

Figure S1. Liquid chromatography-tandem mass spectrometry diagrams. (A) Negative ion mode. (B) Positive ion mode. QC, quality control; CN, negative mode; CP, positive mode.

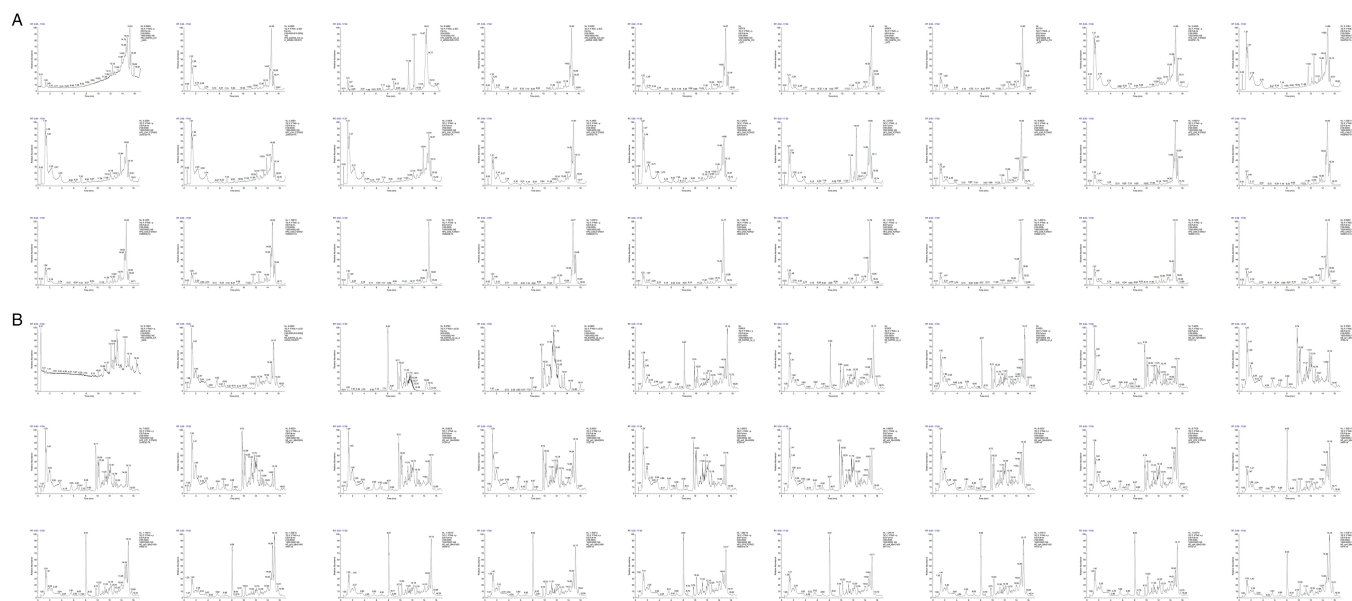




Figure S3. Hierarchical clustering analysis of significantly different metabolites. (A) Positive ion mode. (B) Negative ion mode. PKC, plain normoxia group; HKT, plateau hypoxia group.

A



B

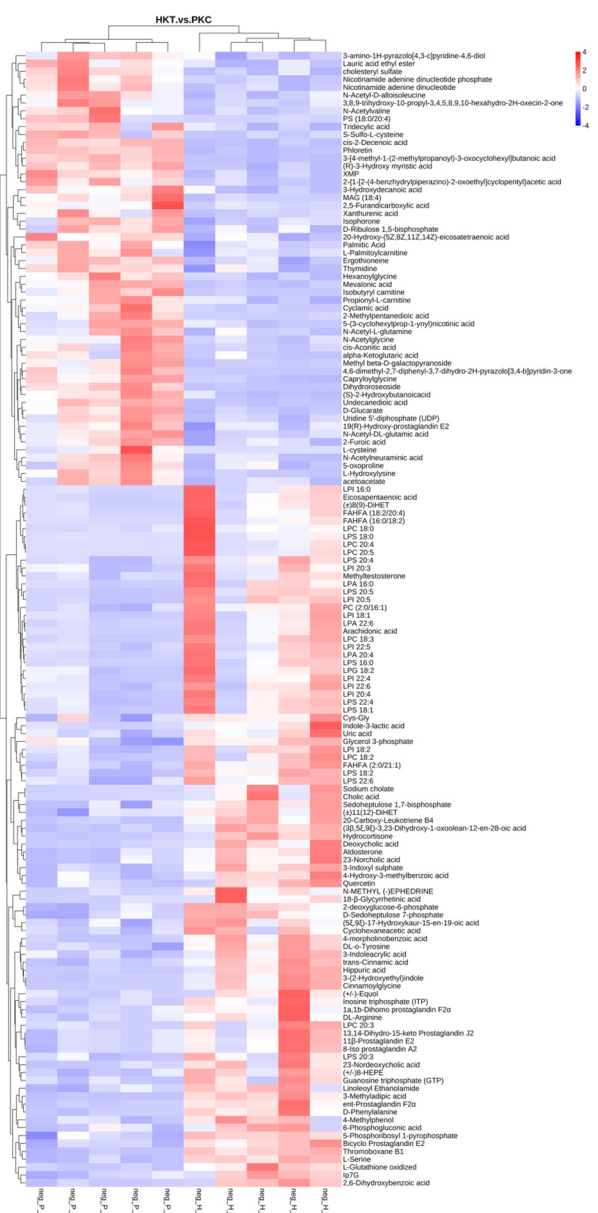


Figure S4. HMDB classification notes of significantly different metabolites. (A) Positive ion mode. (B) Negative ion mode. HMDB, Human Metabolome Database.

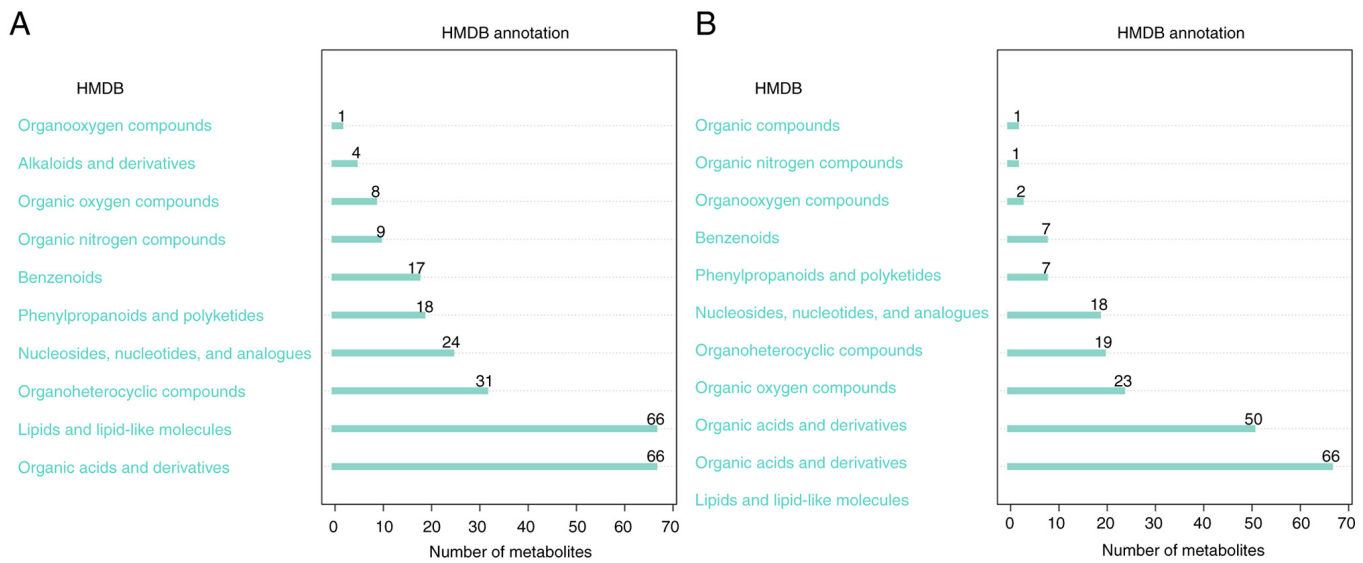


Figure S5. Lipidmaps classification notes of significantly different metabolites. (A) Positive ion mode. (B) Negative ion mode.

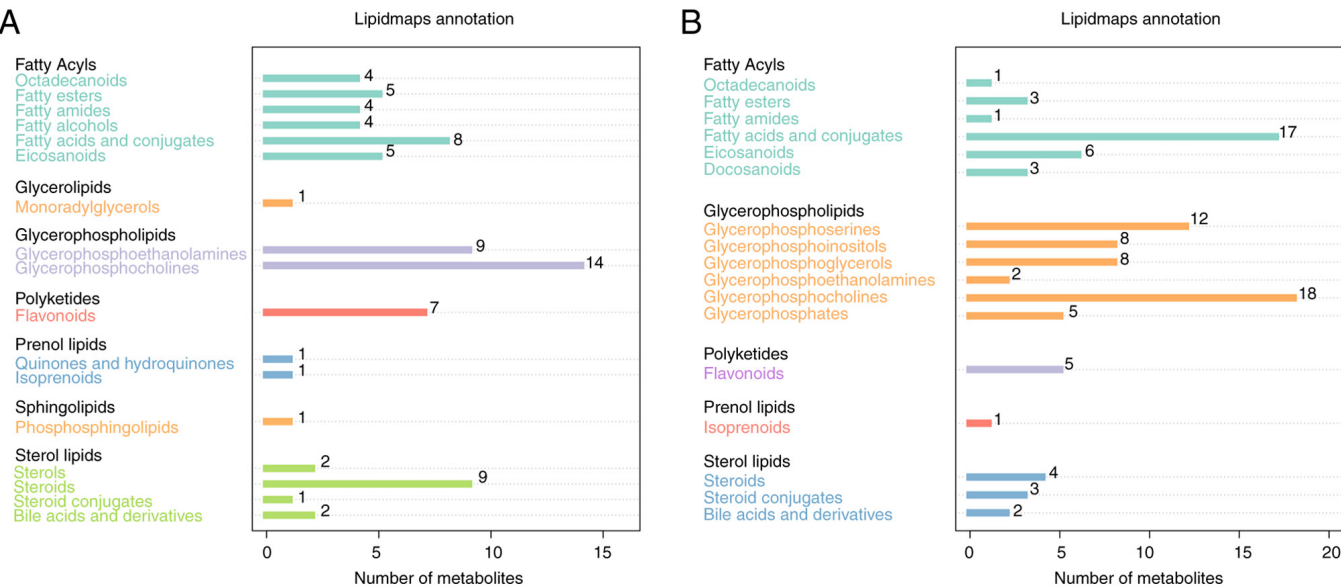


Figure S6. Pearson's correlation coefficient of metabolites involved in amino acid synthesis and nucleotide synthesis.

