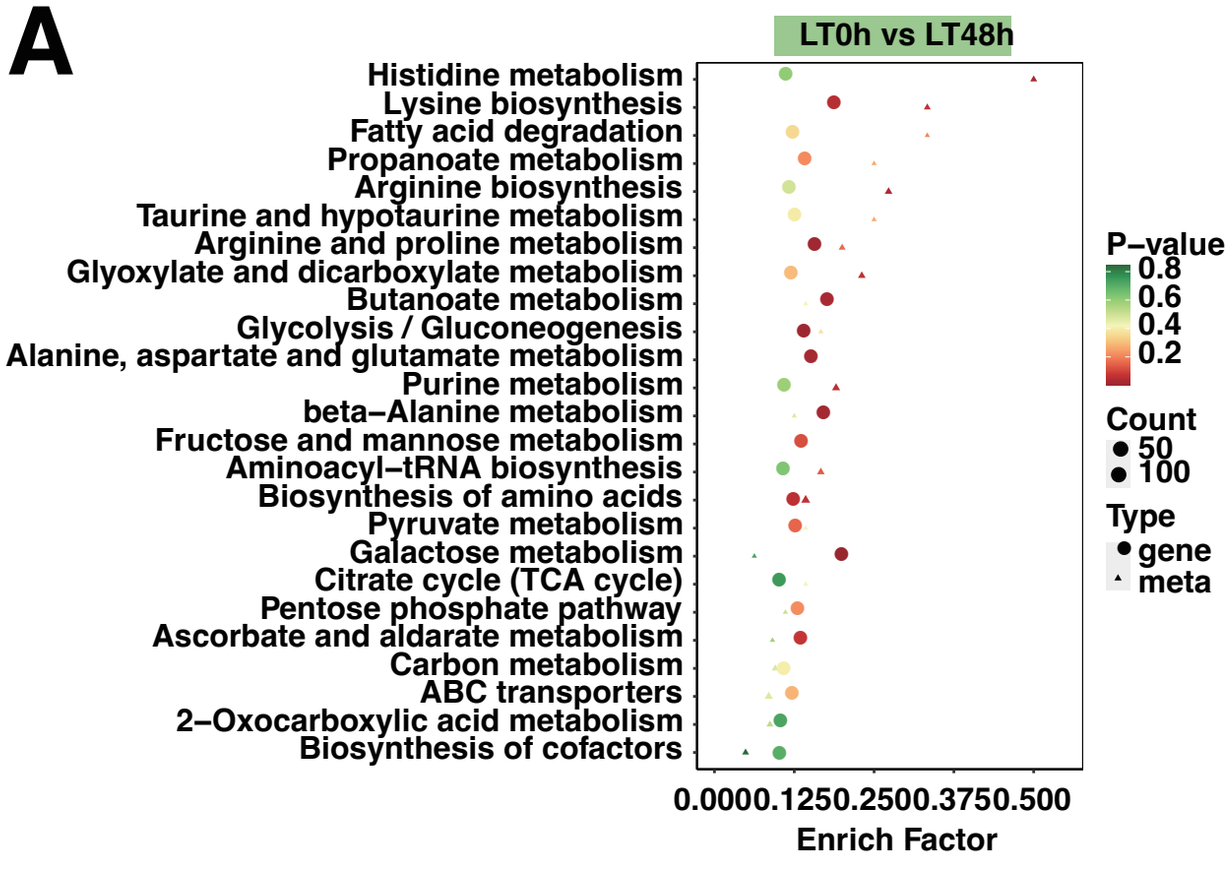
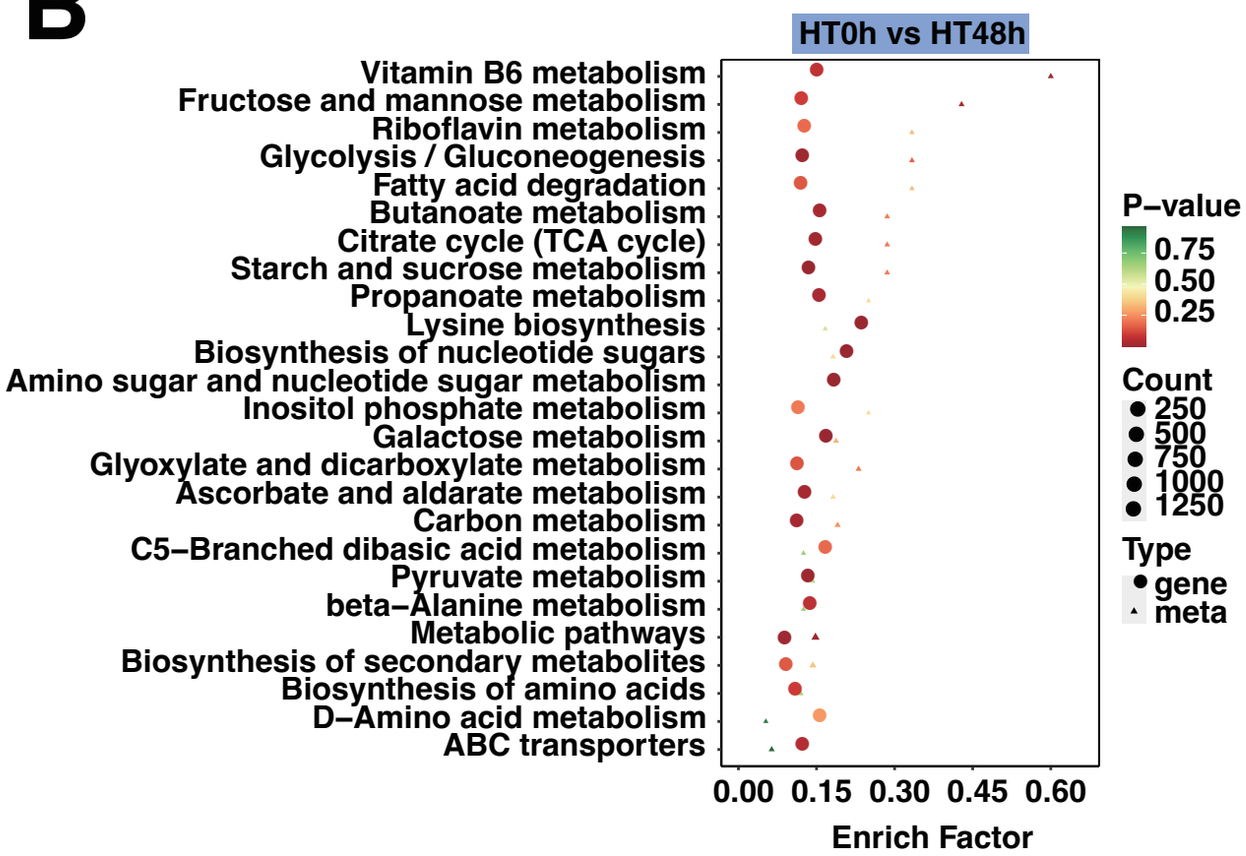
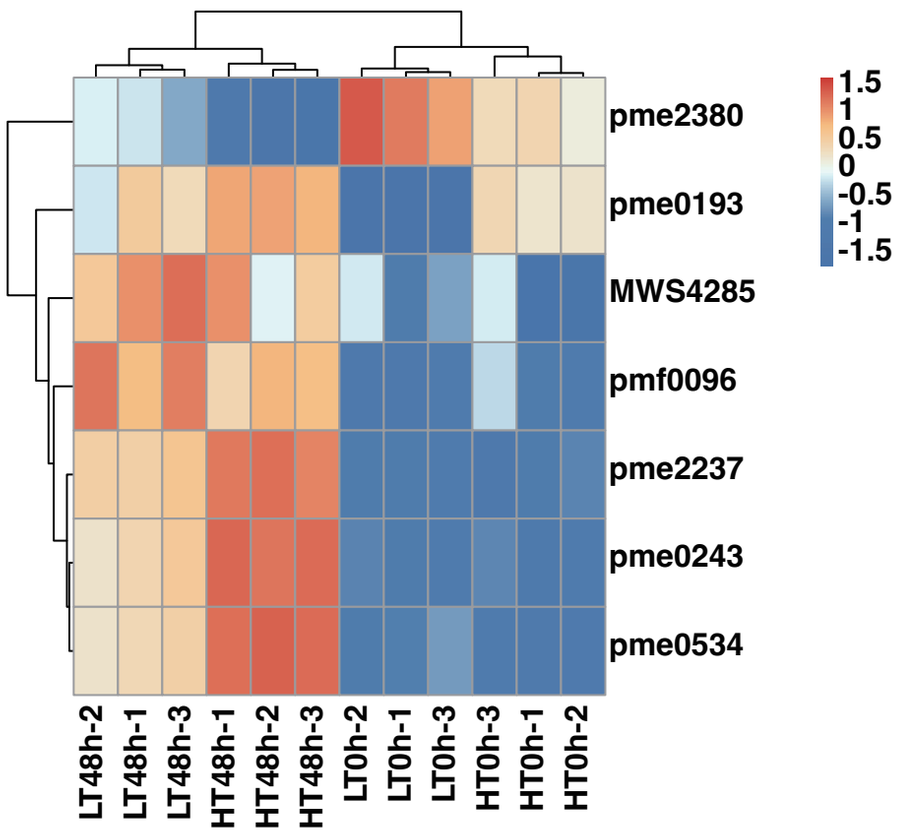
A


LT0h vs LT48h
Histidine metabolism
Lysine biosynthesis
Fatty acid degradation
Propanoate metabolism
Arginine biosynthesis
Taurine and hypotaurine metabolism
Arginine and proline metabolism
Glyoxylate and dicarboxylate metabolism
Butanoate metabolism
Glycolysis / Gluconeogenesis
Alanine, aspartate and glutamate metabolism
Purine metabolism
beta−Alanine metabolism
Fructose and mannose metabolism
Aminoacyl−tRNA biosynthesis
Biosynthesis of amino acids
Pyruvate metabolism
Galactose metabolism
Citrate cycle (TCA cycle)
Pentose phosphate pathway
Ascorbate and aldarate metabolism
Carbon metabolism
ABC transporters
2−Oxocarboxylic acid metabolism
Biosynthesis of cofactors
0.000.125 0.250 0.375 0.500
Enrich Factor
P−value
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0.6
0.4
0.2
Count
50
100
Type
gene
meta

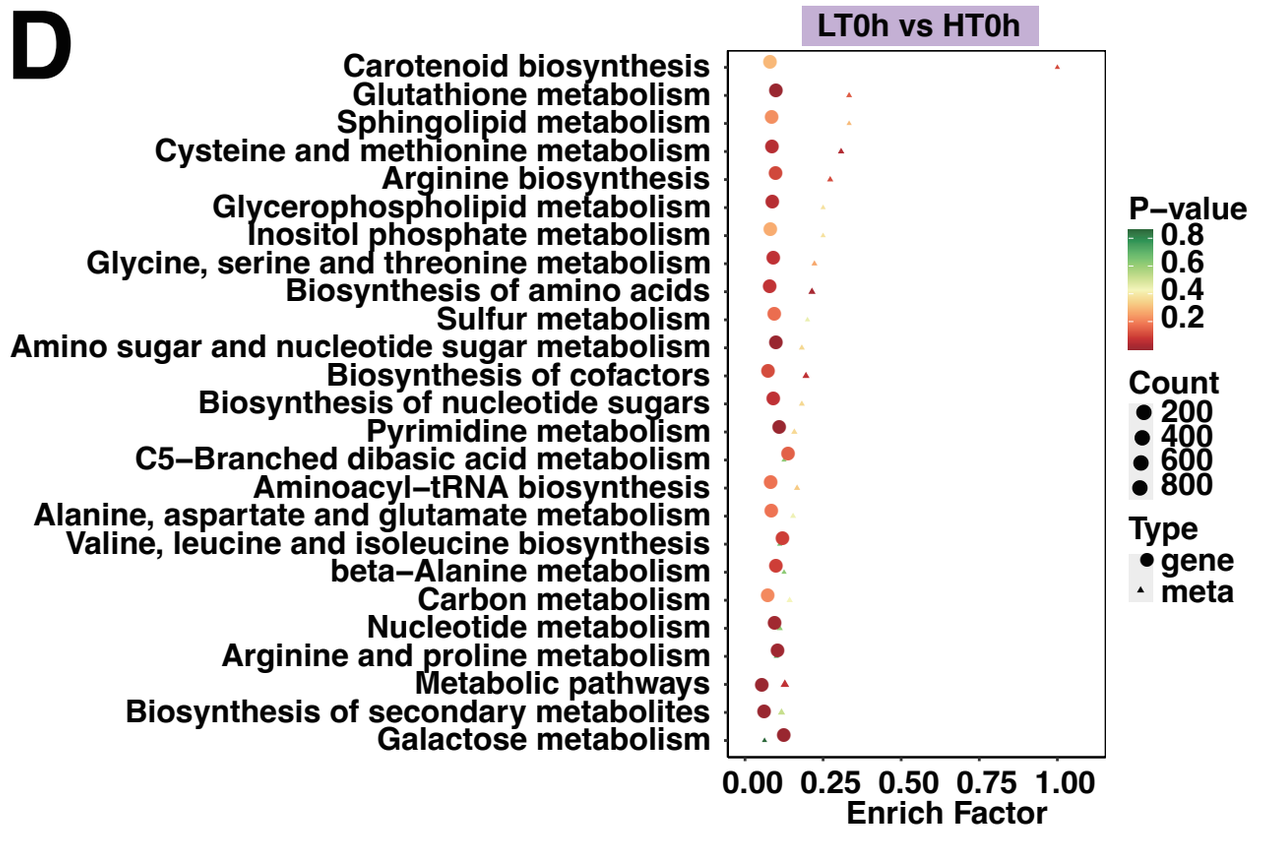
B


HT0h vs HT48h
Vitamin B6 metabolism
Fructose and mannose metabolism
Riboflavin metabolism
Glycolysis / Gluconeogenesis
Fatty acid degradation
Butanoate metabolism
Citrate cycle (TCA cycle)
Starch and sucrose metabolism
Propanoate metabolism
Lysine biosynthesis
Biosynthesis of nucleotide sugars
Amino sugar and nucleotide sugar metabolism
Inositol phosphate metabolism
Galactose metabolism
Glyoxylate and dicarboxylate metabolism
Ascorbate and aldarate metabolism
Carbon metabolism
C5−Branched dibasic acid metabolism
Pyruvate metabolism
beta−Alanine metabolism
Metabolic pathways
Biosynthesis of secondary metabolites
Biosynthesis of amino acids
D−Amino acid metabolism
ABC transporters
0.00 0.15 0.30 0.45 0.60
Enrich Factor
P−value
0.75
0.50
0.25
Count
250
500
750
1000
1250
Type
gene
meta

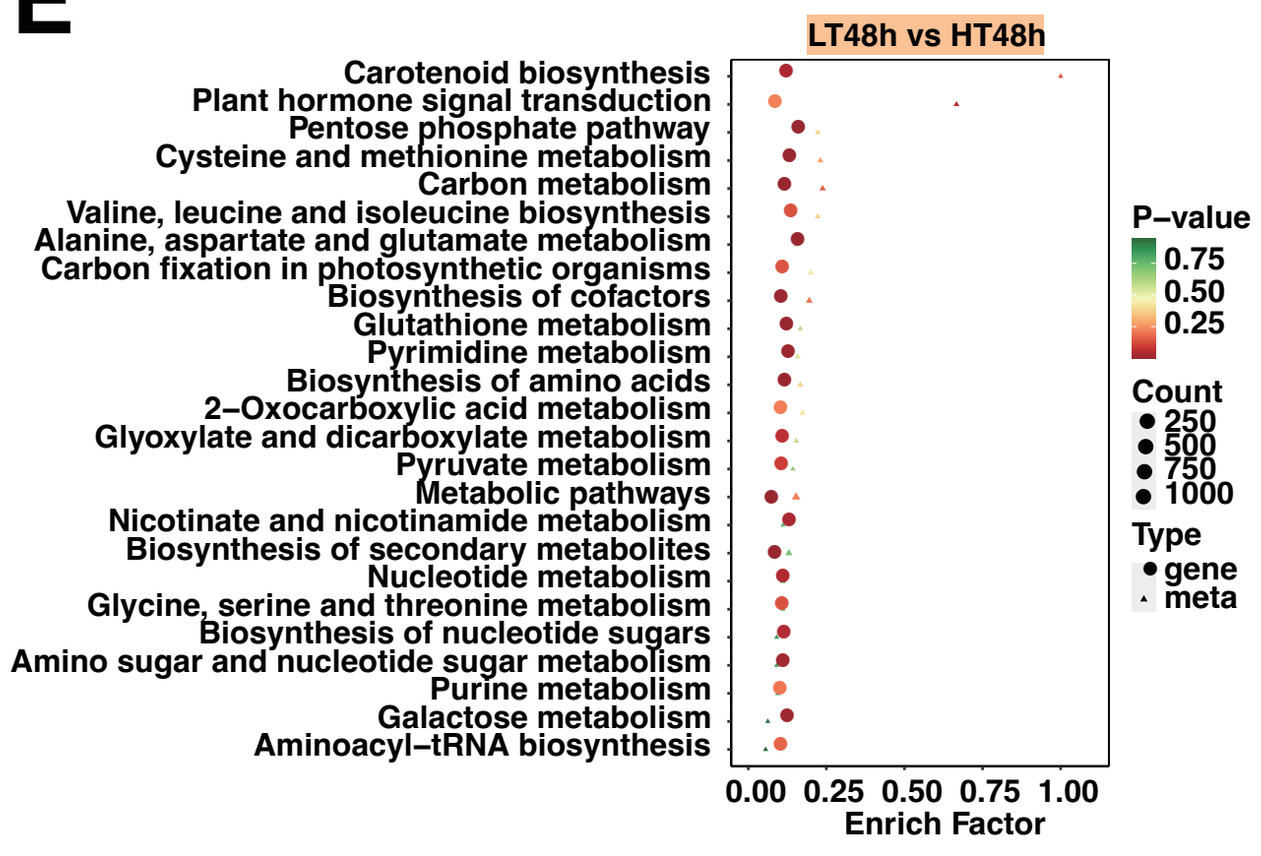
C


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pme0193
MWS4285
pmf0096
pme2237
pme0243
pme0534
1.5
1
0.5
0
-0.5
-1
-1.5
LT48h-2
LT48h-1
LT48h-3
HT48h-1
HT48h-2
HT48h-3
LT0h-2
LT0h-1
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HT0h-1
HT0h-2

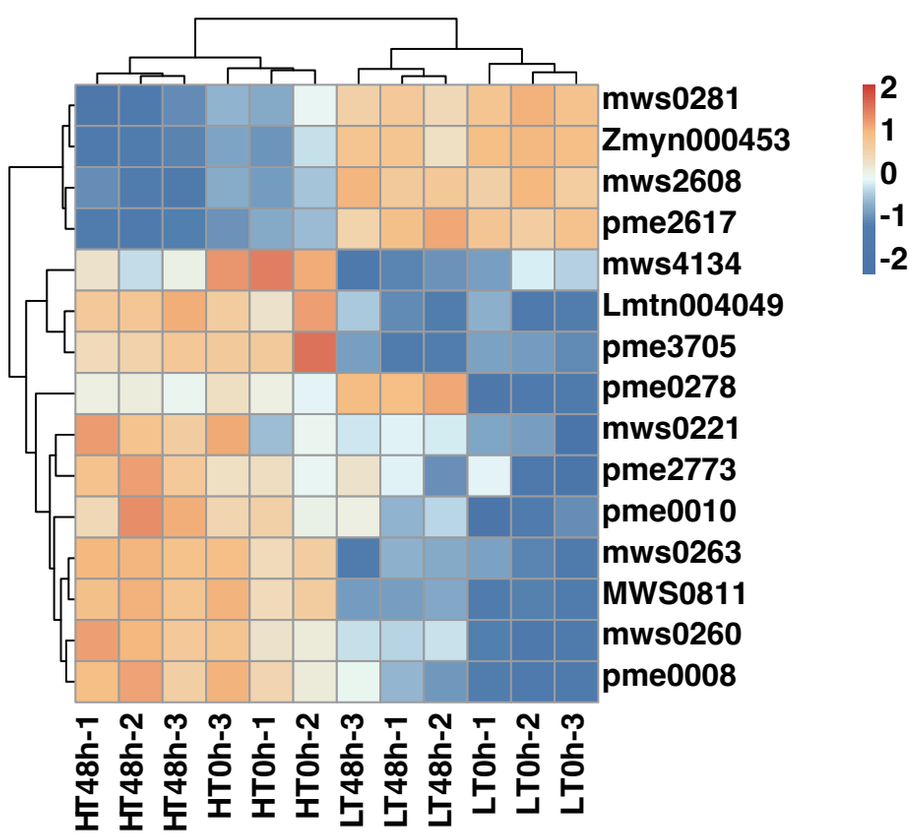
D


LT0h vs HT0h
Carotenoid biosynthesis
Glutathione metabolism
Sphingolipid metabolism
Cysteine and methionine metabolism
Arginine biosynthesis
Glycerophospholipid metabolism
Inositol phosphate metabolism
Glycine, serine and threonine metabolism
Biosynthesis of amino acids
Sulfur metabolism
Amino sugar and nucleotide sugar metabolism
Biosynthesis of cofactors
Biosynthesis of nucleotide sugars
Pyrimidine metabolism
C5−Branched dibasic acid metabolism
Aminoacyl−tRNA biosynthesis
Alanine, aspartate and glutamate metabolism
Valine, leucine and isoleucine biosynthesis
beta−Alanine metabolism
Carbon metabolism
Nucleotide metabolism
Arginine and proline metabolism
Metabolic pathways
Biosynthesis of secondary metabolites
Galactose metabolism
0.00 0.25 0.50 0.75 1.00
Enrich Factor
P−value
0.8
0.6
0.4
0.2
Count
200
400
600
800
Type
gene
meta

E


LT48h vs HT48h
Carotenoid biosynthesis
Plant hormone signal transduction
Pentose phosphate pathway
Cysteine and methionine metabolism
Carbon metabolism
Valine, leucine and isoleucine biosynthesis
Alanine, aspartate and glutamate metabolism
Carbon fixation in photosynthetic organisms
Biosynthesis of cofactors
Glutathione metabolism
Pyrimidine metabolism
Biosynthesis of amino acids
2−Oxocarboxylic acid metabolism
Glyoxylate and dicarboxylate metabolism
Pyruvate metabolism
Metabolic pathways
Nicotinate and nicotinamide metabolism
Biosynthesis of secondary metabolites
Nucleotide metabolism
Glycine, serine and threonine metabolism
Biosynthesis of nucleotide sugars
Amino sugar and nucleotide sugar metabolism
Purine metabolism
Galactose metabolism
Aminoacyl−tRNA biosynthesis
0.00 0.25 0.50 0.75 1.00
Enrich Factor
P−value
0.75
0.50
0.25
Count
250
500
750
1000
Type
gene
meta

F


mws0281
Zmyn000453
mws2608
pme2617
mws4134
Lmtn004049
pme3705
pme0278
mws0221
pme2773
pme0010
mws0263
MWS0811
mws0260
pme0008
2
1
0
-1
-2
HT48h-1
HT48h-2
HT48h-3
HT0h-3
HT0h-1
HT0h-2
LT48h-3
LT48h-1
LT48h-2
LT0h-1
LT0h-2
LT0h-3