Supplementary file 1

Similar metabolic phenotype between samples with high BMI and samples without high BMI

BMI usually changes the urine metabolomic signature. And in many cases, people with high BMI can appear as an outlier during utilizing potential urine biomarkers. In this study, the BMI of include patients ranged from 15.4 to 31.9. But there were only 12 include patients with high BMI (BMI>28.0). To find out whether or not the high BMI could significantly affect the urine metabolomic signature, we firstly used samples without high BMI to construct OPLS-DA model (Figure S1A), and then used the built model to predict the samples with high BMI (Figure S1B). The results showed that the metabolic phenotype was similar between samples with high BMI and samples without high BMI. However, limited by the small sample size, these findings were needed future studies to validate.

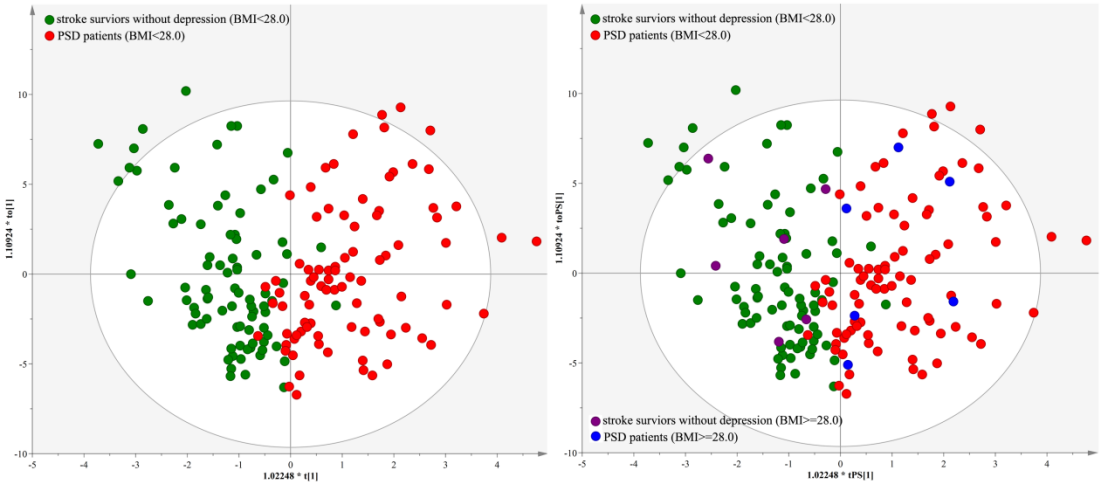

Figure S1 Similar metabolic phenotype between samples with high BMI and samples without high BMI: A) OPLS-DA model showed an obvious separation between PSD patients (BMI<28.0) and stroke survivors without depression (BMI<28.0). B) T-predicted scatter plot from the OPLS-DA model showed that the samples with BMI>=28.0 could be correctly predicted.

Not significantly changed urinary metabolites

In total, 59 urinary metabolites were used to build OPLS-DA model. The built model showed that PSD patients and stroke survivors without depression could be correctly separated with little overlap. Urinary metabolites with VIP>1 in the OPLS-DA model as well as the adjusted p-value<0.05 were selected as differential urinary metabolites responsible for subjects classification. Finally, we identified 12 differential urinary metabolites between PSD patients and those without depression (see Table 2). The urinary metabolites that were not significantly different between PSD patients and those without depression were: β-aminoisobutyric acid, β-alanine, α-hydroxyisobutyric acid, vanillic acid, valine,

threonine, threitol, sucrose, sorbitol, ribose, ribitol, quinolinic acid, pyruvic acid, pseudo uridine, phenylalanine, p-cresol, N-acetyl-D-glucosamine, methylmalonic acid , mannitol, leucine, indoxyl sulphate, homovanillic acid, hippuric acid, Fumaric acid, cysteine, arabitol, aminomalonic acid, aminoethanol, adipic acid, 4-hyroxybenzoic acid, 3-hydroxyisobutyric acid, 3-hydroxyhippuric acid, 2-ketoglutaric acid, 2,4-dihydroxypyrimidine, 5-hydroxyhexanoic acid, (R*,S*)2,3-dihydroxybutanoic acid, 2,4-dihydroxybutyric acid, 1-methylinosine, 2-ethyl-3-hydroxypropionic acid, alanine, citric acid, glycine, 2-methyl-3-hydroxybutyric acid, 3,4-dihydroxybutyric acid, 3-hydroxyphenylacetic acid, hypoxanthine and methylsuccinic acid.

Representative extracted ion chromatograms

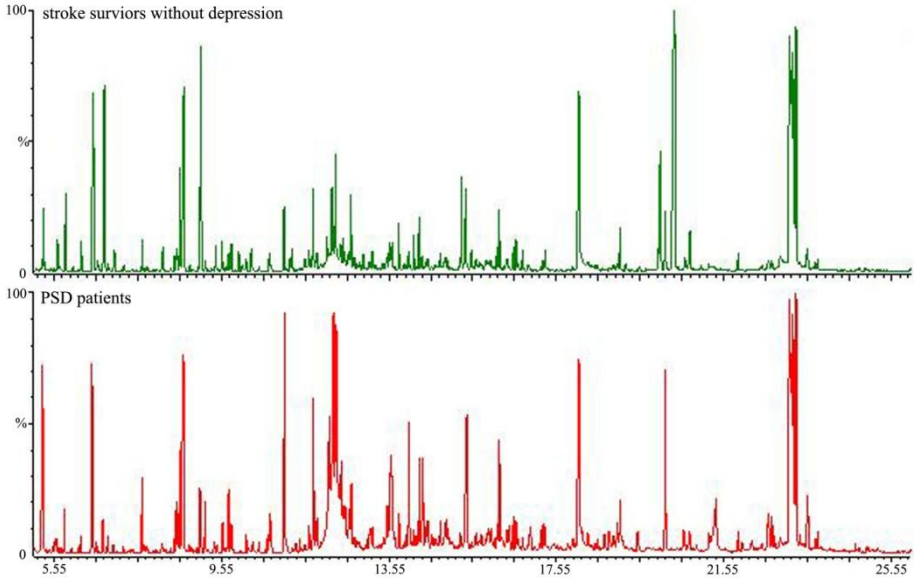

Figure S2 Representative extracted ion chromatograms between the two groups