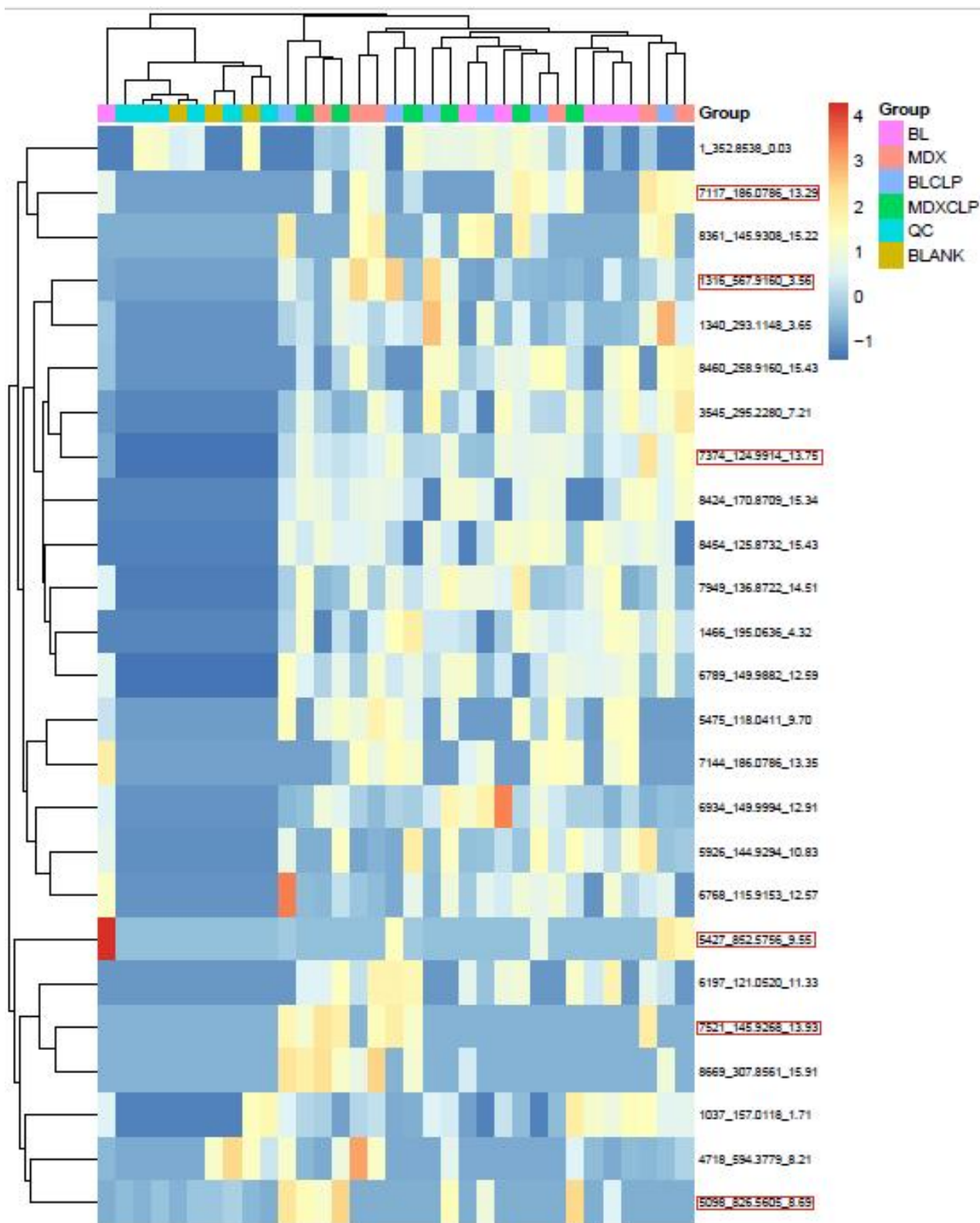




Supplementary Fig. S4 Hierarchical heatmap of the top 25 most significant metabolic features identified by non-parametric Kruskal-Wallis analysis ($P < 0.05$) from LC-MS muscle data acquired in negative ion mode. Feature intensities were z -score normalized to enable relative comparison across samples. Rows represent individual features (m/z -retention time), and columns represent samples colored by experimental group (BL, MDX, BLCLP, MDXCLP, QC, and BLANK). Coordinated abundance patterns and hierarchical clustering highlight systematic metabolic differences among biological groups and confirm analytical stability.