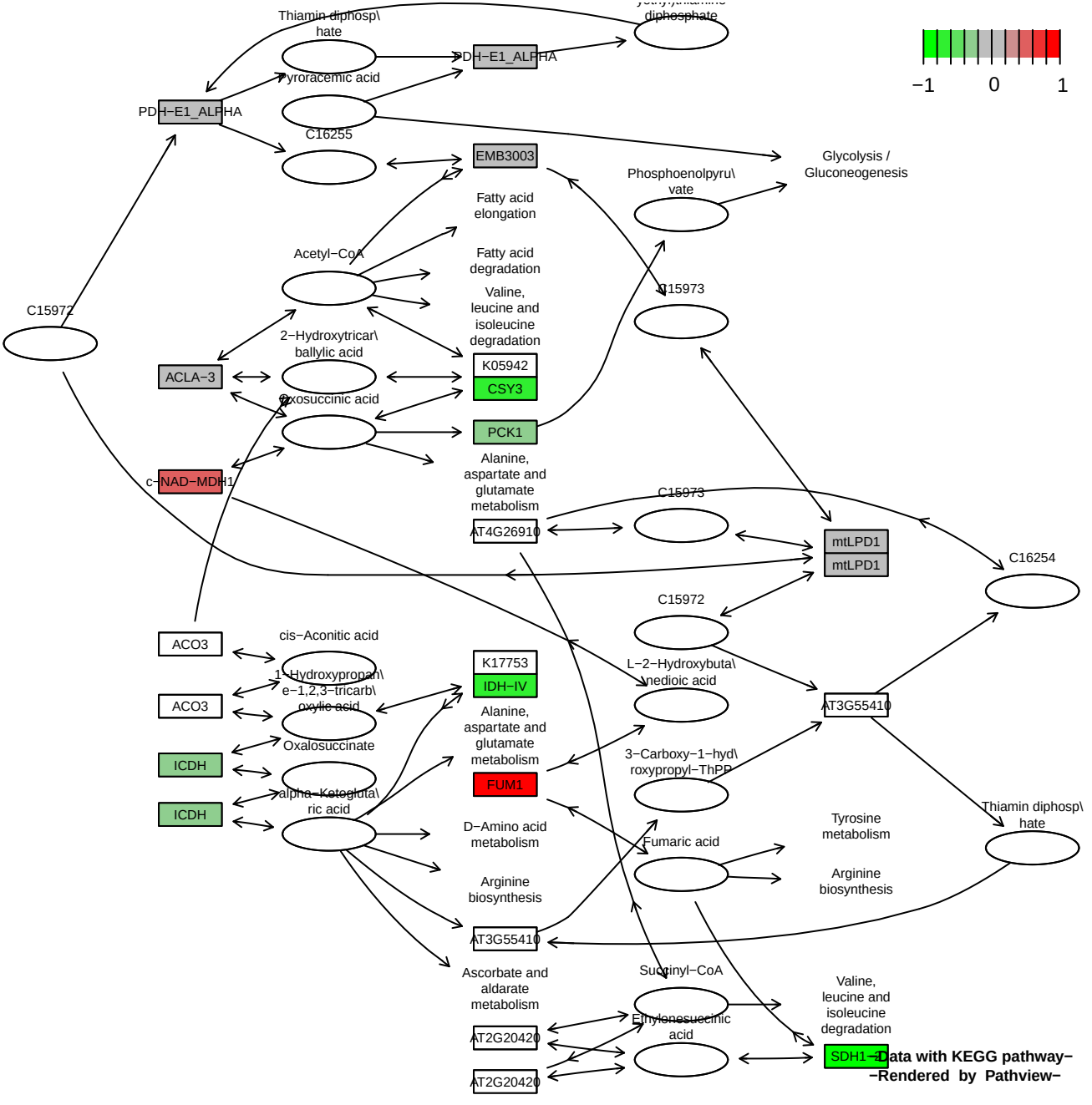
Thiamin diphosp\
hate
diphosphate
PDH−E1_ALPHA
Pyroracemic acid
PDH−E1_ALPHA
C16255
EMB3003
Glycolysis /
Gluconeogenesis
Phosphoenolpyru\
vate
Fatty acid
elongation
Acetyl−CoA
Fatty acid
degradation
Valine,
leucine and
isoleucine
degradation
C15973
C15972
2−Hydroxytricar\
ballylic acid
K05942
CSY3
ACLA−3
Oxosuccinic acid
PCK1
c−NAD−MDH1
Alanine,
aspartate and
glutamate
metabolism
C15973
AT4G26910
mtLPD1
mtLPD1
C16254
C15972
ACO3
cis−Aconitic acid
K17753
IDH−IV
L−2−Hydroxybuta\
nedioic acid
1−Hydroxypropan\
e−1,2,3−tricarb\
oxylic acid
ACO3
AT3G55410
Alanine,
aspartate and
glutamate
metabolism
Oxalosuccinate
ICDH
3−Carboxy−1−hyd\
roxypropyl−ThPP
FUM1
alpha−Ketoglutá\
ric acid
ICDH
Thiamin diphosp\
hate
D−Amino acid
metabolism
Fumaric acid
Tyrosine
metabolism
Arginine
biosynthesis
Arginine
biosynthesis
AT3G55410
Ascorbate and
aldarate
metabolism
Succinyl−CoA
Valine,
leucine and
isoleucine
degradation
Ethylenesuccinic
acid
AT2G20420
SDH1−1
AT2G20420
−1
0
1
−Data with KEGG pathway−
−Rendered by Pathview−

KEGG diagram legend

Edge Types

compound

hidden compound

activation

inhibition

expression

repression

indirect effect

state change

binding/association

dissociation

phosphorylation (+p)

dephosphorylation (−p)

glycosylation (+g)

ubiquitination (+u)

methylation (+m)

others/unknown (?)

Node Types

gene (protein/enzyme)

group (complex)

compound (metabolite/glycan)

map (pathway) — Pathway name