

Supporting Information

Evaluating Sample Normalization Methods for MS-based Multi-omics and the Application to a Neurodegenerative Mouse Model

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TABLE OF CONTENTS

- **Table S1.** The list of internal standards for lipidomics and metabolomics.
- **Fig. S1.** Example LC-MS chromatograms from (A) proteomics, (B) lipidomics, and (C) metabolomics for mouse brain.
- **Fig. S2.** Volcano plots showing the influence of normalization methods on lipidomics.
- **Fig. S3.** Volcano plots showing the influence of normalization methods on metabolomics.
- **Fig. S4.** Example lipid concentrations measured from *GRN* KO vs. WT mouse brains.
- **Supplementary Data (Excel).** The complete datasets for quantitative proteomics, lipidomics and metabolomics in three different sample normalization methods and *GRN* KO mouse brain.

Table S1. The spiked internal standards for lipidomics and metabolomics and their concentration.

Category	Compound name	Adduct	<i>m/z</i>	Spiked conc. (nmol/mL)
Lipidomics	SM (d18:1/18:1-d9)	[M+H] ⁺	738.6475	18.1
Lipidomics	Cer (d18:1-d7/15:0)	[M+H] ⁺	531.5465	25.1
Lipidomics	MG (18:1-d7)	[M+NH ₄] ⁺	381.3704	36.7
Lipidomics	DG (15:0/18:1-d7)	[M+NH ₄] ⁺	605.5849	22.7
Lipidomics	LPC (18:1-d7)	[M+H] ⁺	529.3998	25.2
Lipidomics	LPE (18:1-d7)	[M+H] ⁺	487.3529	27.4
Lipidomics	TG (15:0/18:1-d7/15:0)	[M+NH ₄] ⁺	829.7989	16.4
Lipidomics	CE (18:1-d7)	[M+NH ₄] ⁺	675.6780	20.3
Lipidomics	PC (15:0/18:1-d7)	[M+H] ⁺	753.6138	17.7
Lipidomics	PE (15:0/18:1-d7)	[M+H] ⁺	711.5669	18.8
Lipidomics	PG (15:0/18:1-d7)	[M-H] ⁻	740.5469	17.5
Lipidomics	PS (15:0/18:1-d7)	[M-H] ⁻	753.5422	17.2
Lipidomics	PI (15:0/18:1-d7)	[M-H] ⁻	828.5630	15.7
Metabolomics	¹³ C ₅ , ¹⁵ N folic acid	[M+H] ⁺ [M-H] ⁻	448.1613 446.1462	51.4

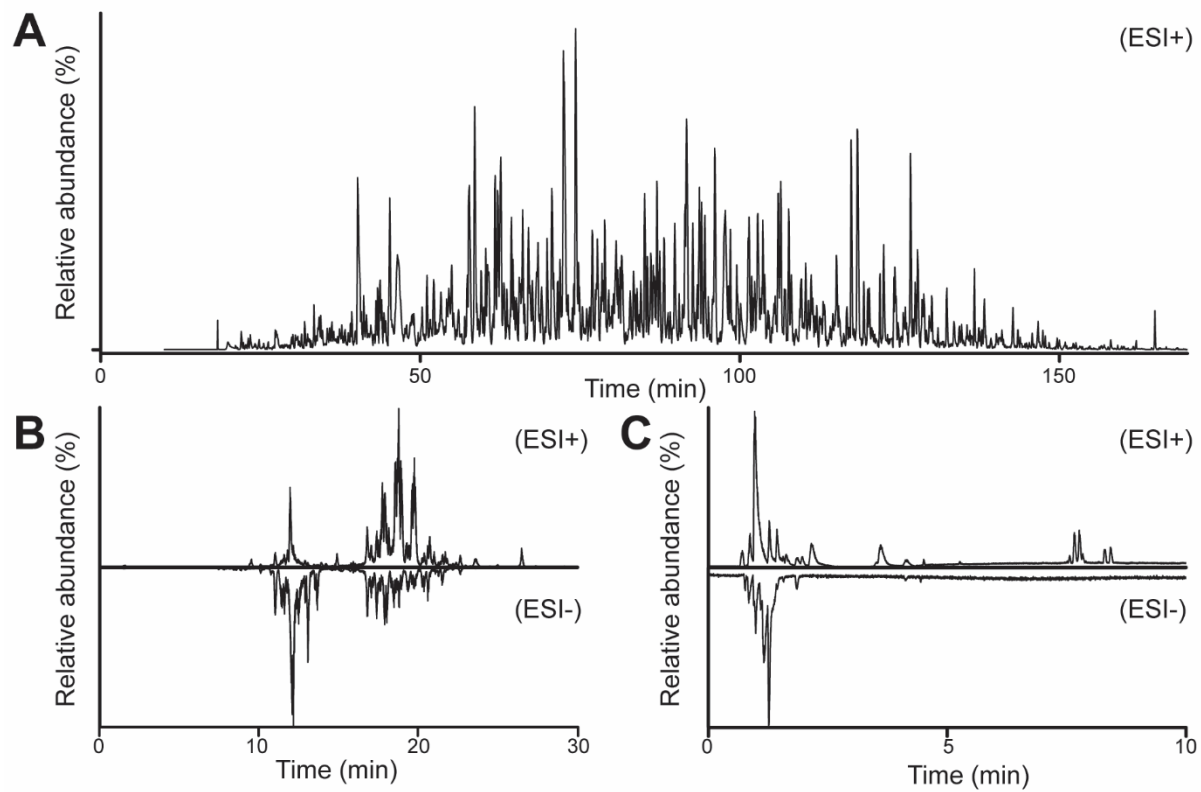


Fig. S1. Example LC-MS chromatograms from (A) proteomics, (B) lipidomics, and (C) metabolomics from mouse brain tissue.

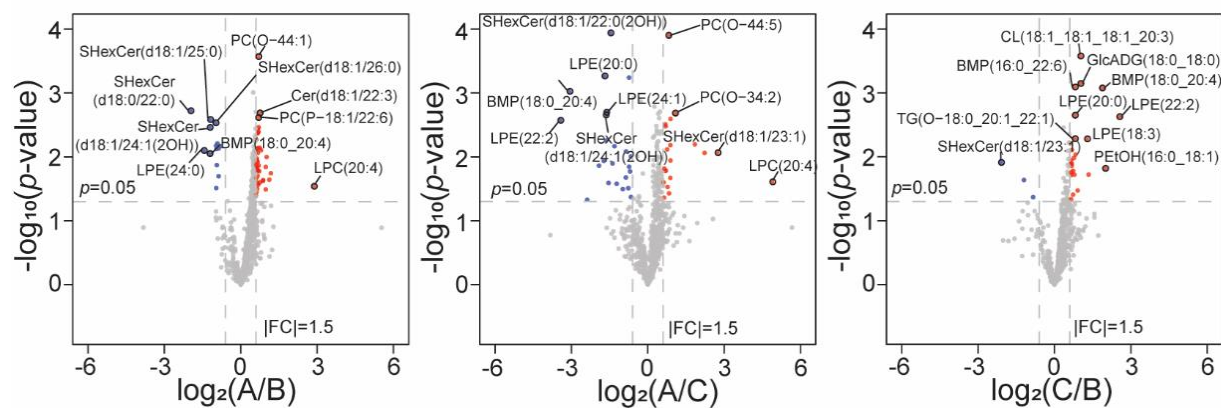


Fig. S2. Volcano plots showing the influence of normalization methods on lipidomics. A, B, C represents three different normalization methods.

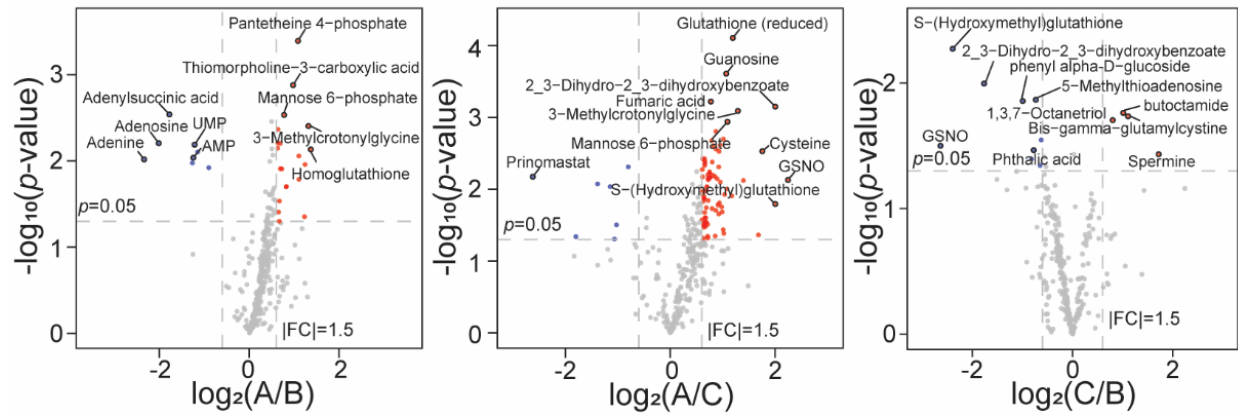


Fig. S3. Volcano plots showing the influence of normalization methods on metabolomics.

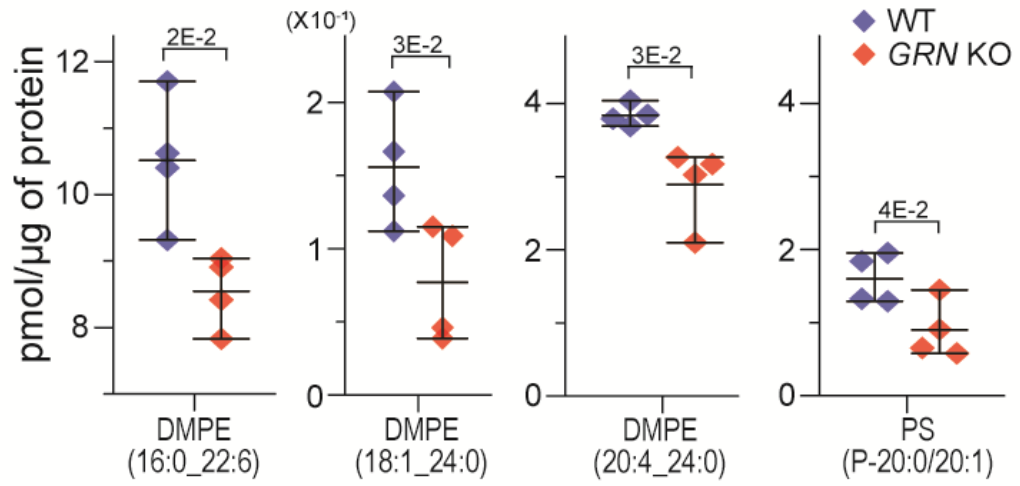


Fig. S4. Example lipid concentrations measured from *GRN* KO vs. WT mouse brains.