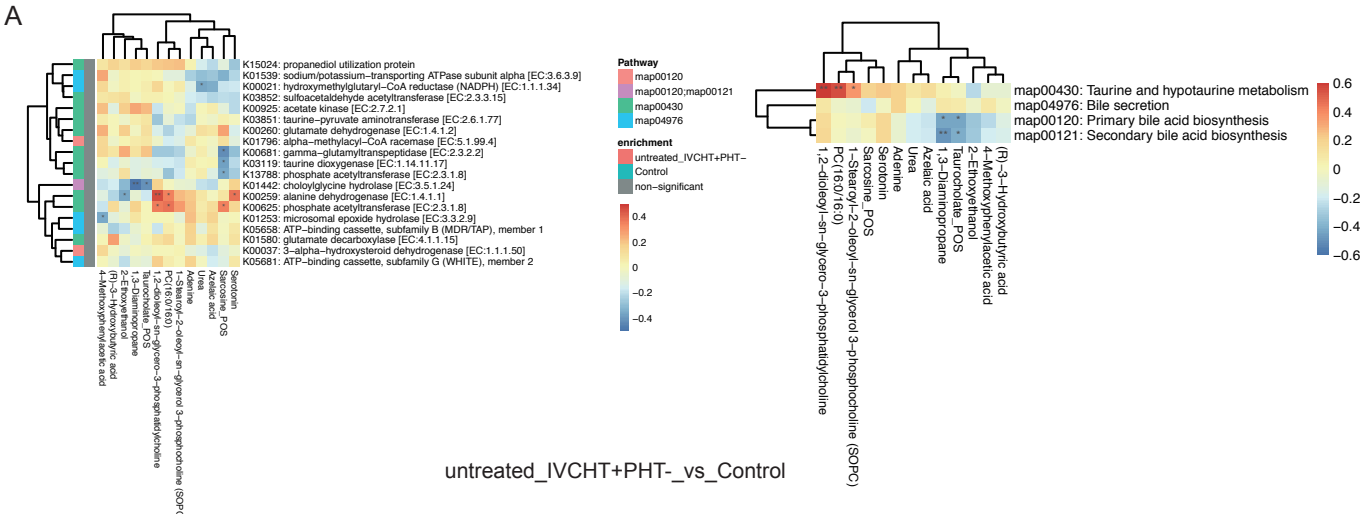
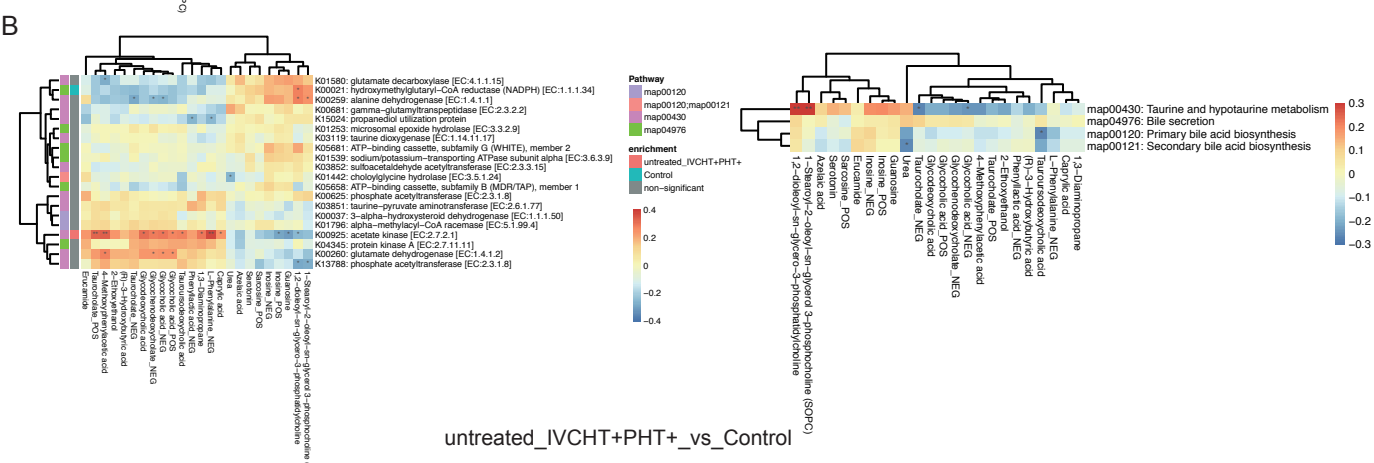

A
K15024: propanediol utilization protein
K01539: sodium/potassium−transporting ATPase subunit alpha [EC:3.6.3.9]
K00021: hydroxymethylglutaryl−CoA reductase (NADPH) [EC:1.1.1.34]
K03852: sulfoacetaldehyde acetyltransferase [EC:2.3.3.15]
K00925: acetate kinase [EC:2.7.2.1]
K03851: taurine−pyruvate aminotransferase [EC:2.6.1.77]
K00260: glutamate dehydrogenase [EC:1.4.1.2]
K01796: alpha−methylacyl−CoA racemase [EC:5.1.99.4]
K00681: gamma−glutamyltranspeptidase [EC:2.3.2.2]
K03119: taurine dioxygenase [EC:1.14.11.17]
K13788: phosphate acetyltransferase [EC:2.3.1.8]
K01442: cholovlglycine hydrolase [EC:3.5.1.24]
K00259: alanine dehydrogenase [EC:1.4.1.1]
K00625: phosphate acetyltransferase [EC:2.3.1.8]
K01253: microsomal epoxide hydrolase [EC:3.3.2.9]
K05658: ATP−binding cassette, subfamily B (MDR/TAP), member 1
K01580: glutamate decarboxylase [EC:4.1.1.15]
K00037: 3−alpha−hydroxysteroid dehydrogenase [EC:1.1.1.50]
K05681: ATP−binding cassette, subfamily G (WHITE), member 2
Serotonin
Sarcosine_POS
Azelaic acid
Urea
Adenine
1−Stearoyl−2−oleoyl−sn−glycerol 3−phosphocholine (SOPC)
1,2−dioleoyl−sn−glycero−3−phosphatidylcholine
PC(16:0/16:0)
1,3−Diaminopropane
Taurocholate_POS
2−Ethoxyethanol
(R)−3−Hydroxybutyric acid
4−Methoxyphenylacetic acid
Pathway
map00120
map00120;map00121
map00430
map04976
enrichment
untreated_IVCHT+PHT−
Control
non−significant
0.4
0
−0.2
−0.4
untreated_IVCHT+PHT-_vs_Control
(R)−3−Hydroxybutyric acid
4−Methoxyphenylacetic acid
2−Ethoxyethanol
Taurocholate_POS
1,3−Diaminopropane
Azelaic acid
Urea
Adenine
Serotonin
Sarcosine_POS
1−Stearoyl−2−oleoyl−sn−glycerol 3−phosphocholine (SOPC)
PC(16:0/16:0)
1,2−dioleoyl−sn−glycero−3−phosphatidylcholine
map00430: Taurine and hypotaurine metabolism
map04976: Bile secretion
map00120: Primary bile acid biosynthesis
map00121: Secondary bile acid biosynthesis
0.6
0.4
0.2
0
−0.2
−0.4
−0.6


B
K01580: glutamate decarboxylase [EC:4.1.1.15]
K00021: hydroxymethylglutaryl−CoA reductase (NADPH) [EC:1.1.1.34]
K00259: alanine dehydrogenase [EC:1.4.1.1]
K00681: gamma−glutamyltranspeptidase [EC:2.3.2.2]
K15024: propanediol utilization protein
K01253: microsomal epoxide hydrolase [EC:3.3.2.9]
K03119: taurine dioxygenase [EC:1.14.11.17]
K05681: ATP−binding cassette, subfamily G (WHITE), member 2
K01539: sodium/potassium−transporting ATPase subunit alpha [EC:3.6.3.9]
K03852: sulfoacetaldehyde acetyltransferase [EC:2.3.3.15]
K01442: cholovlglycine hydrolase [EC:3.5.1.24]
K05658: ATP−binding cassette, subfamily B (MDR/TAP), member 1
K00625: phosphate acetyltransferase [EC:2.3.1.8]
K03851: taurine−pyruvate aminotransferase [EC:2.6.1.77]
K00037: 3−alpha−hydroxysteroid dehydrogenase [EC:1.1.1.50]
K01796: alpha−methylacyl−CoA racemase [EC:5.1.99.4]
K00925: acetate kinase [EC:2.7.2.1]
K04345: protein kinase A [EC:2.7.11.11]
K00260: glutamate dehydrogenase [EC:1.4.1.2]
K13788: phosphate acetyltransferase [EC:2.3.1.8]
Ceramide
Taurocholate_POS
(R)−3−Hydroxybutyric acid
2−Ethoxyethanol
4−Methoxyphenylacetic acid
Taurocholate_NEG
Glycocholic acid
Glycocholic acid_NEG
Glycochenodeoxycholate
Glycochenodeoxycholate_NEG
Phenylacetic acid_NEG
Taurodeoxycholic acid
L−Phenylalanine_NEG
Capryl acid
Azelaic acid
Serotonin
Sarcosine_POS
Urea
Adenine
Inosine_POS
Inosine_NEG
Guanosine
1−Stearoyl−2−oleoyl−sn−glycerol 3−phosphocholine (SOPC)
1,2−dioleoyl−sn−glycero−3−phosphatidylcholine
Pathway
map00120
map00120;map00121
map00430
map04976
enrichment
untreated_IVCHT+PHT+
Control
non−significant
0.4
0.2
0
−0.2
−0.4
untreated_IVCHT+PHT+_vs_Control
1,3−Diaminopropane
Capryl acid
L−Phenylalanine_NEG
Taurodeoxycholic acid
(R)−3−Hydroxybutyric acid
Phenylacetic acid_NEG
2−Ethoxyethanol
Taurocholate_POS
4−Methoxyphenylacetic acid
Glycocholic acid_NEG
Glycochenodeoxycholate_NEG
Glycodeoxycholic acid
Taurocholate_NEG
Urea
Guanosine
Inosine_POS
Inosine_NEG
Erucamide
Serotonin
Sarcosine_POS
Azelaic acid
1−Stearoyl−2−oleoyl−sn−glycerol 3−phosphocholine (SOPC)
1,2−dioleoyl−sn−glycero−3−phosphatidylcholine
map00430: Taurine and hypotaurine metabolism
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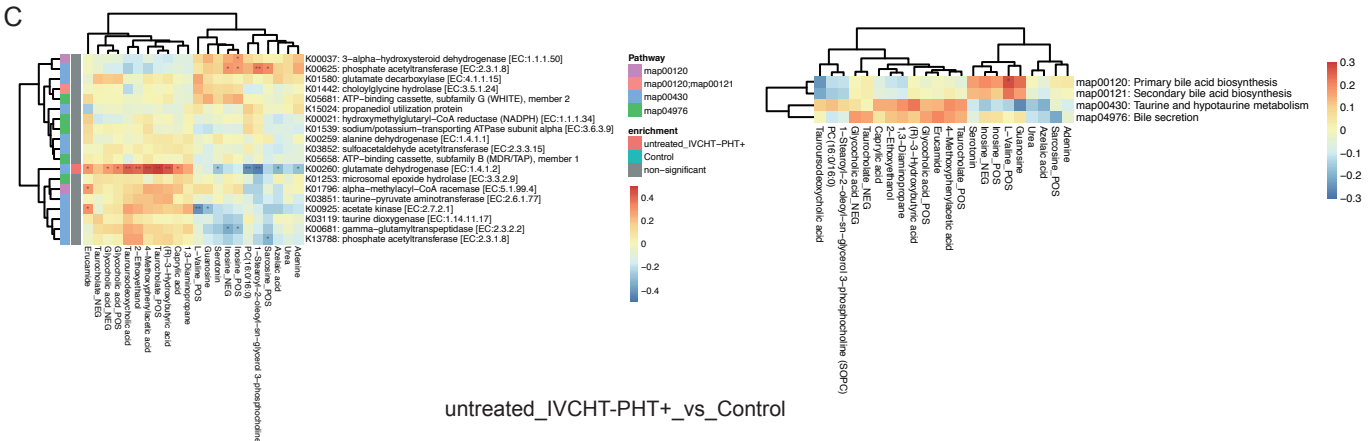
map00120: Primary bile acid biosynthesis
map00121: Secondary bile acid biosynthesis
0.3
0.2
0.1
0
−0.1
−0.2
−0.3


C
K00037: 3−alpha−hydroxysteroid dehydrogenase [EC:1.1.1.50]
K00625: phosphate acetyltransferase [EC:2.3.1.8]
K01580: glutamate decarboxylase [EC:4.1.1.15]
K01442: cholovlglycine hydrolase [EC:3.5.1.24]
K05681: ATP−binding cassette, subfamily G (WHITE), member 2
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K01539: sodium/potassium−transporting ATPase subunit alpha [EC:3.6.3.9]
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K05658: ATP−binding cassette, subfamily B (MDR/TAP), member 1
K00260: glutamate dehydrogenase [EC:1.4.1.2]
K01253: microsomal epoxide hydrolase [EC:3.3.2.9]
K01796: alpha−methylacyl−CoA racemase [EC:5.1.99.4]
K03851: taurine−pyruvate aminotransferase [EC:2.6.1.77]
K00925: acetate kinase [EC:2.7.2.1]
K03119: taurine dioxygenase [EC:1.14.11.17]
K00681: gamma−glutamyltranspeptidase [EC:2.3.2.2]
K13788: phosphate acetyltransferase [EC:2.3.1.8]
Erucamide
Taurocholate_POS
Glycocholic acid_NEG
Glycocholic acid_POS
Taurocholate_NEG
(R)−3−Hydroxybutyric acid
4−Methoxyphenylacetic acid
2−Ethoxyethanol
Taurocholate_POS
Capryl acid
1,3−Diaminopropane
Guanosine
Serotonin
Inosine_POS
Inosine_NEG
PC(16:0/16:0)
1−Stearoyl−2−oleoyl−sn−glycerol 3−phosphocholine (SOPC)
Azelaic acid
Urea
Adenine
Pathway
map00120
map00120;map00121
map00430
map04976
enrichment
untreated_IVCHT−PHT+
Control
non−significant
0.4
0.2
0
−0.2
−0.4
untreated_IVCHT-PHT+_vs_Control
Adenine
Sarcosine_POS
Urea
Azelaic acid
Guanosine
L−Valine_POS
Inosine_POS
Inosine_NEG
Serotonin
Taurocholate_NEG
Taurocholate_POS
4−Methoxyphenylacetic acid
Erucamide
Glycocholic acid_POS
(R)−3−Hydroxybutyric acid
1,3−Diaminopropane
2−Ethoxyethanol
Capryl acid
Taurodeoxycholic acid
PC(16:0/16:0)
1−Stearoyl−2−oleoyl−sn−glycerol 3−phosphocholine (SOPC)
map00120: Primary bile acid biosynthesis
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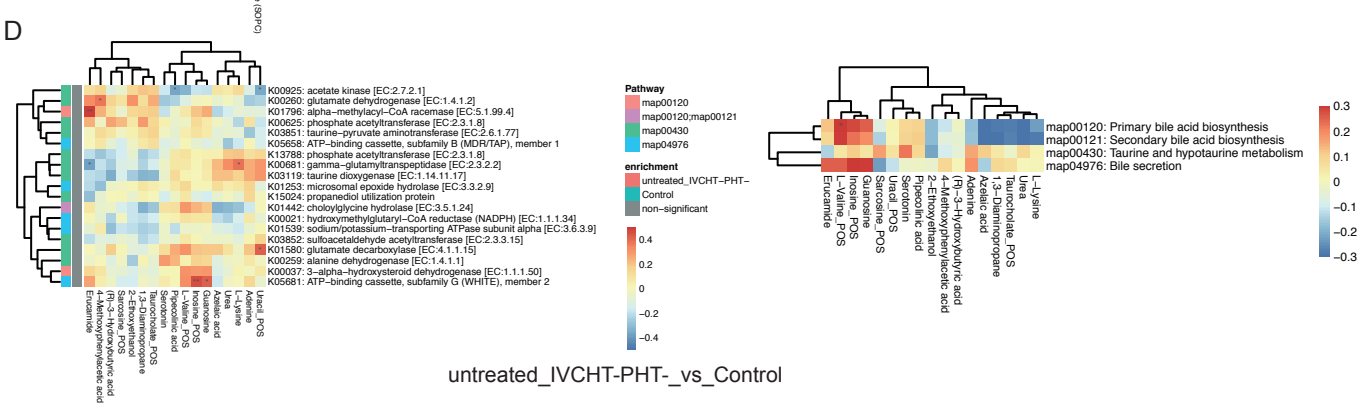
map04976: Bile secretion
0.3
0.2
0.1
0
−0.1
−0.2
−0.3


D
K00925: acetate kinase [EC:2.7.2.1]
K00260: glutamate dehydrogenase [EC:1.4.1.2]
K01796: alpha−methylacyl−CoA racemase [EC:5.1.99.4]
K00625: phosphate acetyltransferase [EC:2.3.1.8]
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K05658: ATP−binding cassette, subfamily B (MDR/TAP), member 1
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K15024: propanediol utilization protein
K01442: cholovlglycine hydrolase [EC:3.5.1.24]
K00021: hydroxymethylglutaryl−CoA reductase (NADPH) [EC:1.1.1.34]
K01539: sodium/potassium−transporting ATPase subunit alpha [EC:3.6.3.9]
K03852: sulfoacetaldehyde acetyltransferase [EC:2.3.3.15]
K01580: glutamate decarboxylase [EC:4.1.1.15]
K00259: alanine dehydrogenase [EC:1.4.1.1]
K00037: 3−alpha−hydroxysteroid dehydrogenase [EC:1.1.1.50]
K05681: ATP−binding cassette, subfamily G (WHITE), member 2
Erucamide
(R)−3−Hydroxybutyric acid
4−Methoxyphenylacetic acid
Sarcosine_POS
2−Ethoxyethanol
Taurocholate_POS
Serotonin
Pipecolinic acid
L−Valine_POS
Guanosine
Azelaic acid
Urea
L−Lysine
Adenine
Uracil_POS
Pathway
map00120
map00120;map00121
map00430
map04976
enrichment
untreated_IVCHT−PHT−
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−0.4
untreated_IVCHT-PHT-_vs_Control
Erucamide
L−Valine_POS
Inosine_POS
Inosine_NEG
Guanosine
Sarcosine_POS
Uracil_POS
Serotonin
Pipecolinic acid
2−Ethoxyethanol
4−Methoxyphenylacetic acid
(R)−3−Hydroxybutyric acid
Adenine
Azelaic acid
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Taurocholate_POS
Urea
L−Lysine
map00120: Primary bile acid biosynthesis
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map00430: Taurine and hypotaurine metabolism
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0.3
0.2
0.1
0
−0.1
−0.2
−0.3