Supporting Information

High-Resolution Live-Cell Imaging and Analysis by Laser Desorption/Ionization Droplet Delivery Mass Spectrometry

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Validation of analyte identities secreted from PC12 cells with LC-MS MRM

LC–MS analyses with MRM of the biological and control samples were performed on an Agilent 1100 LC (Agilent, Santa Clara, CA) equipped with an Eclipse Plus 5 μm phenyl-hexyl column, 100 Å pore size, 150 mm x 2.1 mm (Agilent, Santa Clara, CA) and coupled to an ESI Quattro Premier triple quadrupole MS (Waters, Milford, MA). Separation of the analytes was performed by injection of 10 μL of sample solution. A binary solvent system was used on the LC, with buffer A (H_2O with 0.1% formic acid) and buffer B (acetonitrile with 0.1% formic acid). The column temperature was kept at 25°C. A 250 μL/min flow rate was used with gradient elution where buffer B increased linearly over the course of a 10-minute run as follows: 0–2 min 0% B, 2–5 min 0–25% B, 5–6 min 25–70% B, 6–7 min 70% B, 7–8 min 70–0%B, 8–10 min 0% B. MS parameters used for MRM were: capillary voltage 5 kV, source temperature 110°C, desolvation temperature 350°C. Cone voltage was parent-ion dependent and collision energy was daughter-ion dependent. For phenethylamine (m/z 122), the cone voltage was set to 18 V; collision energy 25 eV (to m/z 76.8), 19 eV (to m/z 78.7), 21 eV (to m/z 102.7) and 12 eV (to m/z 104.8). For tyramine (m/z 138), the cone voltage was set to 15 V; 25 eV (to m/z 76.7) and 9 eV (to m/z 120.8). Dwell times were 50 ms per transition.

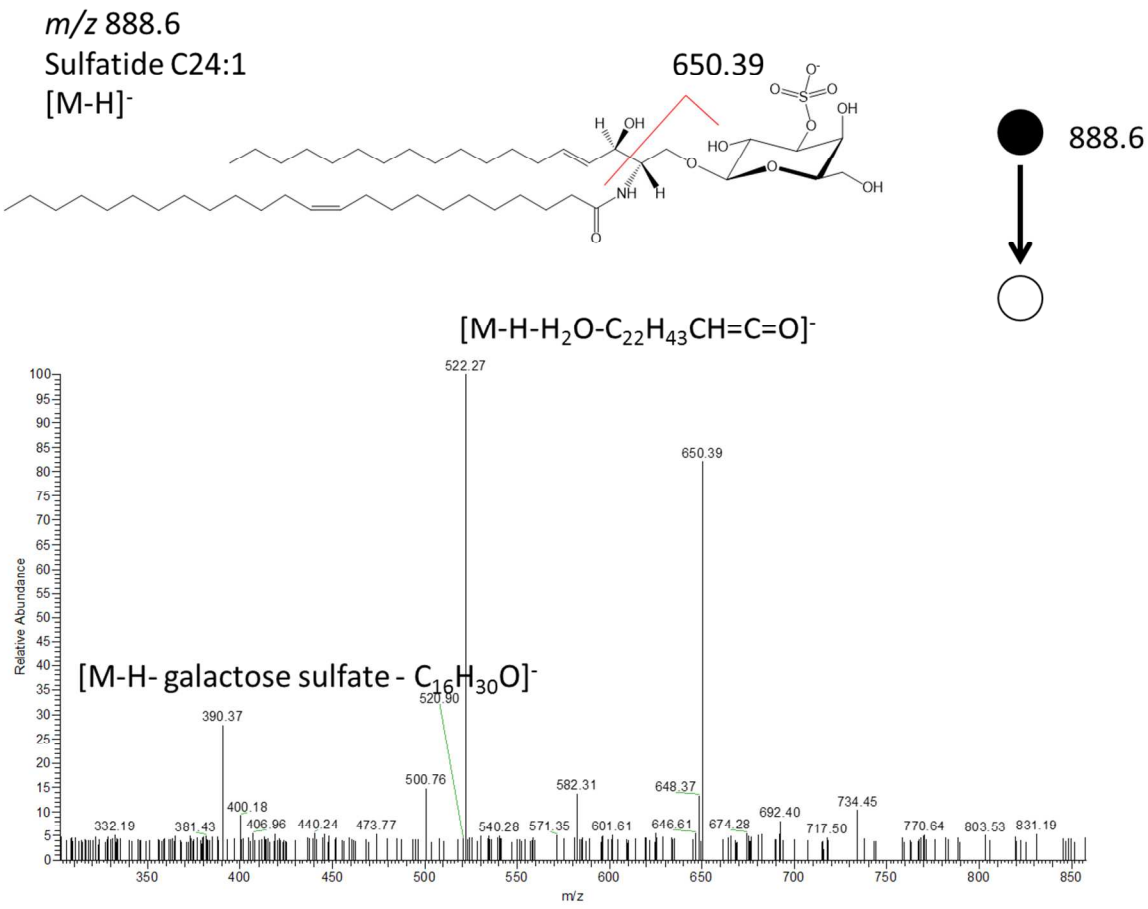

Figure S1. Negative ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 888.6

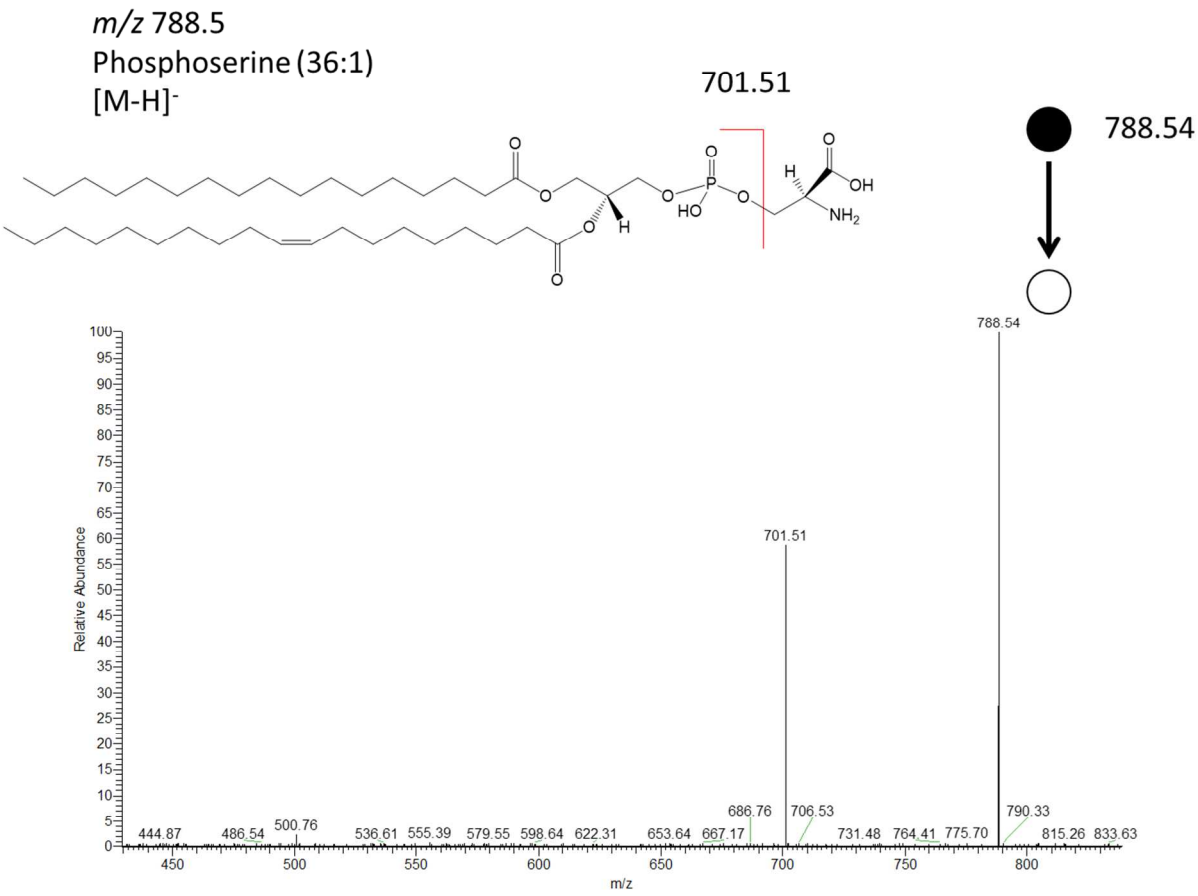

Figure S2. Negative ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 788.54

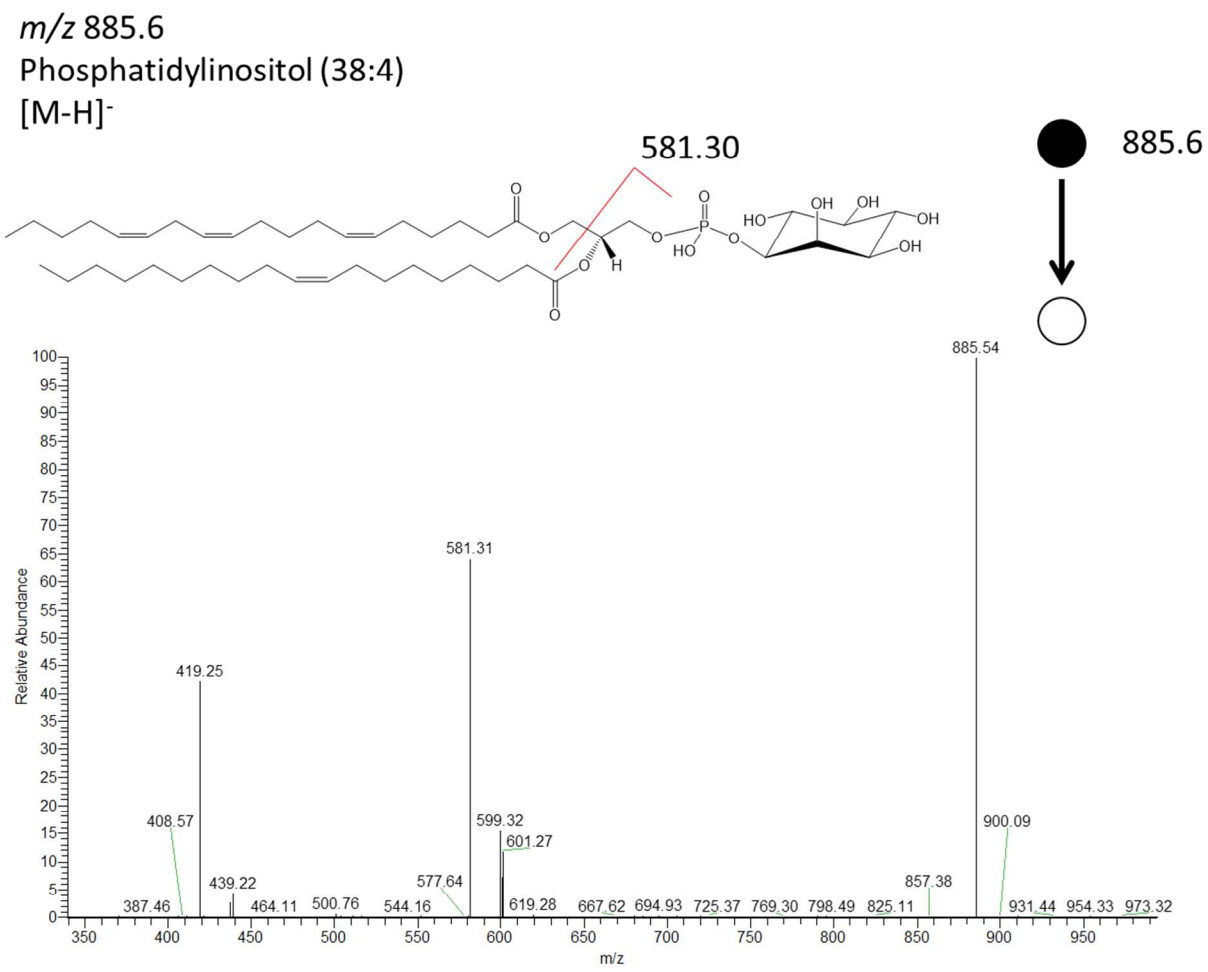

Figure S3. Negative ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 885.6

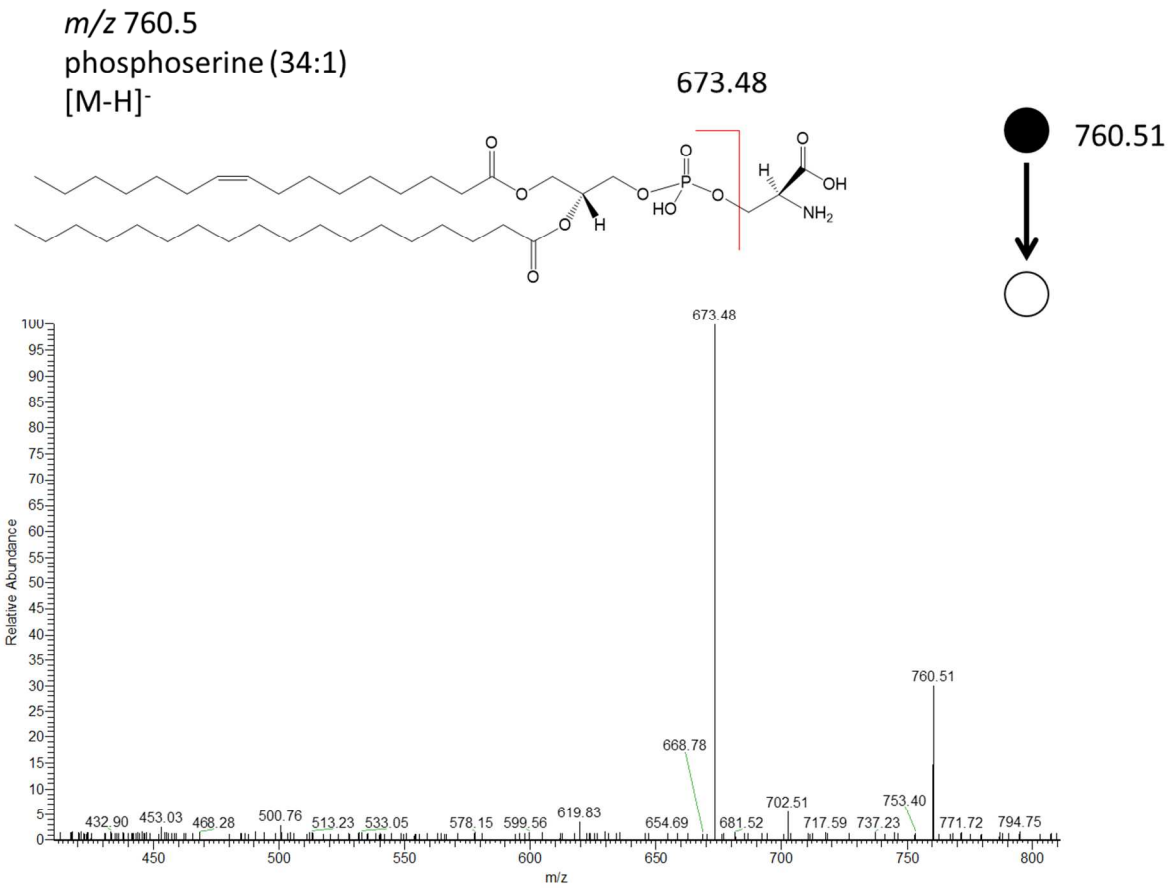

Figure S4. Negative ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 760.51

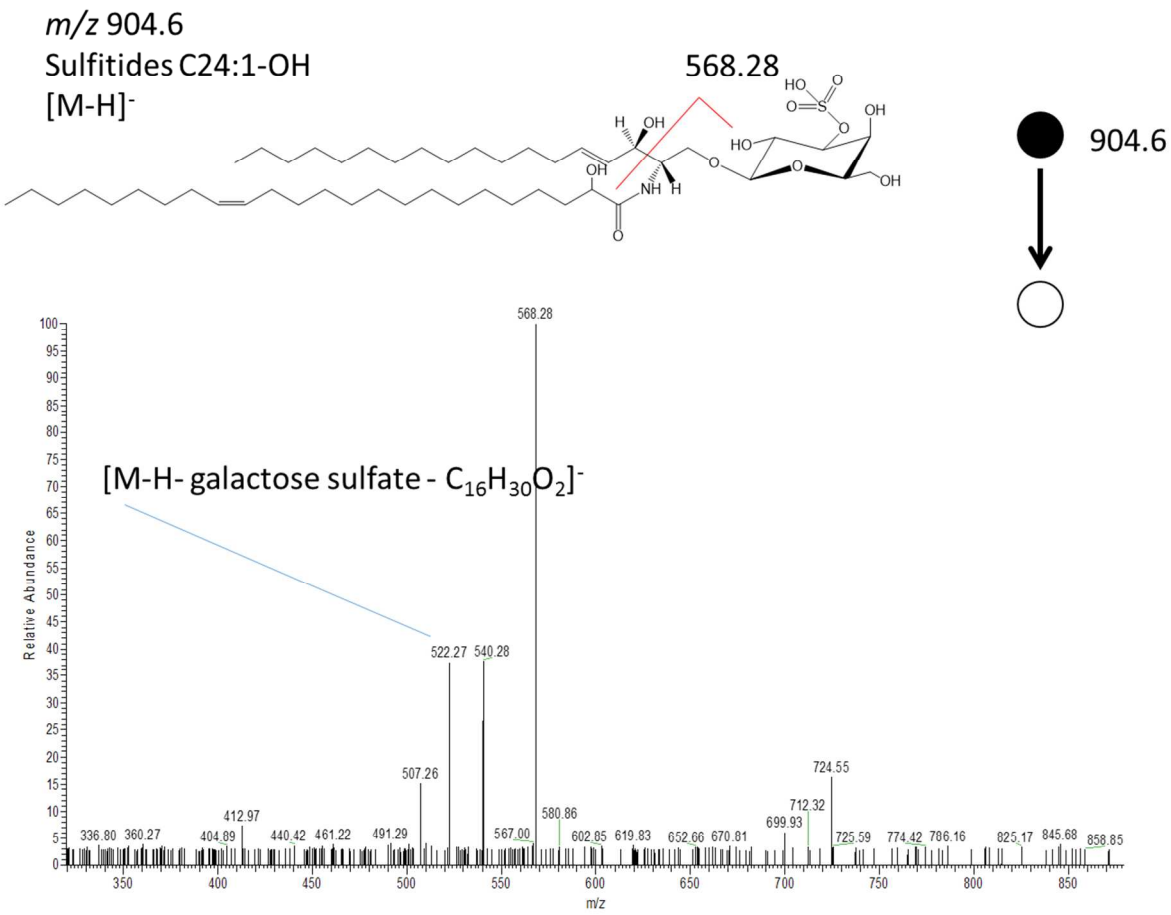

Figure S5. Negative ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 904.6

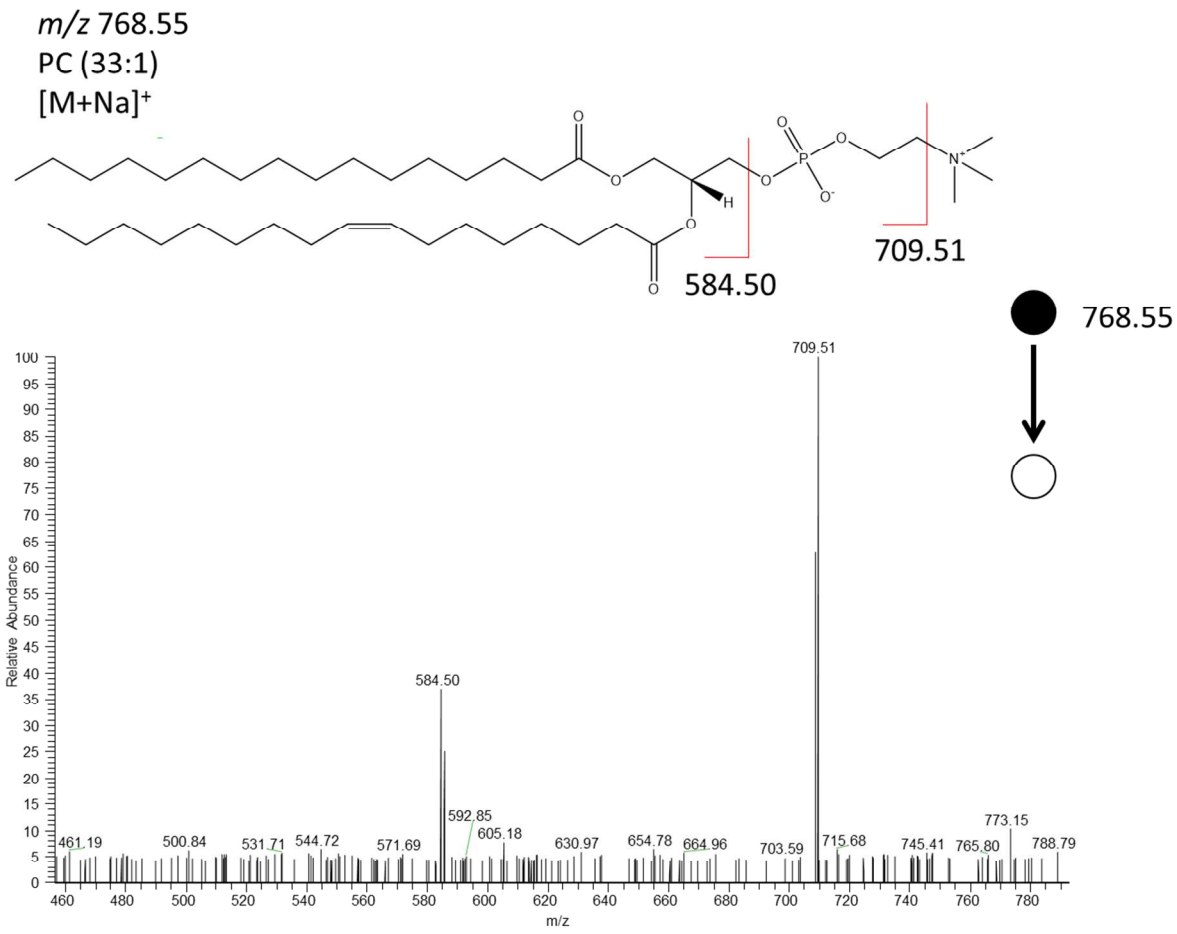

Figure S6. Positive ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 768.55

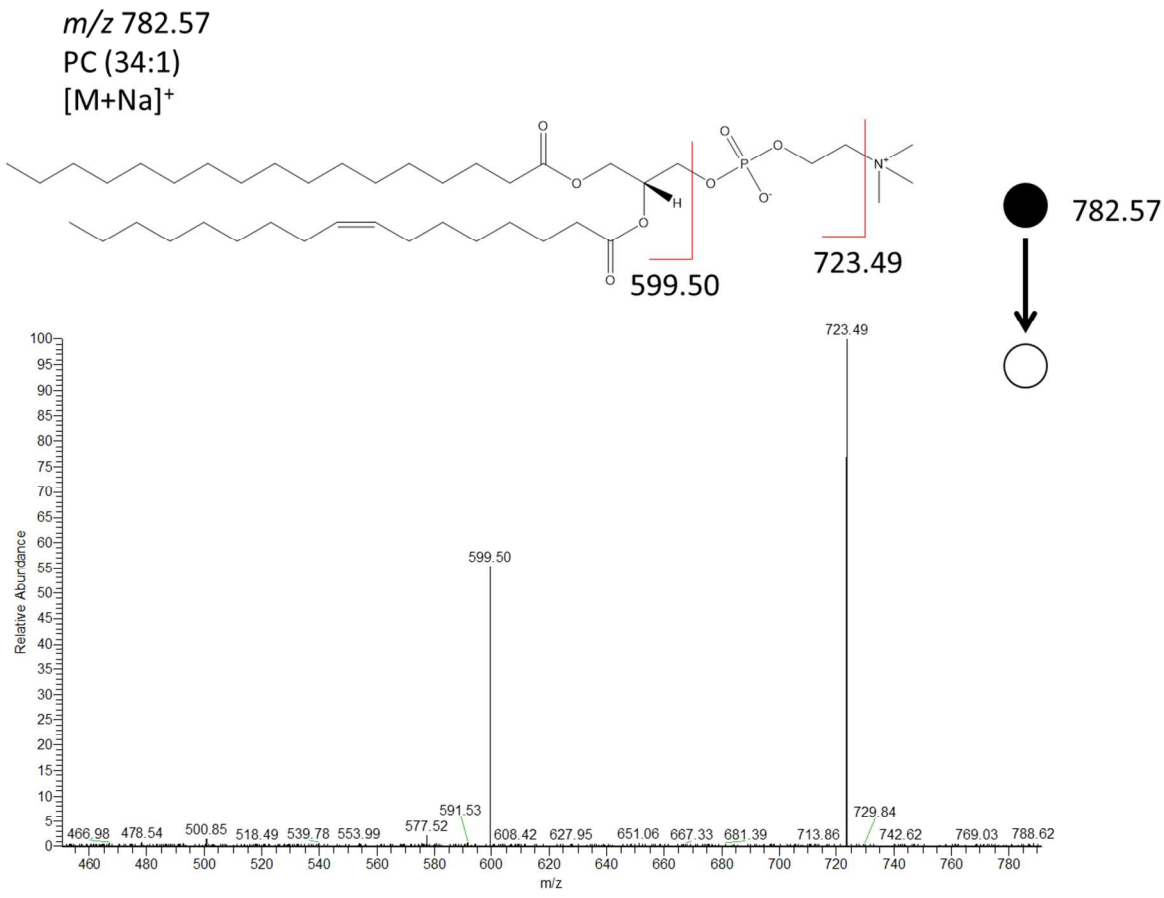

Figure S7. Positive ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 782.57

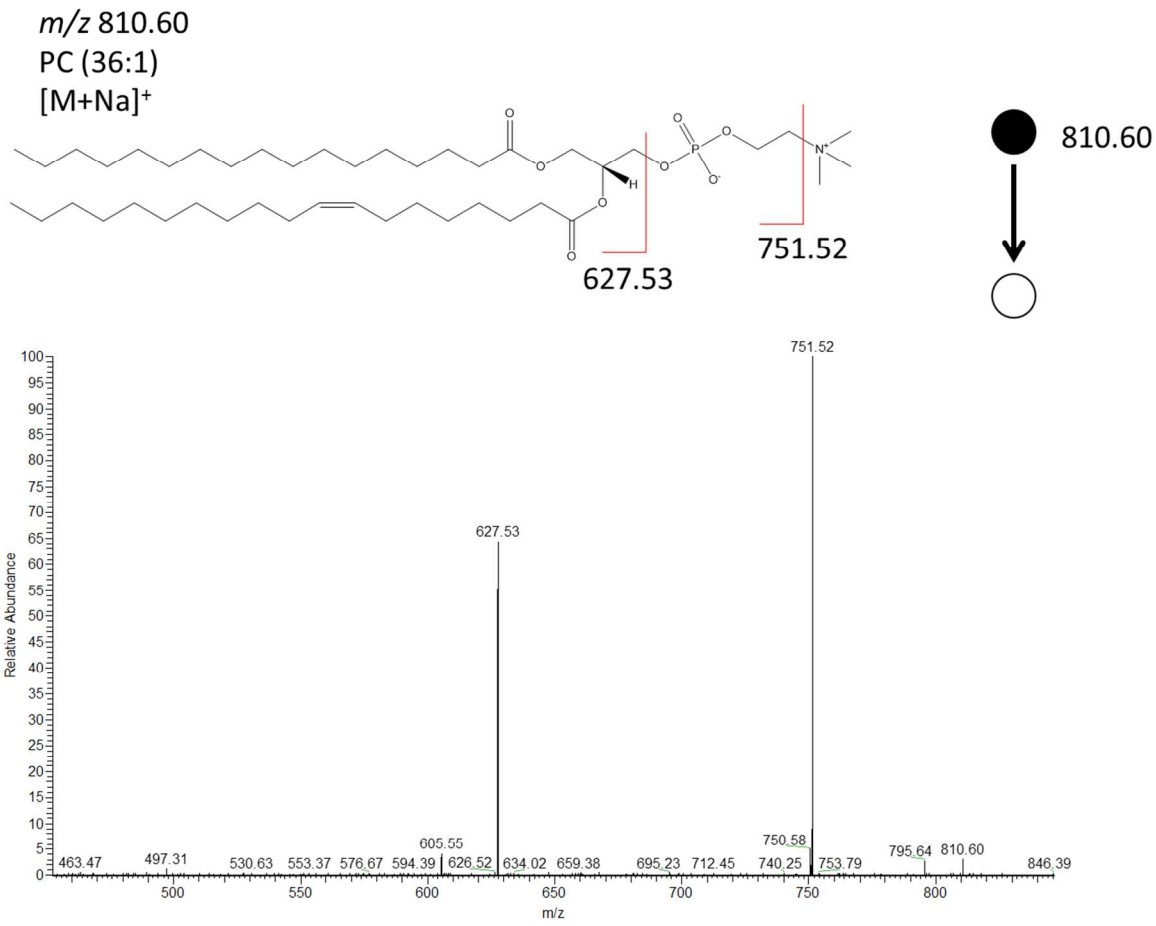

Figure S8. Positive ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 810.60

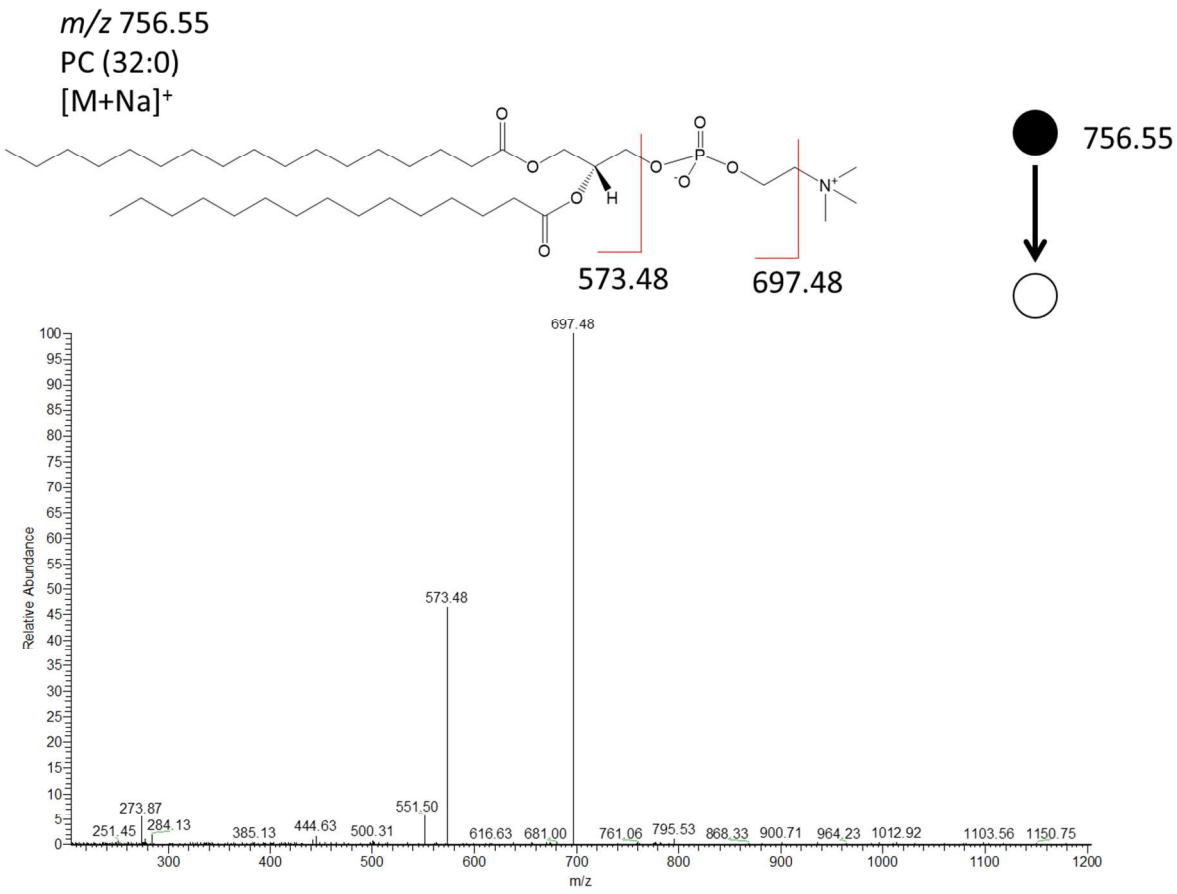

Figure S9. Positive ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 756.55

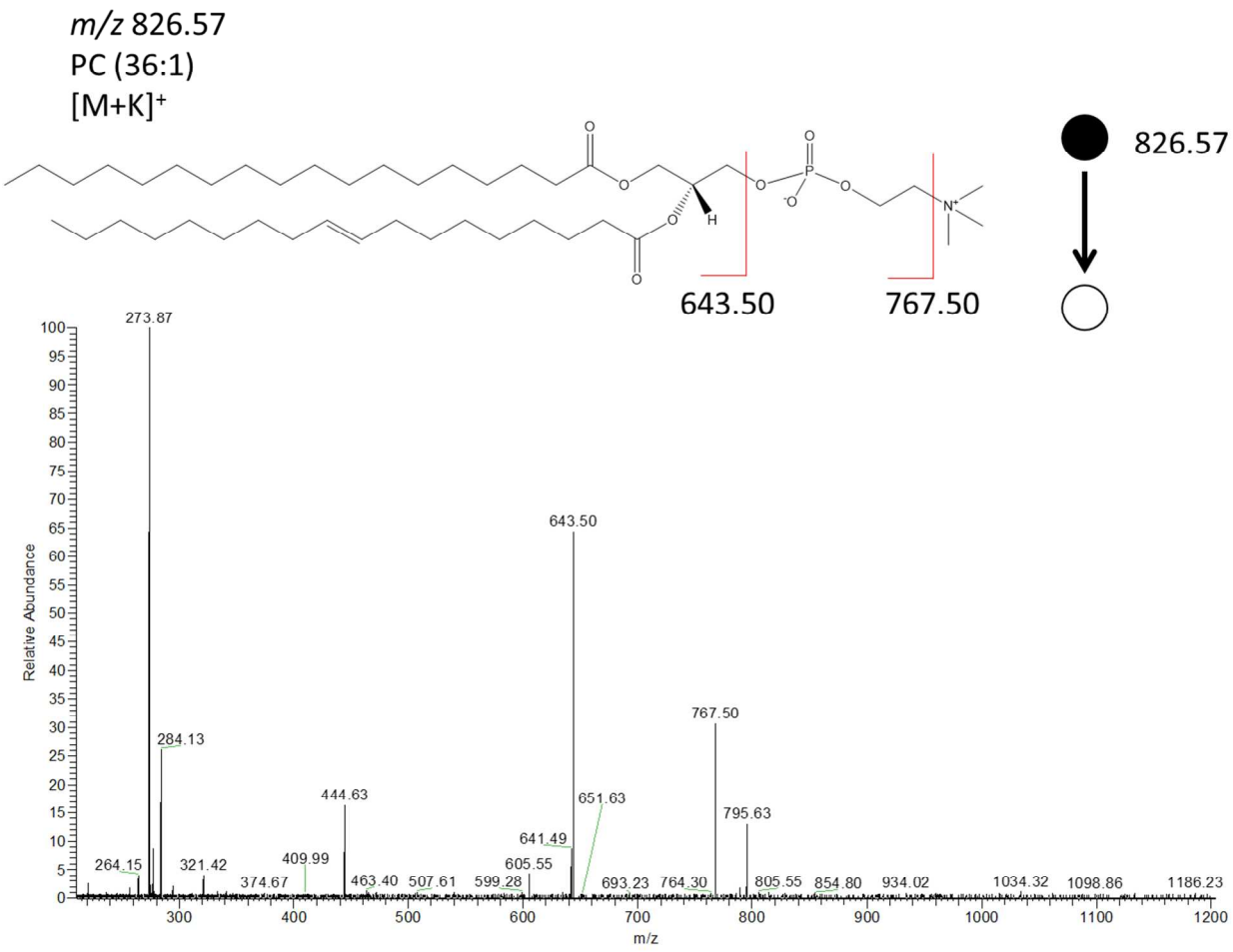

Figure S10. Positive ion mode tandem mass spectrometry analysis of the precursor ion at *m/z* 826.57

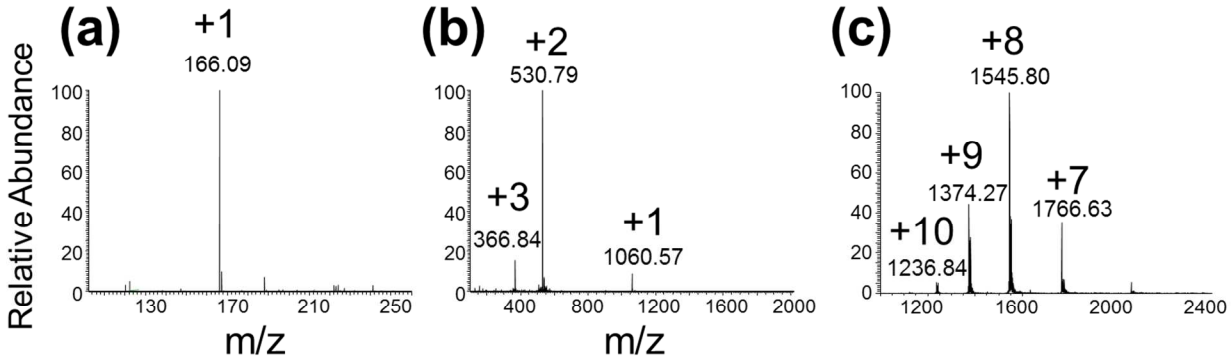

Figure S11. Mass spectra of the samples in liquid phase including (a) 100 μM phenylalanine, (b) 100 μM bradykinin, and (c) 100 μM cytochrome *c*. The charge state of the ions is indicated by +*z*.

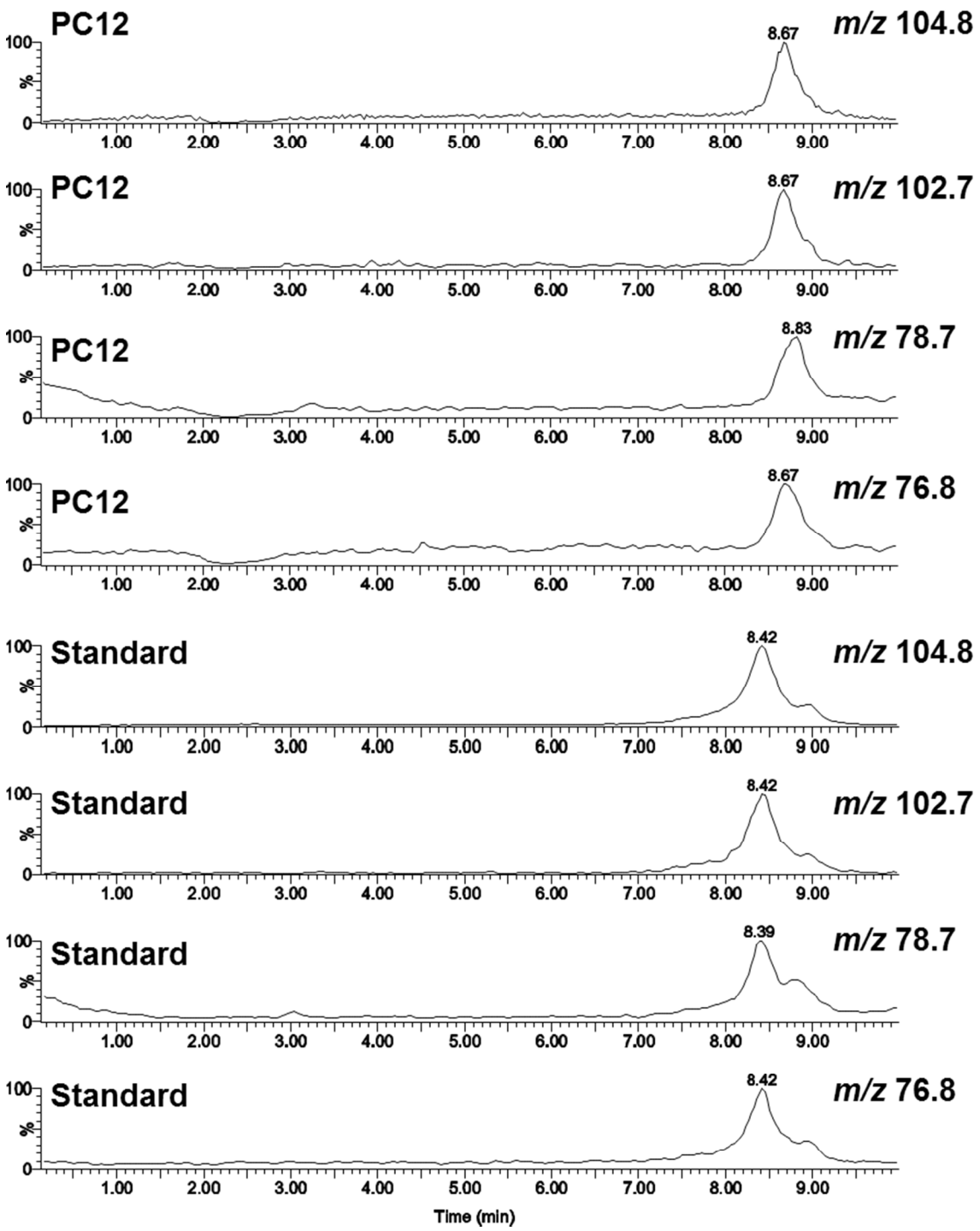

Figure S12. Multiple reaction monitoring LC–MS for phenethylamine showing a comparison of the biological sample with analytical standard sample (0.2 μM phenethylamine). The matching of four unique fragments of phenethylamine (*m/z* 122) at *m/z* 104.8, *m/z* 102.7, *m/z* 78.7 and *m/z* 76.8, between the releasates from PC12 cells and the analytical standard confirmed the identity of the releasate as phenethylamine.

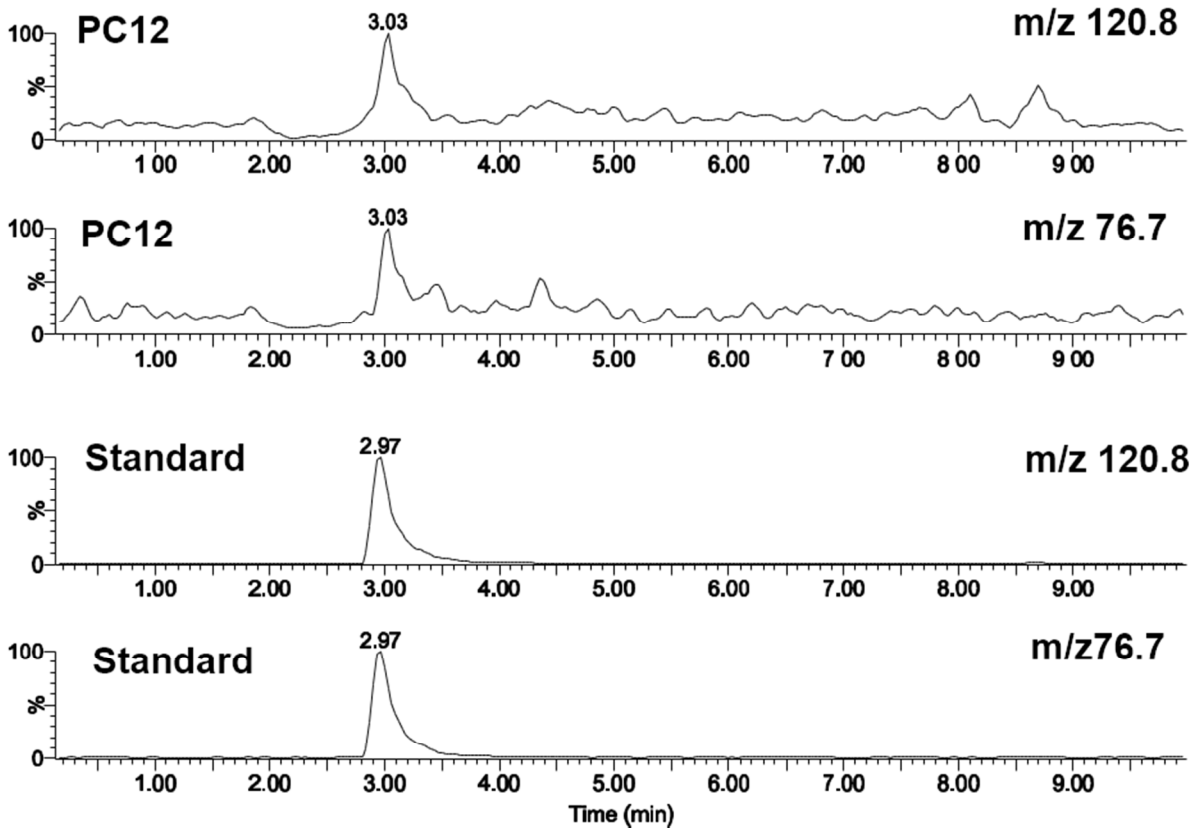

Figure S13. Multiple reaction monitoring LC–MS for tyramine showing a comparison of biological sample with analytical standard sample (0.2 μM tyramine). The matching of two unique fragments from tyramine (*m/z* 138) at *m/z* 120.8 and *m/z* 76.3, between the releasates from PC12 cells and the analytical standard confirmed the identity of the releasate as tyramine.