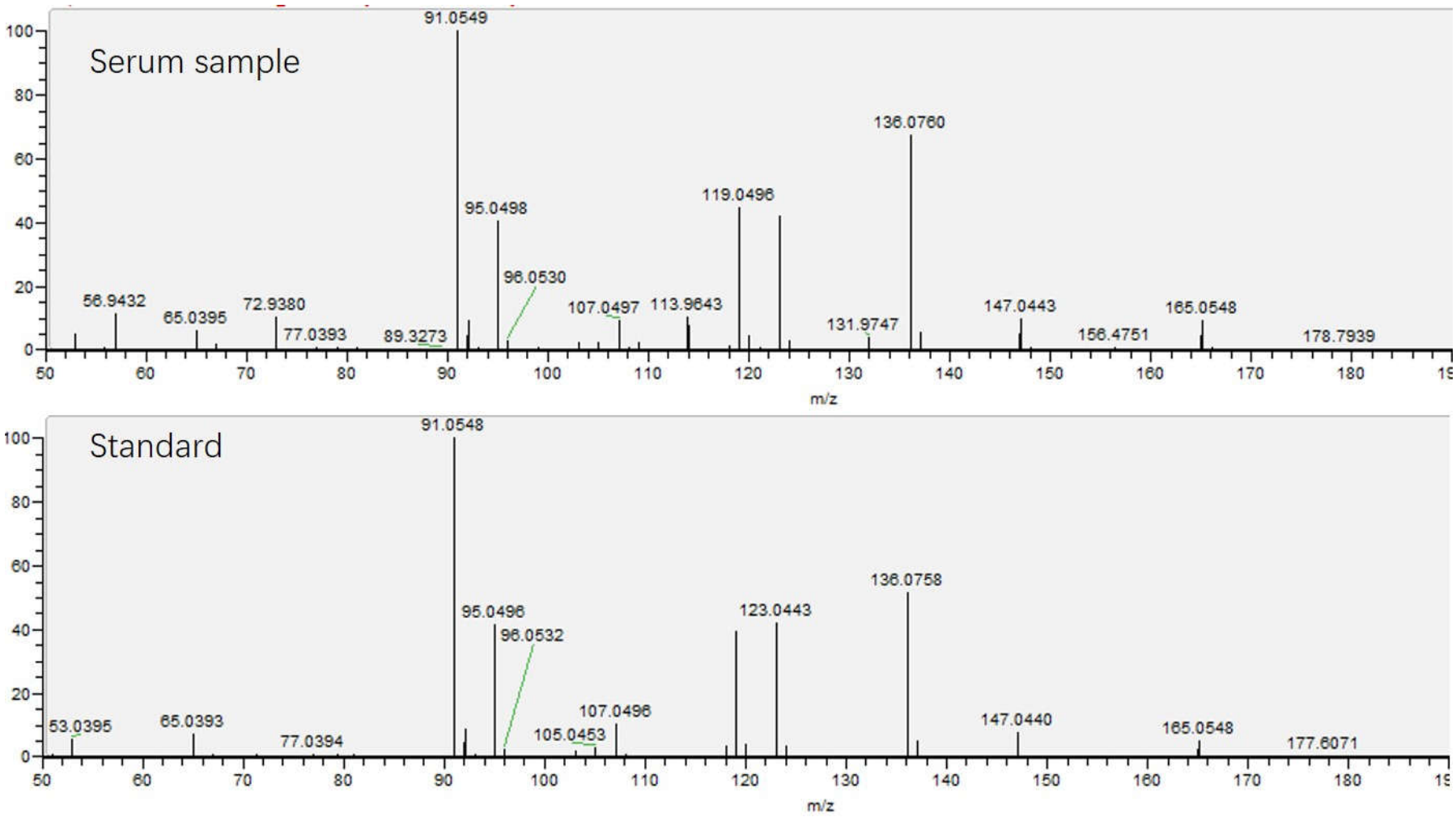
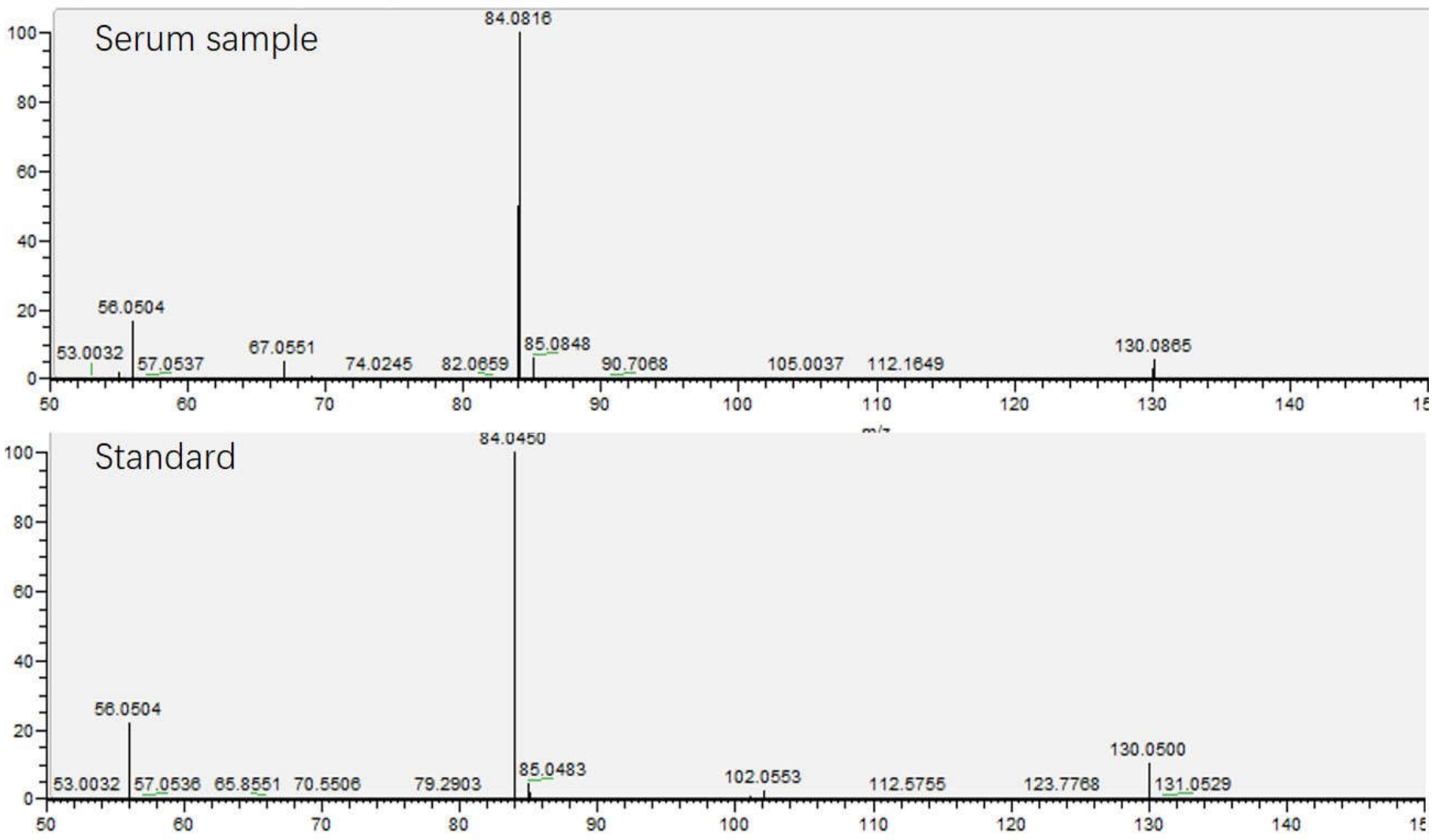
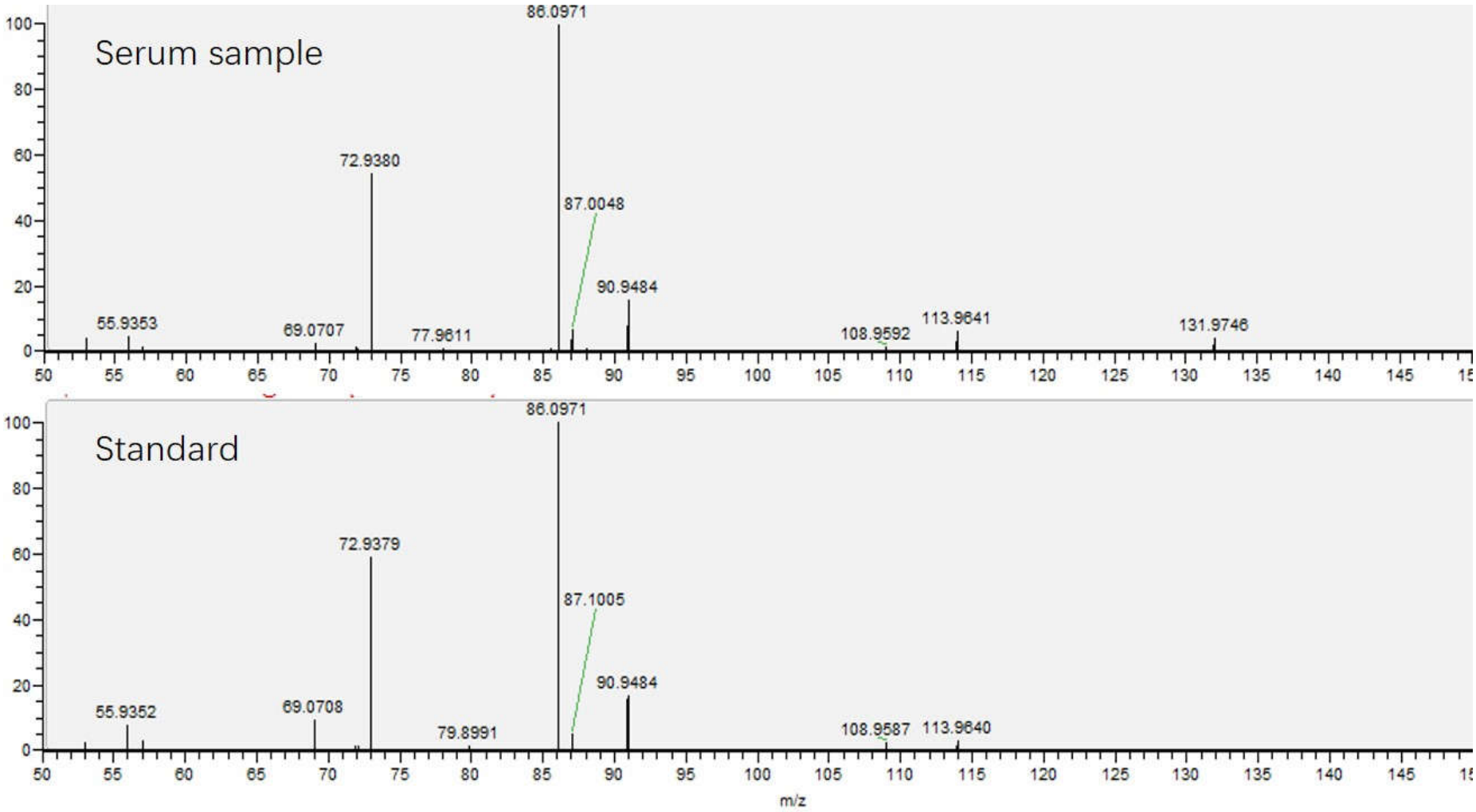


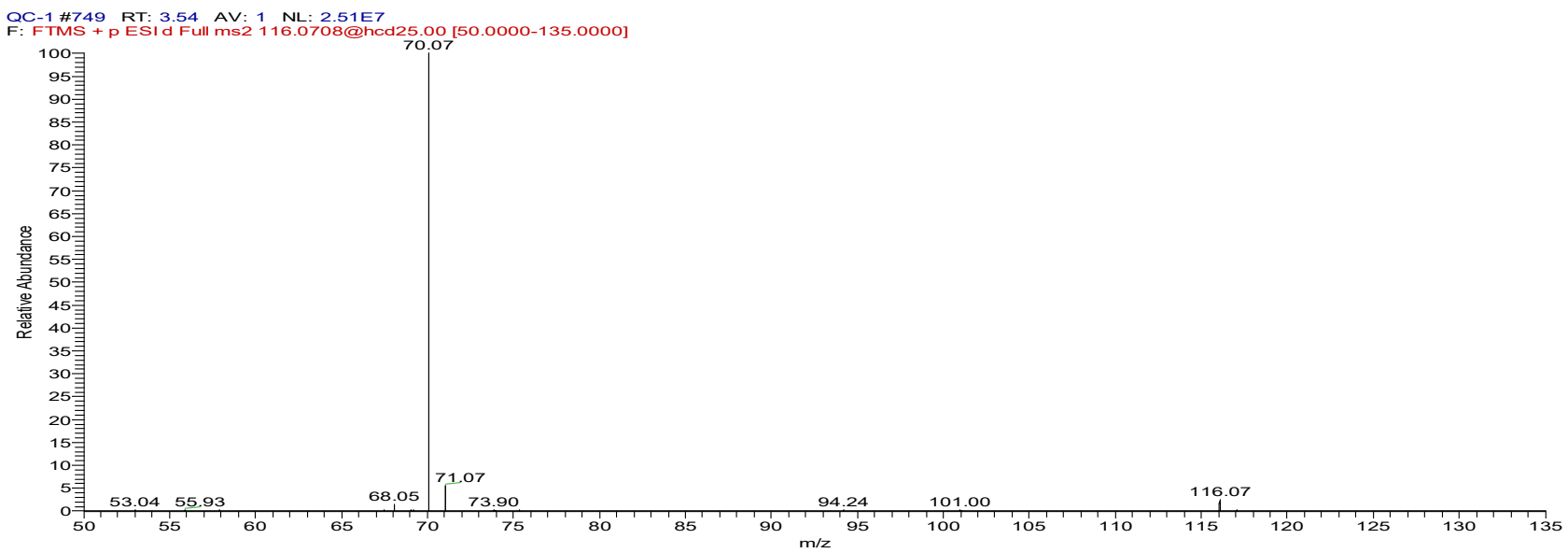
Supplementary Figure 1. MS/MS identification of tyrosine.



Supplementary Figure 2. MS/MS identification of glutamine.



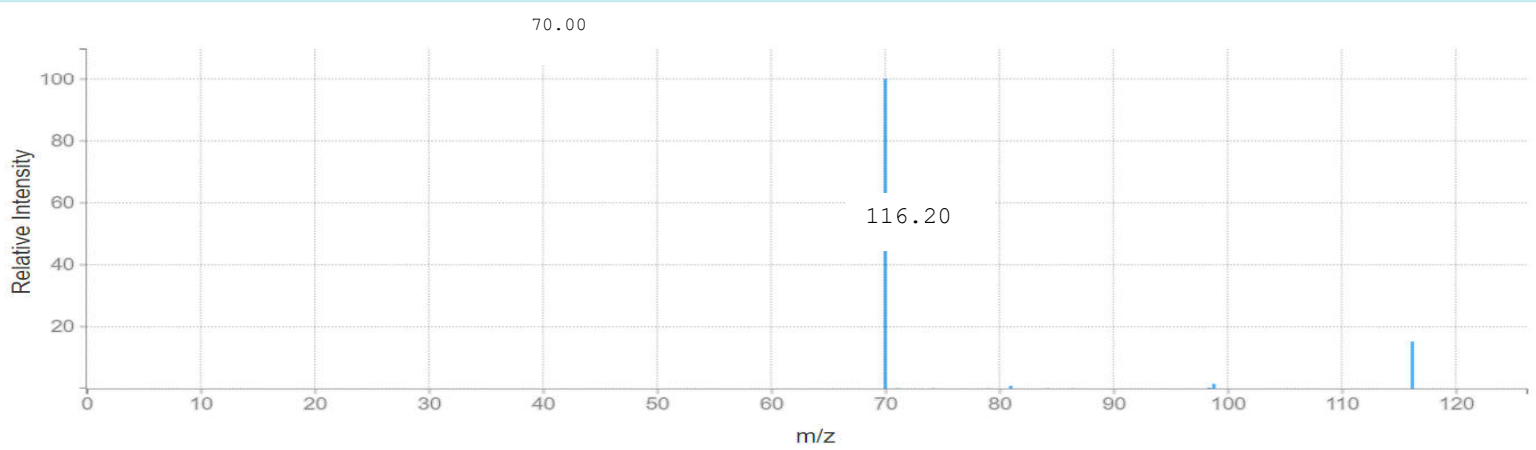
Supplementary Figure 3. MS/MS identification of leucine.



Spectrum Details

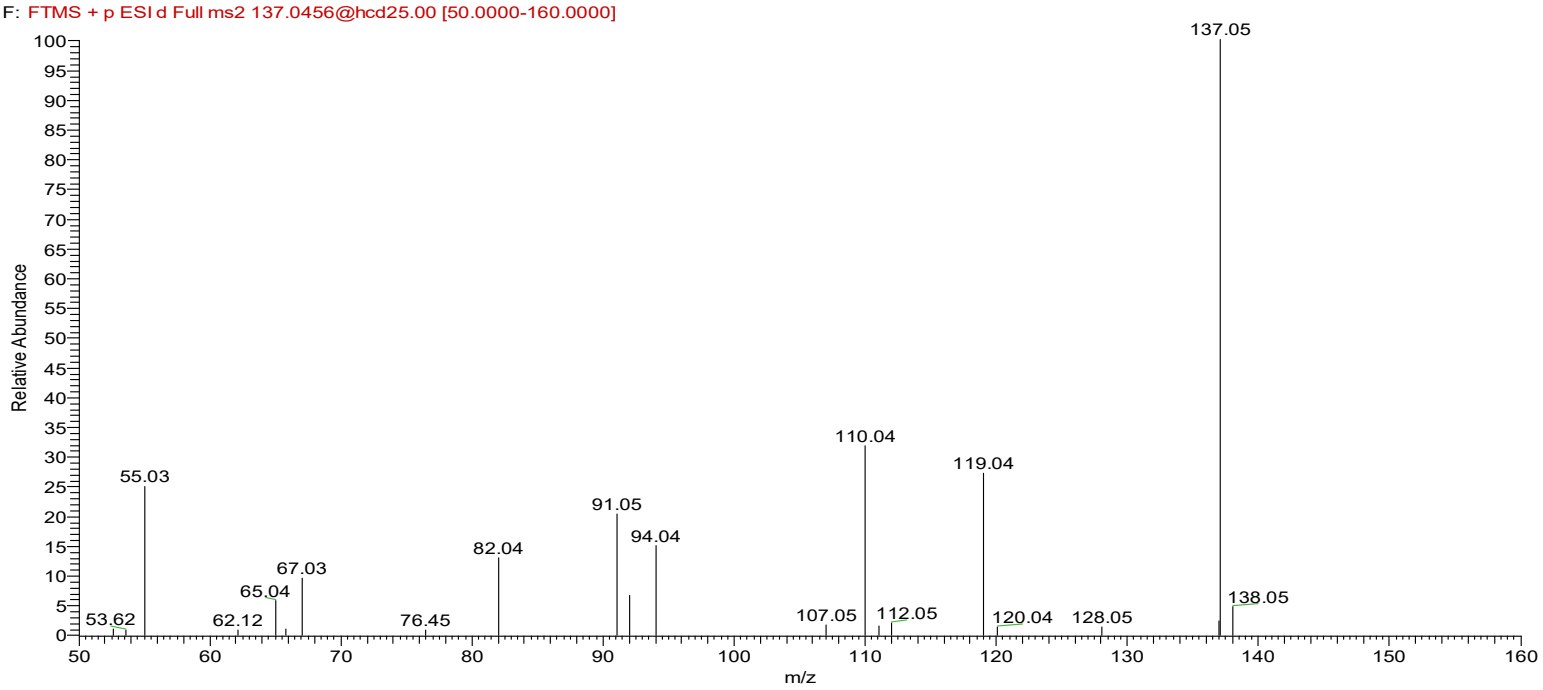
HMDB ID: HMDB0000162
Compound name: L-Proline
Spectrum type: LC-MS/MS Spectrum - LC-ESI-QQ (API3000, Applied Biosystems) 20V, Positive
Splash Key: splash10-00di-9100000000-8169367f5127c57fae12 View in MoNA

Spectrum View



http://www.hmdb.ca/spectra/ms_ms/3246

Supplementary Figure 4. MS/MS identification of proline.

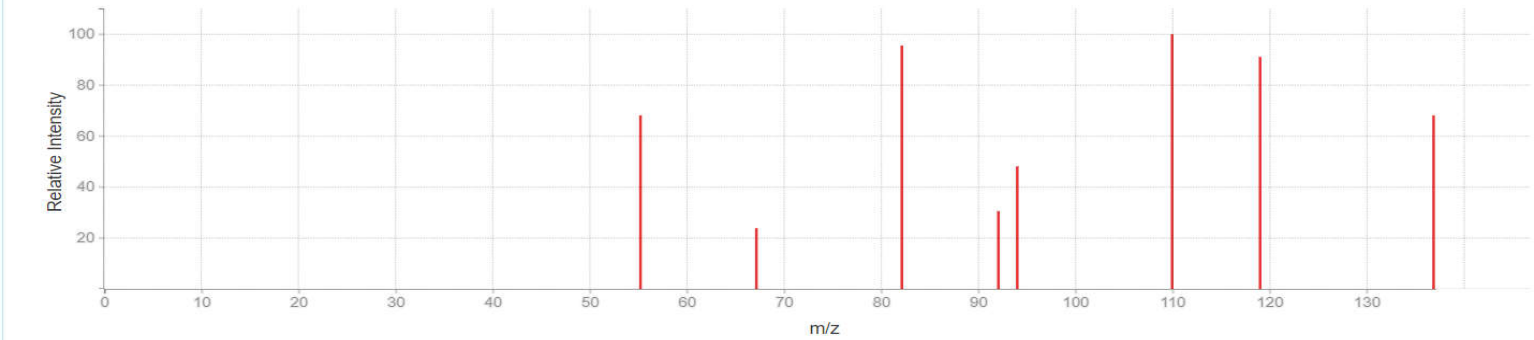


Spectrum Details

HMDB ID: HMDB0000157
Compound name: Hypoxanthine
Spectrum type: LC-MS/MS Spectrum - Quattro_QQQ 25V, Positive (Annotated)
Splash Key: splash10-0api-9800000000-fb4e3cccb7d27d119feb View in MoNA

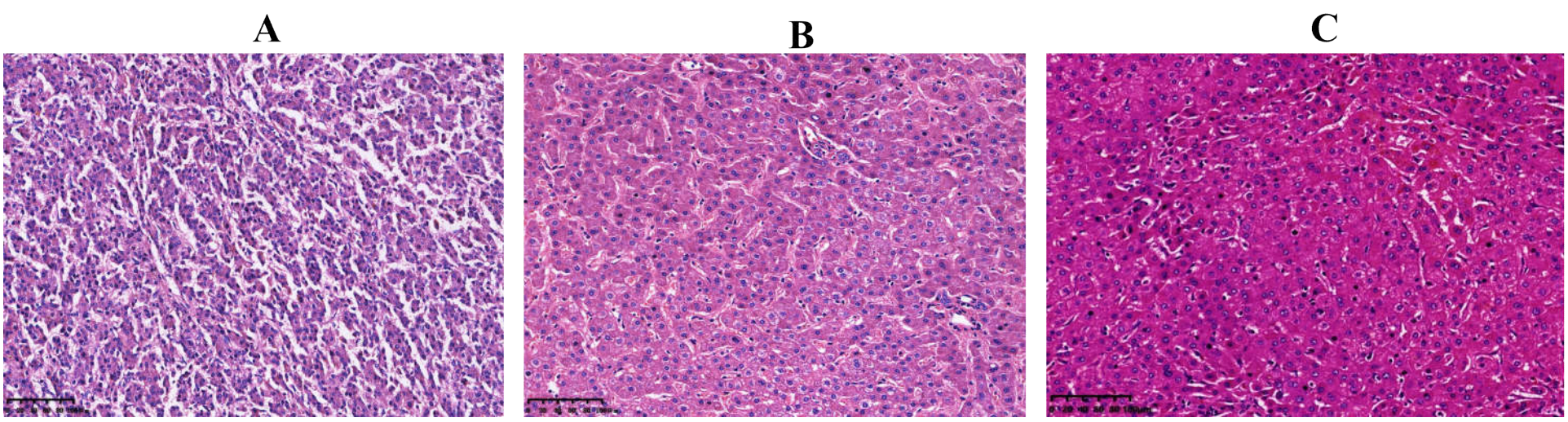
Spectrum View

Image Viewer



http://www.hmdb.ca/spectra/ms_ms/243

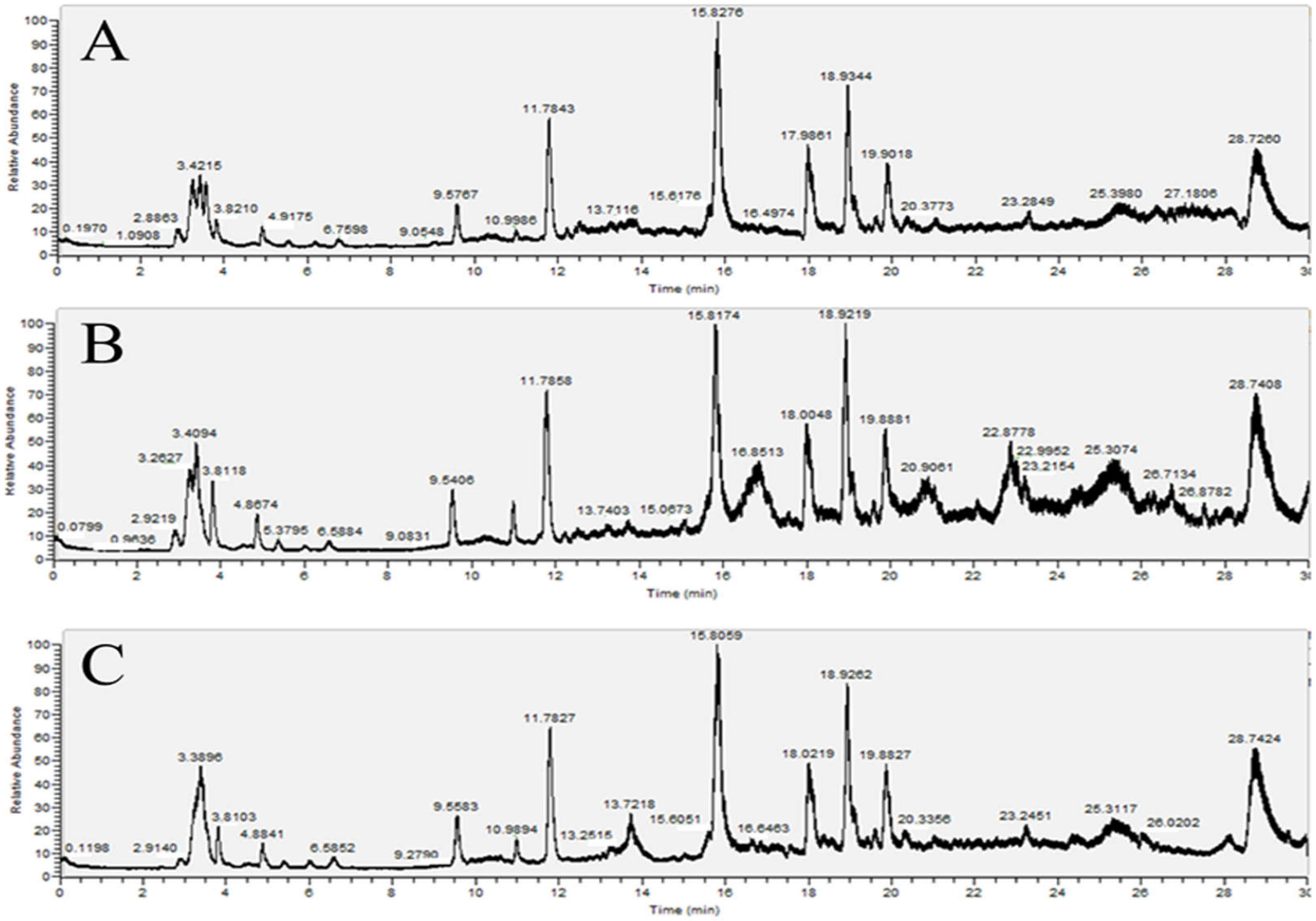
Supplementary Figure 5. MS/MS identification of hydroxypurine.



Supplementary Figure 6. Histopathological examination (HE staining).

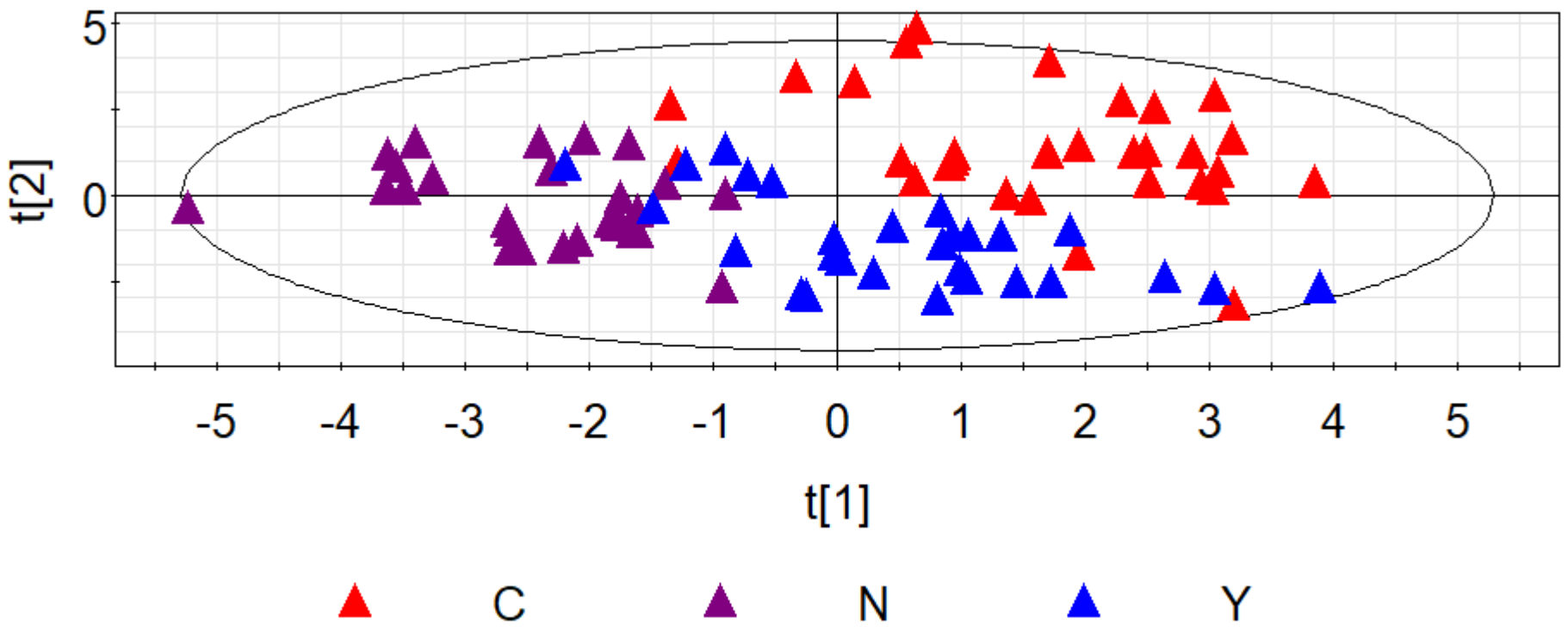
(A) Hepatocellular Carcinoma tissues. The tumor cells are arranged in the form of cord and flake, and the size of the tumor cells is different. The multinuclear giant cells are visible, the nucleus is deeply dyed, the nuclear division is increasing, some of the tumor cells are rich in cytoplasm and red dye, and the nuclei are round or oval. (B) Cirrhosis tissues. The structure of normal hepatic lobule is replaced by pseudolobuli. The pseudolobuli is composed of regenerated hepatocyte nodules and remnant hepatic lobules, containing two or three central veins or a central vein at the edge. The hepatocytes of the pseudolobuli were denatured or even necrotic in varying degrees. The area of the portal area is widened because of connective

tissue hyperplasia, with varying degrees of infiltration of inflammatory cells and small bile duct like structures (pseudo bile ducts). (C) Hepatic tissues of health controls.

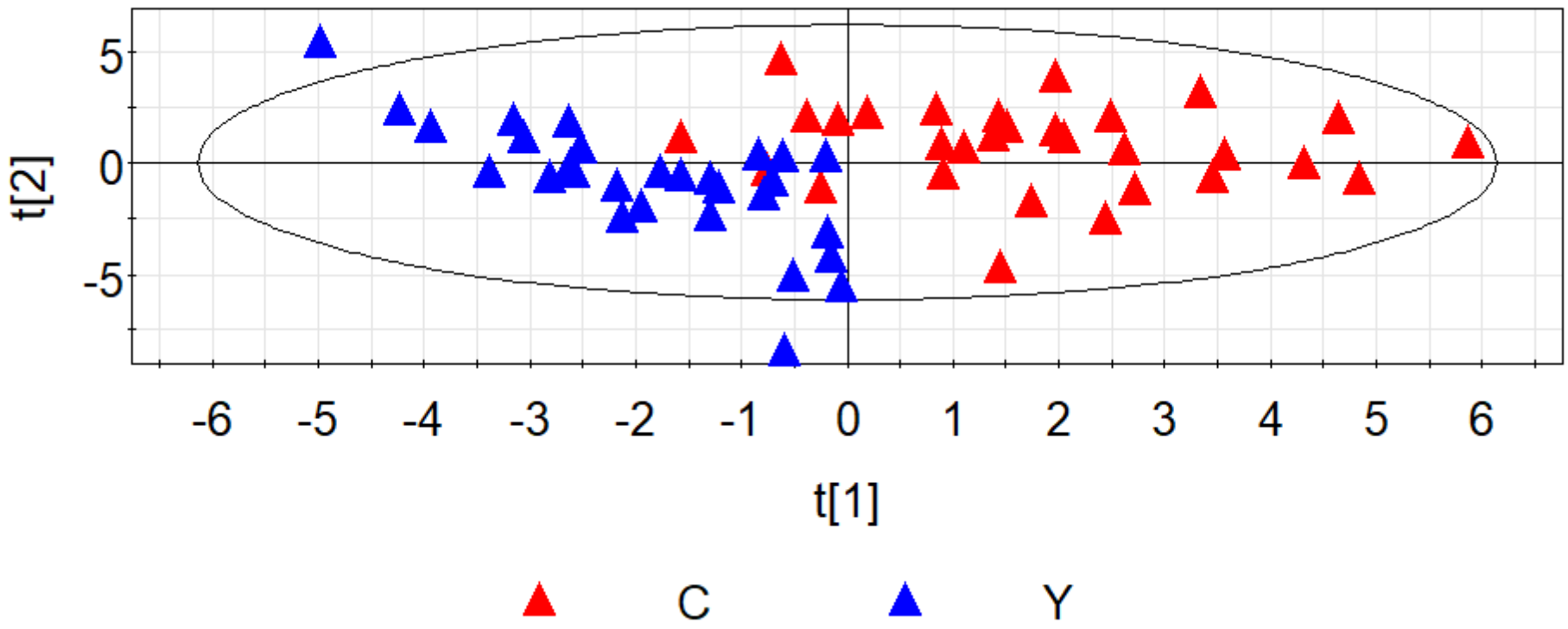


Supplementary Figure 7. Base peak intensity chromatogram of serum from HCC, cirrhosis and health controls.

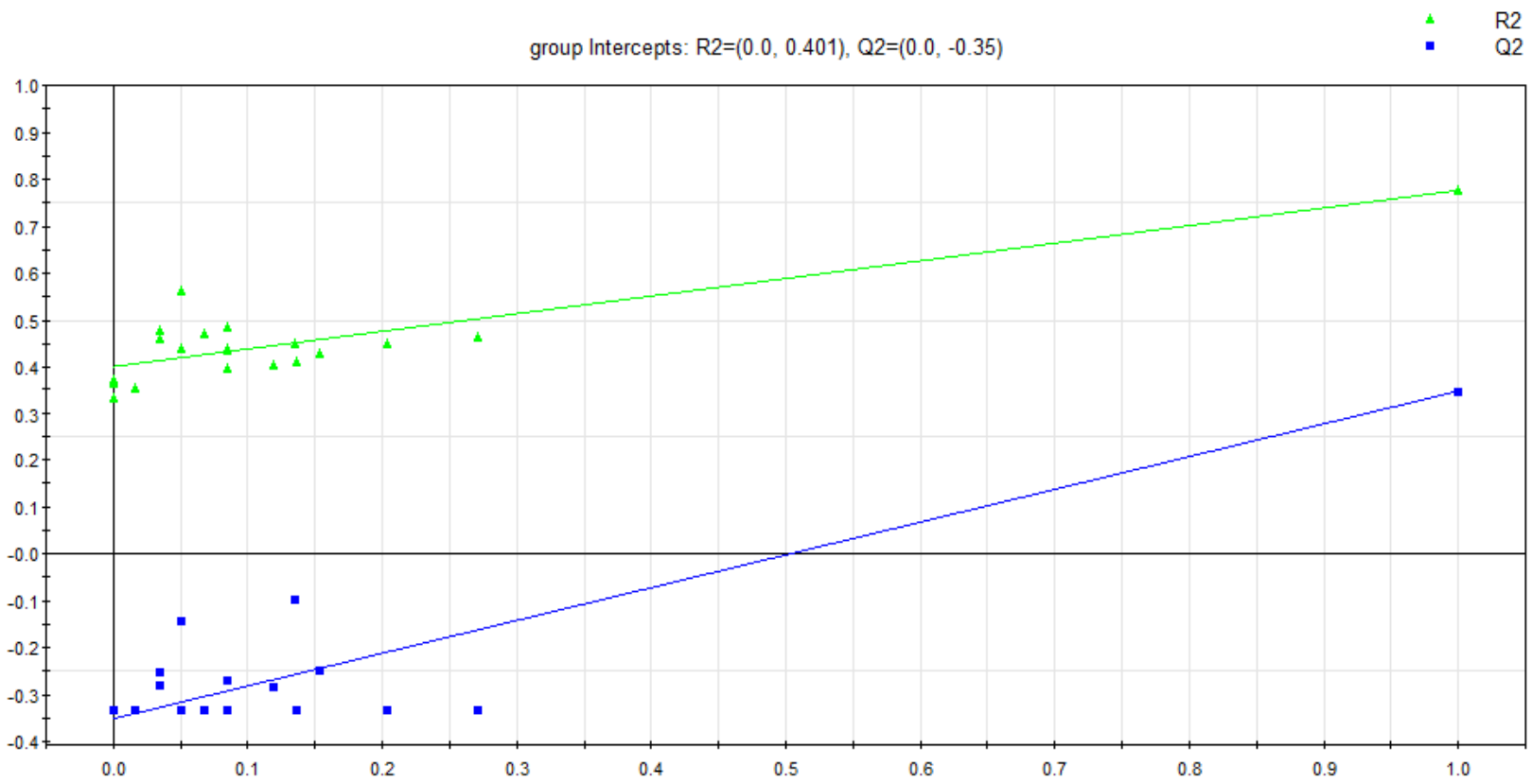
(A) HCC, (B) cirrhosis, (C) Health Controls.



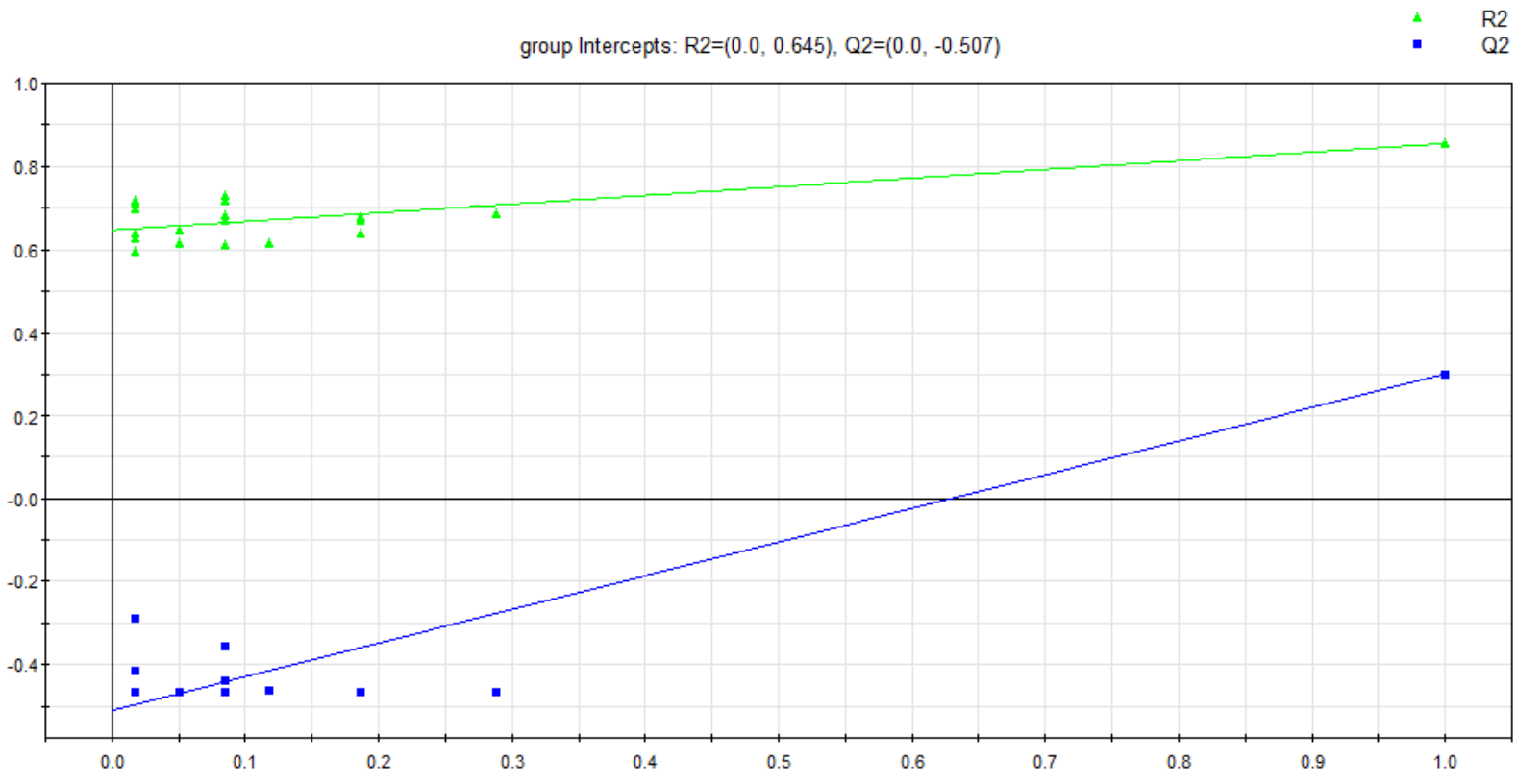
Supplementary Figure 8. The PLS-DA score plot of all the three groups (HCC (C group) and cirrhosis groups (Y group), and health controls (N group). R2X=0.258cum, R2Y=0.777cum, Q2=0.349cum.



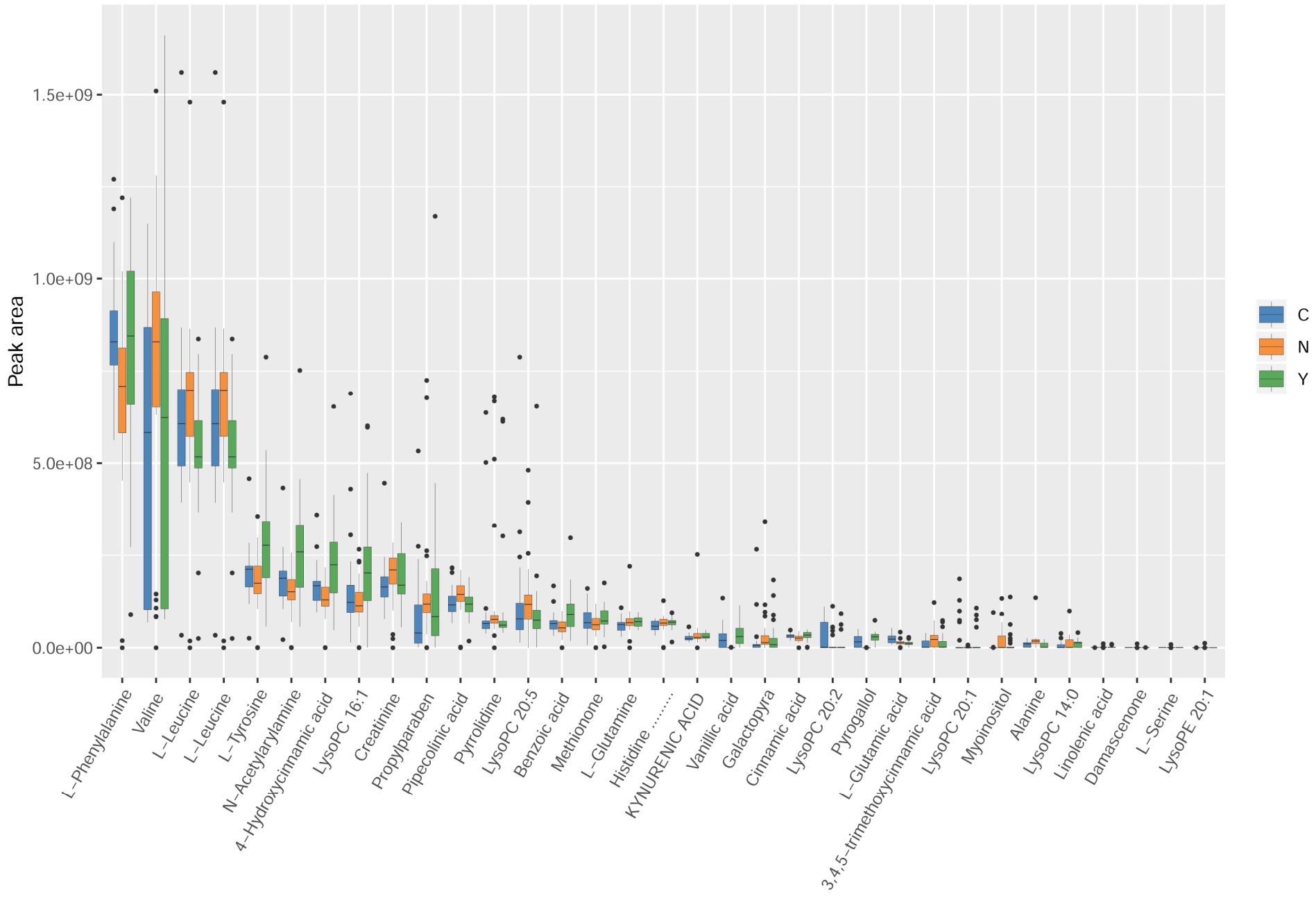
Supplementary Figure 9. The PLS-DA score plot of C group and Y group. R2X=0.345cum, R2Y=0.853cum, Q2=0.301cum.



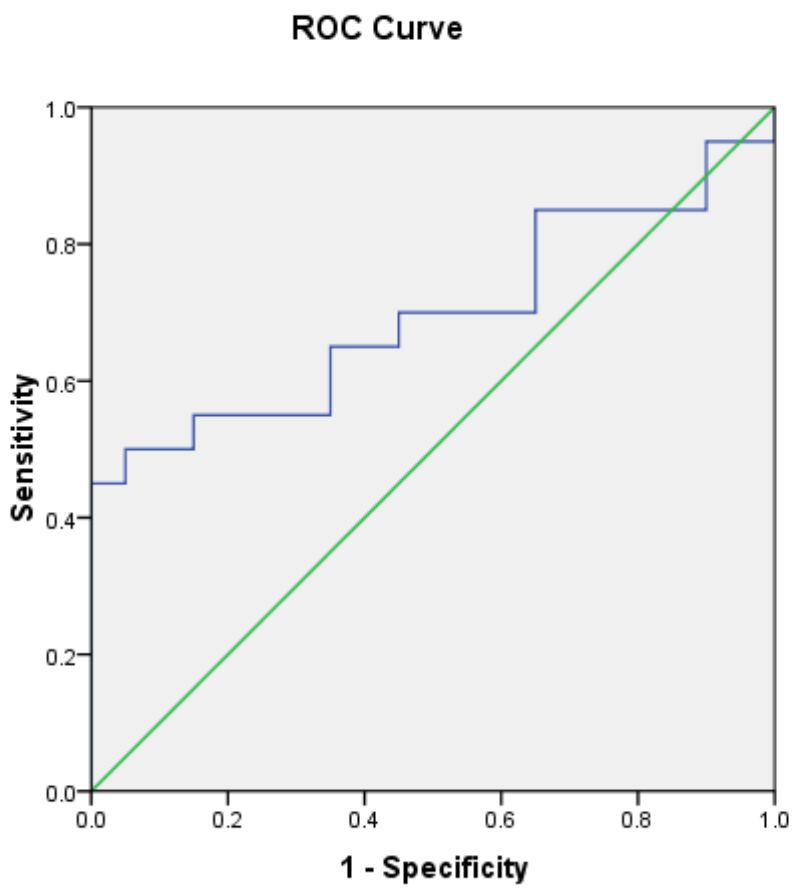
Supplementary Figure 10. Cross validation of PLS-DA score plot of all the three groups.



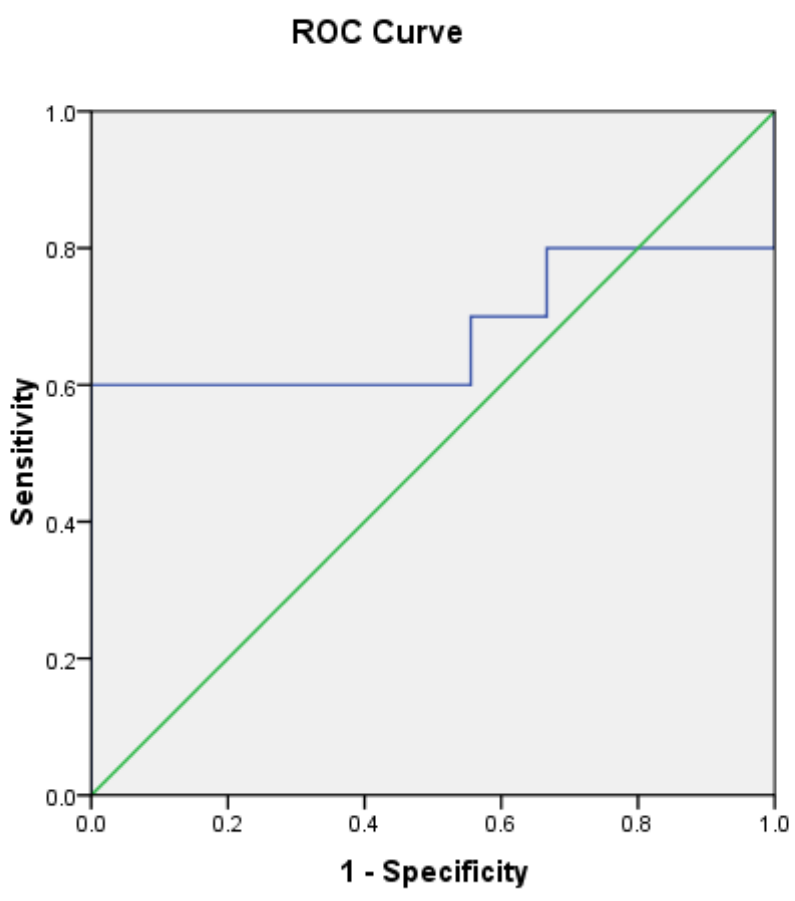
Supplementary Figure 11. Cross validation of PLS-DA score plot of C group and Y group.



Supplementary Figure 12. **The relative abundance of significantly altered metabolites in HCC, cirrhosis and health controls.**



Supplementary Figure 13. ROC of AFP in discrimination of HCC and cirrhosis patients (Training samples). Area Under Curve were 0.69 (95% CI: 0.52-0.86)



Supplementary Figure 14. ROC of AFP in discrimination of HCC and cirrhosis patients (Validation samples). Area Under Curve were 0.68 (95% CI: 0.41-0.94)