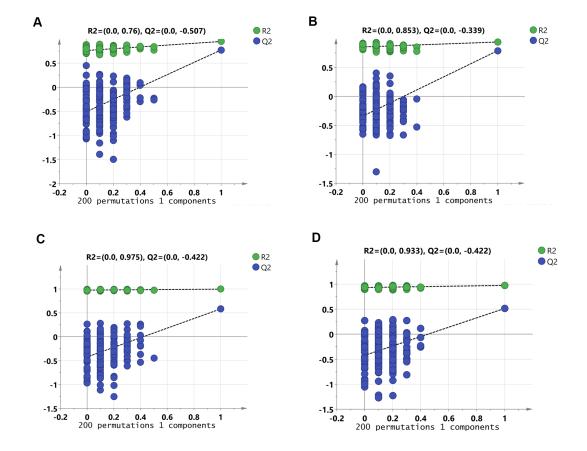
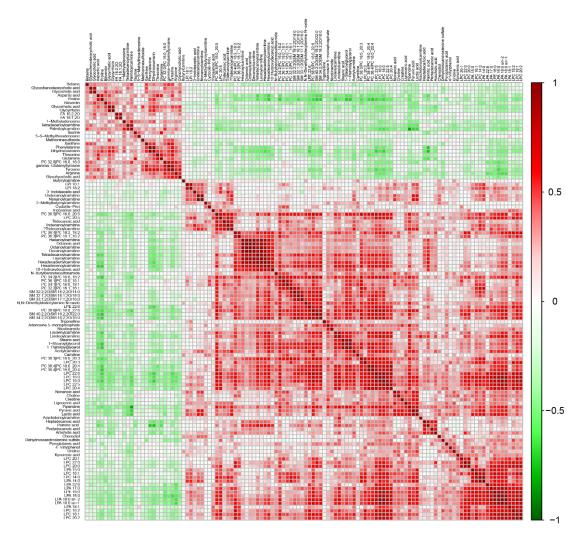


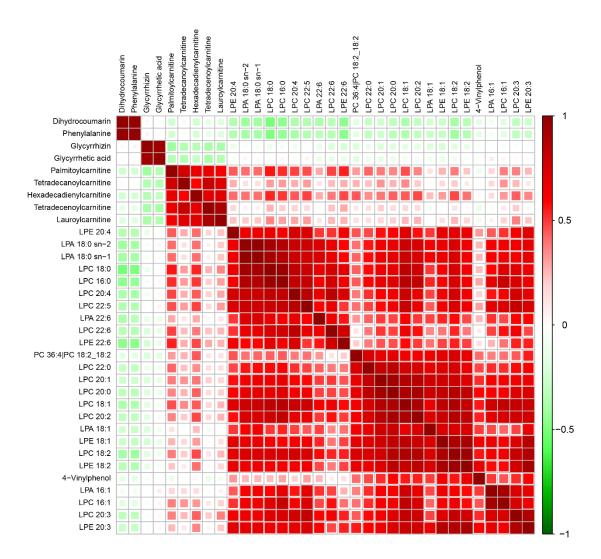
Supplemental Figure 1. The PCA plot for healthy, pre-TACE and post-TACE groups as well as QC. (A) The positive ion mode; (B) The negative ion mode. $R^2X=0.679$ for positive ion mode and $R^2X=0.511$ for negative ion mode. $R^2X>0.5$ indicates reliable model quality.



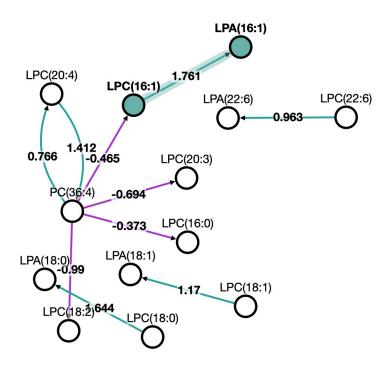
Supplemental Figure 2. The permutation tests for OPLS-DA model. (A, B) The permutation tests for positive ion and negative ion between healthy and pre-TACE groups, respectively. (C, D) The permutation tests for positive ion and negative ion between pre-TACE and post-TACE groups, respectively.



Supplemental Figure 3. Correlation matrix of different metabolites in healthy and pre-TACE groups. The Pearson Correlation was conducted for the quantitative information of these metabolites.



Supplemental Figure 4. Correlation matrix of different metabolites in pre-TACE and pro-TACE groups. The Pearson Correlation was conducted for the quantitative information of these metabolites.



Supplemental Figure 5. Lipid network graphs exported from BioPAN from the 34 differential metabolites between pre-TACE and post-TACR groups. Reactions with a positive Z score have green arrows while negative Z scores are colored purple