

Table S1. Identification of urinary biomarkers in HCV cases.

| No. | Rt | Name | Trend | VIP |
|-----|------|------------------------------|-------|----------|
| 1 | 9.38 | Glycine | ↑ | 18.0218 |
| 2 | 4.49 | Succinic acid | ↓ | 11.79101 |
| 3 | 9.17 | Acetate | ↑ | 7.47369 |
| 4 | 8.46 | Hippuric | ↑ | 7.36361 |
| 5 | 5.46 | Carnitine | ↓ | 6.28862 |
| 6 | 3.95 | Citrate | ↑ | 6.00245 |
| 7 | 7.9 | Ethyl citrate | ↓ | 5.91743 |
| 8 | 3.41 | Arginine | ↑ | 5.70033 |
| 9 | 2.58 | Betaine | ↑ | 5.28267 |
| 10 | 6.47 | histidine | ↑ | 5.26471 |
| 11 | 5.53 | Indolebutyric acid | ↓ | 5.02477 |
| 12 | 5.46 | Leucine | ↑ | 9.01045 |
| 13 | 3.39 | Valine | ↓ | 8.20191 |
| 14 | 3.60 | N-Benzoylglycine ethyl ester | ↑ | 7.23011 |
| 15 | 8.08 | Phthalic acid | ↑ | 6.71478 |
| 16 | 3.77 | Octanedioic acid | ↑ | 6.31235 |
| 17 | 8.23 | Propanedioic acid | ↑ | 5.72351 |
| 18 | 5.58 | Aspartic acid | ↑ | 5.6574 |
| 19 | 8.43 | Taurine | ↓ | 5.34362 |
| 20 | 1.72 | L-Tyrosine | ↓ | 5.03689 |

Note: ↑, content increased; ↓, content decreased

Table S2. Result from ingenuity pathway analysis with MetPA.

| No. | Pathway Name | Total | Hits | Impact |
|-----|---|-------|------|---------|
| 1 | Aminoacyl-tRNA biosynthesis | 75 | 6 | 0 |
| 2 | Nitrogen metabolism | 39 | 4 | 0 |
| 3 | Phenylalanine metabolism | 45 | 3 | 0.0315 |
| 4 | Citrate cycle (TCA cycle) | 20 | 2 | 0.07773 |
| 5 | Taurine and hypotaurine metabolism | 20 | 2 | 0.33094 |
| 6 | Thiamine metabolism | 24 | 2 | 0 |
| 7 | Alanine, aspartate and glutamate metabolism | 24 | 2 | 0.02279 |
| 8 | Valine, leucine and isoleucine biosynthesis | 27 | 2 | 0.0265 |
| 9 | beta-Alanine metabolism | 28 | 2 | 0.01119 |
| 10 | Propanoate metabolism | 35 | 2 | 0.00134 |
| 11 | Valine, leucine and isoleucine degradation | 40 | 2 | 0.02232 |
| 12 | Lysine degradation | 47 | 2 | 0 |
| 13 | Primary bile acid biosynthesis | 47 | 2 | 0.01644 |
| 14 | Glycine, serine and threonine metabolism | 48 | 2 | 0.21111 |
| 15 | Glyoxylate and dicarboxylate metabolism | 50 | 2 | 0.00326 |
| 16 | D-Arginine and D-ornithine metabolism | 8 | 1 | 0 |
| 17 | Tyrosine metabolism | 76 | 2 | 0.04724 |
| 18 | Cyanoamino acid metabolism | 16 | 1 | 0 |
| 19 | Sulfur metabolism | 18 | 1 | 0.03307 |
| 20 | Selenoamino acid metabolism | 22 | 1 | 0.00321 |
| 21 | Pantothenate and CoA biosynthesis | 27 | 1 | 0 |
| 22 | Phenylalanine, tyrosine and tryptophan biosynthesis | 27 | 1 | 0.00738 |
| 23 | Glycolysis or Gluconeogenesis | 31 | 1 | 0.00046 |
| 24 | Pyruvate metabolism | 32 | 1 | 0.09947 |
| 25 | Methane metabolism | 34 | 1 | 0 |
| 26 | Ubiquinone and other terpenoid-quinone biosynthesis | 36 | 1 | 0 |
| 27 | Glutathione metabolism | 38 | 1 | 0 |
| 28 | Butanoate metabolism | 40 | 1 | 0.01774 |
| 29 | Histidine metabolism | 44 | 1 | 0.13988 |
| 30 | Pyrimidine metabolism | 60 | 1 | 0 |
| 31 | Arginine and proline metabolism | 77 | 1 | 0.12632 |
| 32 | Purine metabolism | 92 | 1 | 0 |
| 33 | Porphyrin and chlorophyll metabolism | 104 | 1 | 0 |

Note: Total is the total number of compounds in the pathway; the Hits is the actually matched number from the user uploaded data; the Impact is the pathway impact value calculated from pathway topology analysis.