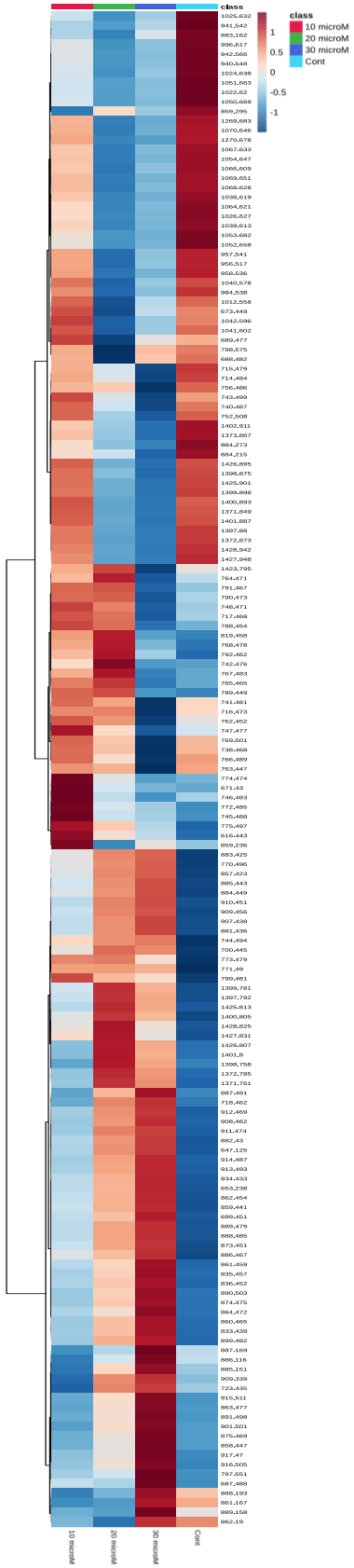
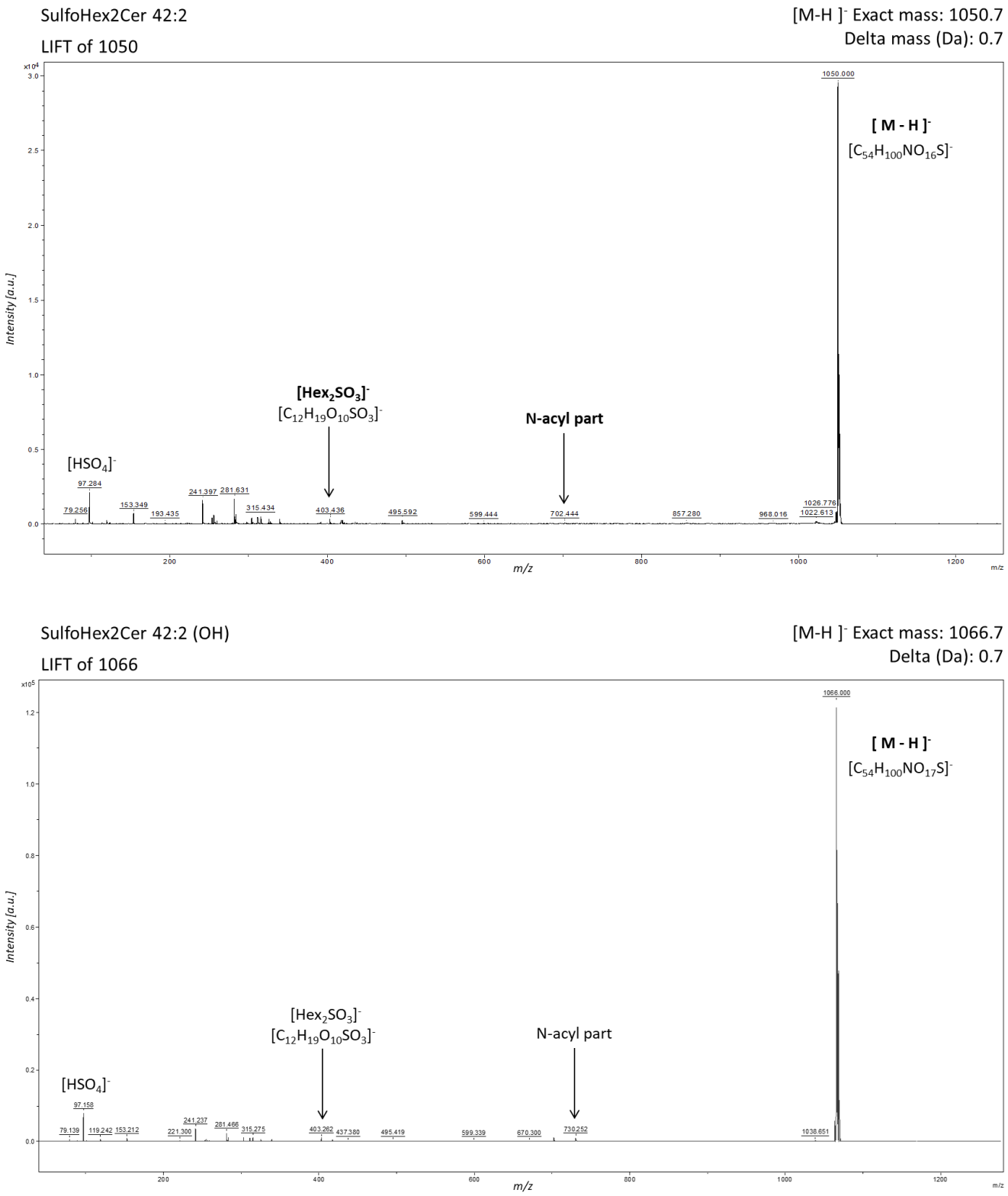
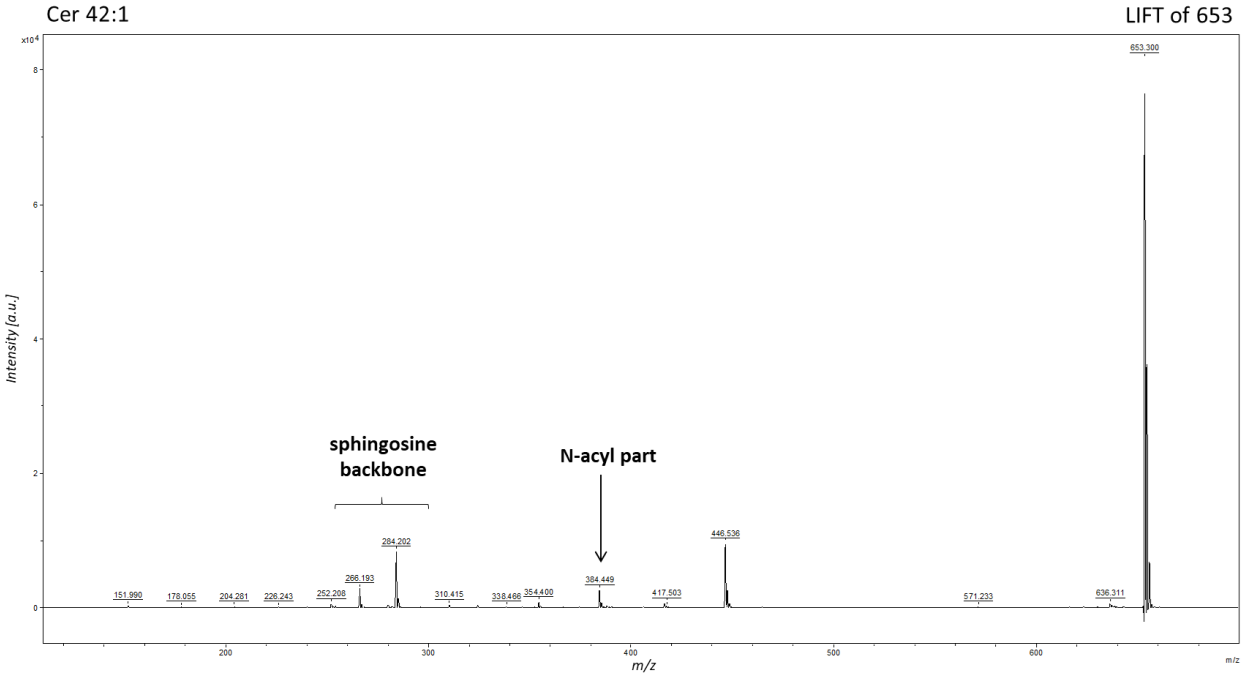


Supplementary Figure 1. Heatmap of MALDI-MS lipid ions in HepG2 cells treated with eliglustat. Peak alignment was performed using SCiLs Lab 2026 Pro software, and the aligned m/z values were imported into MetaboAnalyst v5 for heatmap generation. Columns represent control cells and cells treated with increasing concentrations of eliglustat (10, 20 and 30 µM), whereas rows correspond to the aligned m/z features. Colors indicate row-wise normalized ion abundance (Z-scores), with red and blue representing relatively higher and lower signal intensities, respectively



Supplementary Figure 2. Negative-ion MALDI-MS/MS characterization of SulfoHex2Cer species at m/z 1050 and m/z 1066. Diagnostic fragment ions at m/z 97, 241, and 403, corresponding to sulfate-, sulfated hexose-, and sulfated dihexose-containing fragments, respectively, confirm the sulfoglycosphingolipid nature of both precursors. The m/z 1066 species shows a fragmentation pattern consistent with a hydroxylated fatty acyl chain.



Supplementary Figure 3. Cer42:1 assignment is tentative and based on negative-ion MALDI-MS/MS fragmentation. The product ions at m/z 266 was tentatively assigned as sphingoid base-related fragment. The product ion at m/z 384 may originate from a hydroxylated C24 fatty acyl moiety (Hsu & Turk, 2004, 2008). Additionally, the low-intensity peak observed at m/z 637 likely represents an in-source dehydration product or a minor co-selected, non-hydroxylated form containing a standard C24:0 fatty acid chain.