SUPPORTING INFORMATION

Matrix Effects in Biological Mass Spectrometry Imaging: Identification and Compensation

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Figure S1. Mass spectra showing A) [PC 25:0+Na]⁺ (m/z 658.44) and [PC 25:0+K]⁺ (m/z 674.41), and B) [PC 43:6+Na]⁺ (m/z 898.628) and [PC 43:6+K]⁺ (m/z 914.602). Red traces show spectra from brain tissue acquired without standards in the solvent and black traces show spectra from brain tissue acquired with PC 25:0 and PC 43:6 in the nano-DESI solvent. Peaks originating from the standards are marked blue.



Figure S2. A) $[M+K]^+$ of endogenous LPC 16:0 normalized to $[M+K]^+$ of LPC 13:0; B) $[M+H]^+$ of endogenous PC 34:1 normalized to TIC, C) $[M+H]^+$ of endogenous PC 34:1 normalized to $[M+H]^+$ of PC 25:0, and D) Standard LPC 13:0 $[M+K]^+$ normalized to standard PC 25:0 $[M+K]^+$.



Figure S3. Line scan over brain tissue showing traces of A) [PC 34:0 + Na]⁺ at m/z 784.57, B) [PC 38:4 + Na]⁺ at m/z 832.58, C) [PC 38:6 + Na]⁺ at m/z 828.55, D) Standard [PC 21:0/22:6 + Na]⁺ at m/z 898.63, E) [PC 34:0 + K]⁺ at m/z 800.53, F) PC 38:4 + K] at m/z 848.56, G) [PC 38:6 + K]⁺ at m/z 844.53, and H) Standard [PC 21:0/22:6 + K]⁺ at m/z 914.61. Gray

traces show normalization to the TIC, black traces show normalization to the standard (PC 25:0 $[M+Na]^+$ (*m/z* 658.44) or $[M+K]^+$ (*m/z* 674.41) respectively), dotted traces show the nonnormalized signal. The primary y axis shows normalized intensity where normalization to TIC is taken times 150 and normalization to standard is divided by four. The secondary y-axis shows the relative abundance of the non-normalized ion. The line scan was performed from left to right in the optical (shown in Figure S3). Red fields mark the injured striatum and green fields mark the healthy striatum. Data is median filtrated (n=9) for clarity.



Figure S4. Optical image of the mouse brain tissue section, blue trace shows the location of the line scan discussed in Figure S2 (from left to right). Scale bar shows 2 mm.