

Supplement Figures/Tables

Mixed Venous Metabolites

Metabolite	KEGG ID
Betaine	C00719
Malonate	C00383
Histidine	C00135
Lactate	C00186
3-Hydroxyisobutyrate	C01089
Hypoxanthine	C00262
Succinate	C00042
Phenylalanine	C00079
Tyrosine	C00082
Isoleucine	C00407
2-Oxoisocaproate	C00233
Methionine	C00073
Ornithine	C00077
Valine	C00183
Serine	C00065
Glutamine	C00025
AMP	C00020
Alanine	C00041
Creatine	C00300
Glutamate	C00064
Glutathione	C00051
IMP	C00130
Proline	C00148
Threonine	C00188
Trimethylamine N-oxide	C01104
<i>Choline</i>	C00114
<i>ATP</i>	C00002
<i>Glycine</i>	C00037
ADP	C00008
Glucose	C00031
Formate	C00058
Pyruvate	C00022
Taurine	C00245
Betaine	C00719

Urine Metabolites

Metabolite	KEGG ID
2-Hydroxyisobutyrate	N/A
3-I Oxyisulfate	N/A
N-Isovaleroylglycine	N/A
Lactate	C00186
Trimethylamine	C00565
Isobutyrate	C02632
Trimethylamine N-oxide	C01104
Xanthosine	C01762
Glucose	C00031
Trigonelline	C01004
2-Oxoisocaproate	C00233
Methylamine	C00218
Taurine	C00245
Glycine	C00037
Betaine	C00719
Urea	C00086
3-Hydroxyisobutyrate	C01188
N-Phenylacetylglycine	C05598
Hippurate	C01586
Formate	C00058

Table 2a-b: List of all metabolites studied in this protocol, along with their KEGG IDs (Kyoto Encyclopedia of Genes and Genomes), from both **(a)** Mixed Venous (MV) blood (n=34) and **(b)** urine (n=20) sources.

Supplemental Metabolic Pathway Relationships of MV RP/Metabolite Correlates

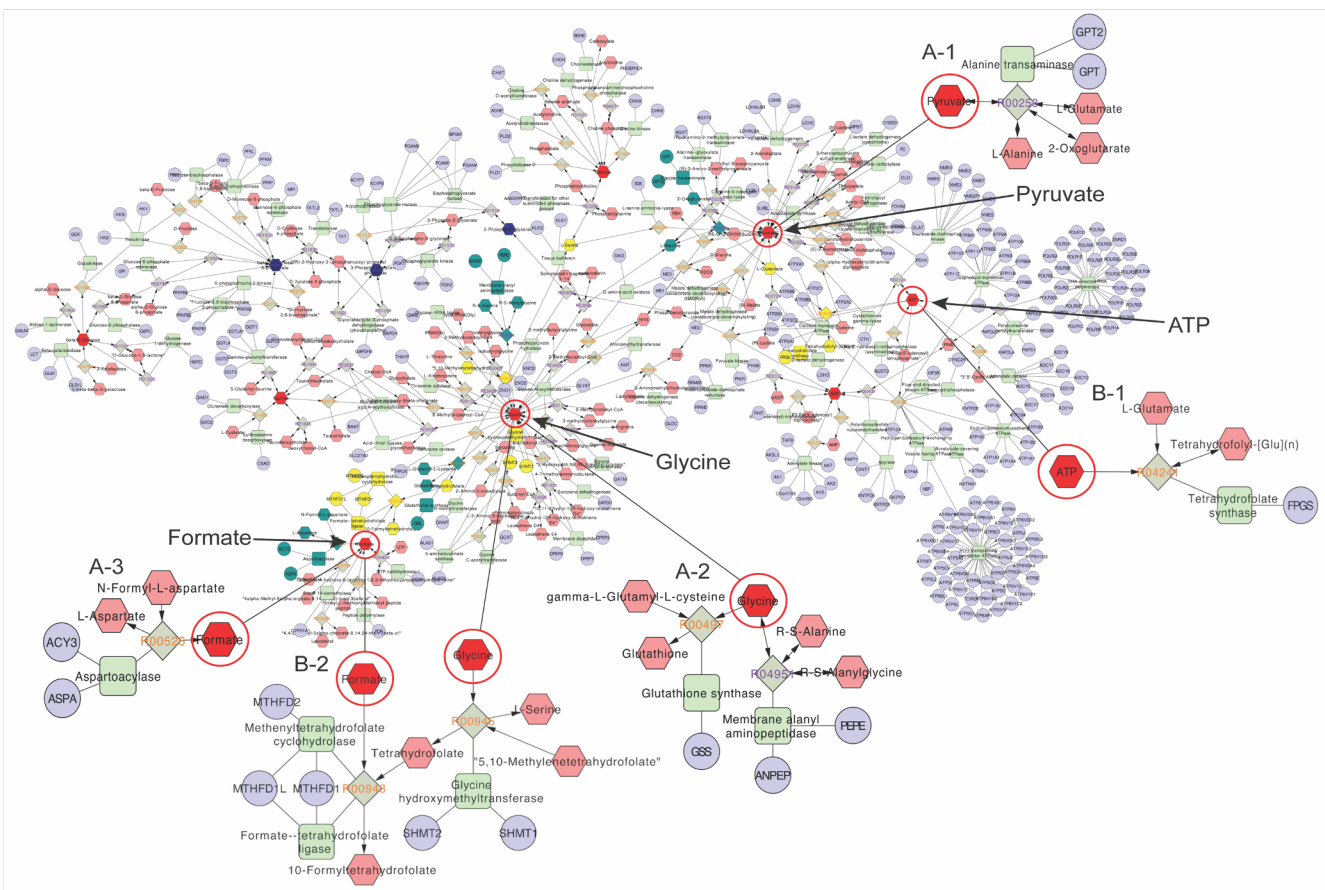


Figure 4 - The urea cycle and metabolism of arginine, proline, glutamate, aspartate, and asparagine pathway, as well as vitamin B9 (folate) metabolism with highlighted metabolites identified by the MV LASSO regression model. The KEGG IDs of meaningful MV metabolites were uploaded into Metscape (<http://metscape.ncibi.org/>), and the compound-reaction-enzyme-gene function resulted the two connected networks (center) in which the glycolysis and gluconeogenesis pathway was common to both, as presented in Figure 3 in the main manuscript. The subnetworks of the urea cycle (dark green highlighted nodes) and vitamin B9 (yellow highlighted nodes) are broadly distributed in the parent network. Subnetworks (A1-3) are those associated with the urea cycle and metabolism of arginine, proline, glutamate, aspartate, and asparagine. Subnetworks (B1-2) are associated with vitamin B9 (folate) metabolism. In the illustration, the subnetworks are not spatially oriented to the parent network. Compounds are represented by red hexagons (labeled metabolites are those that were uploaded into Metscape; the dark blue metabolites are those added to connect the initially generated two networks; see figure 3 in the main manuscript). Reactions by denoted by grey squares and enzymes by green round corner squares and genes by blue circles.