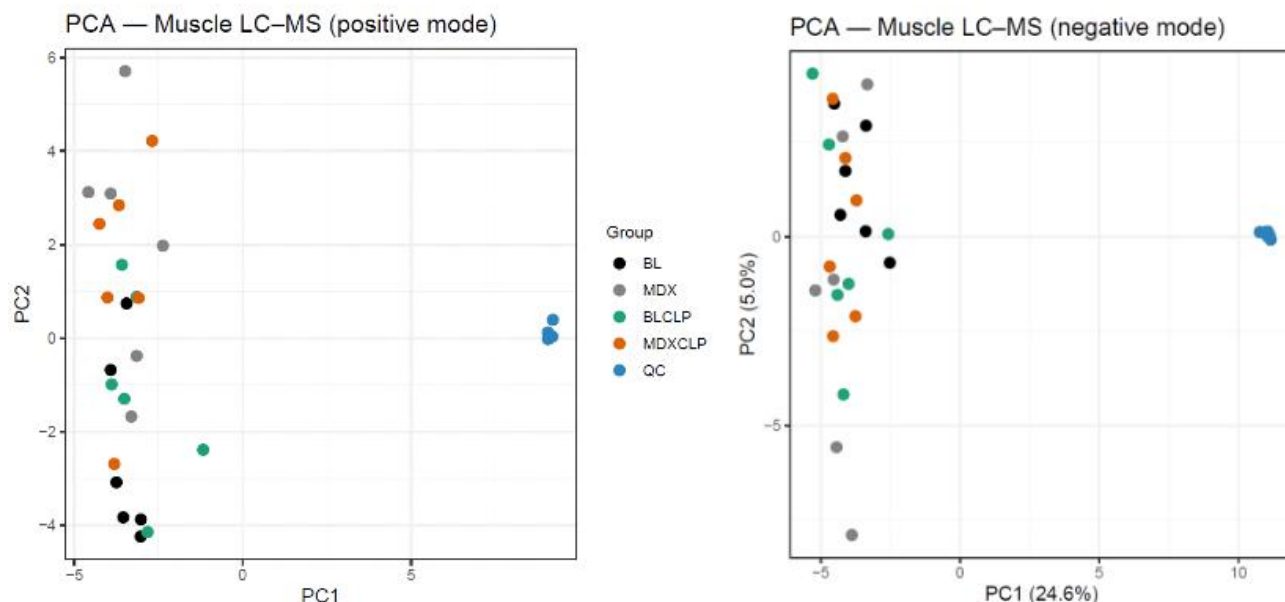




**Supplementary Fig. S2.** Principal component analysis (PCA) of muscle metabolomic profiles obtained by LC-MS (negative ion mode). The scores plot depicts the distribution of samples along the first two principal components (PC1 and PC2), with PC1 explaining 24.6% of the total variance and PC2 explaining 5.0%. BLANK samples were excluded, while QC samples were retained and clustered consistently, indicating good instrumental reproducibility and analytical stability. Samples are color-coded according to experimental groups: BL (black), MDX (gray), BLCLP (green), MDXCLP (orange), and QC (blue). The biological groups exhibit distinct distribution patterns and a tendency toward separation in the multivariate space, suggesting global metabolic differences associated with the MDX (MDX) genotype and the CLP290 condition.