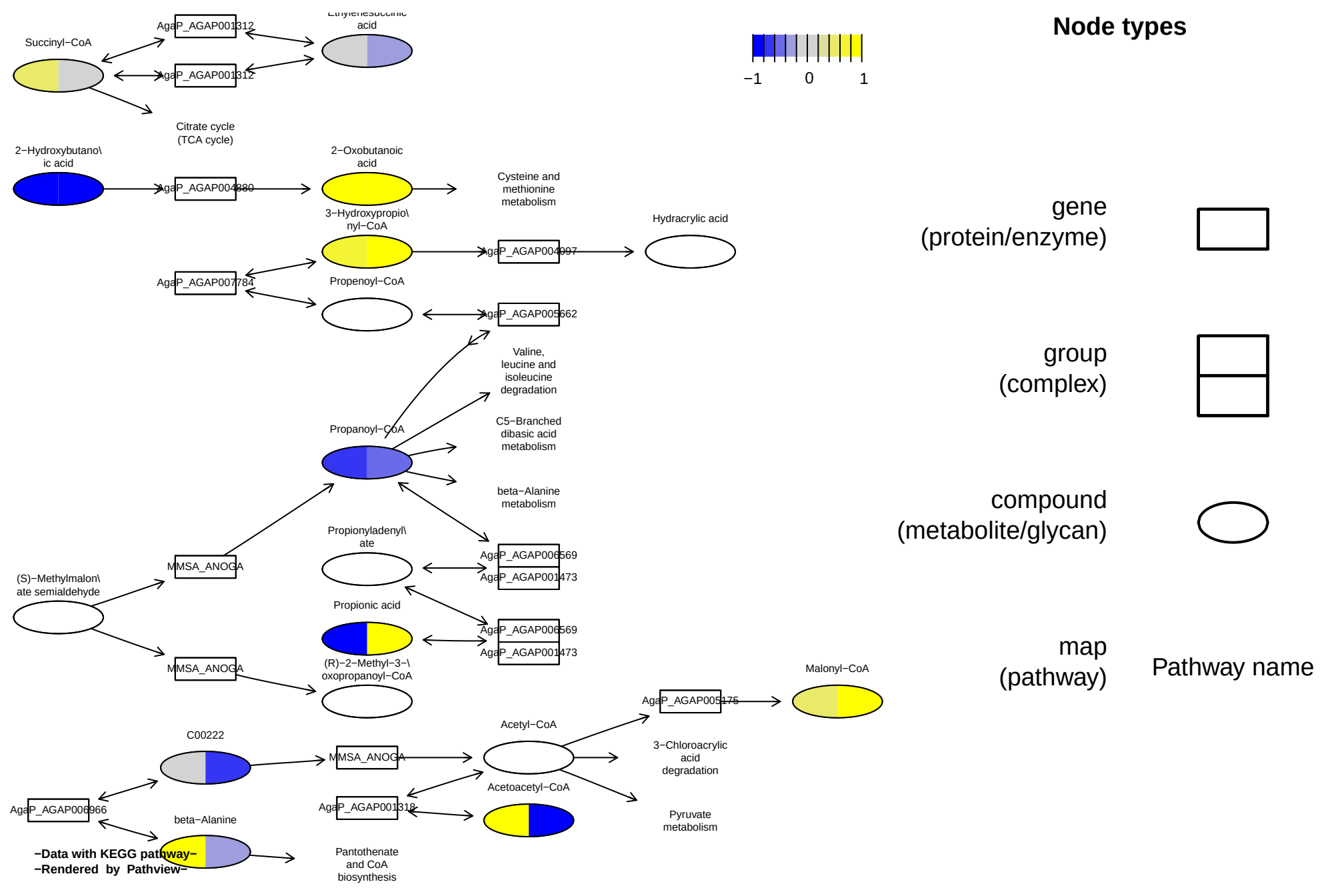
Node types
−1
0
1
gene
(protein/enzyme)
group
(complex)
compound
(metabolite/glycan)
map
(pathway)
Pathway name
Succinyl−CoA
AgaP_AGAP001312
AgaP_AGAP001312
Ethylenesuccinic acid
Citrate cycle
(TCA cycle)
2−Hydroxybutano\ ic acid
AgaP_AGAP004880
2−Oxobutanoic acid
Cysteine and methionine metabolism
3−Hydroxypropio\ nyl−CoA
AgaP_AGAP004997
Hydracrylic acid
AgaP_AGAP007784
Propenoyl−CoA
AgaP_AGAP005662
Valine, leucine and isoleucine degradation
C5−Branched dibasic acid metabolism
Propanoyl−CoA
beta−Alanine metabolism
Propionyladenyl\ ate
AgaP_AGAP006569
AgaP_AGAP001473
MMSA_ANOGA
(S)−Methylmalon\ ate semialdehyde
Propionic acid
AgaP_AGAP006569
AgaP_AGAP001473
MMSA_ANOGA
(R)−2−Methyl−3−\ oxopropanoyl−CoA
Malonyl−CoA
AgaP_AGAP005175
Acetyl−CoA
C00222
MMSA_ANOGA
3−Chloroacrylic acid degradation
Acetoacetyl−CoA
AgaP_AGAP006966
AgaP_AGAP001318
Pyruvate metabolism
beta−Alanine
−Data with KEGG pathway−
−Rendered by Pathview−
Pantothenate and CoA biosynthesis