversa Nanomate automated nano-ESI source.

4 Measurements were performed in both positive and negative ion modes.

5 External mass calibration was conducted weekly to maintain <5 ppm mass accuracy.

6 Lipids were identified using LipotypeXplorer software based on MS1 and MS/MS data.

7 Quantification data were normalized to internal standards, and data were reported in both pmol and mol% formats

8 Lipid species with signal intensities ≥5-fold above blank and noise thresholds were retained.

9 Reproducibility was confirmed using quality control samples (mammalian blood) with a median coefficient of variation (CV) of ~4%.