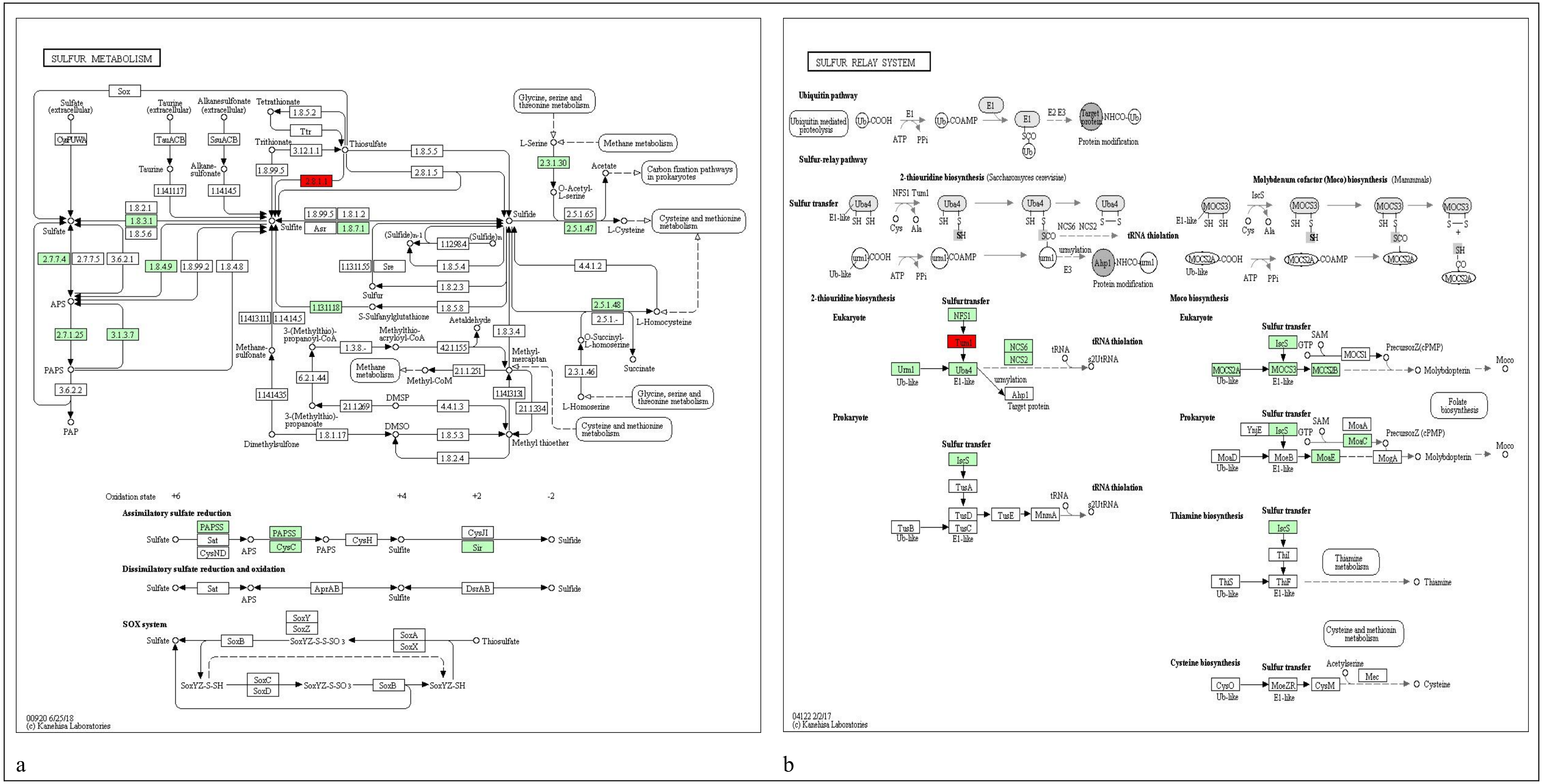
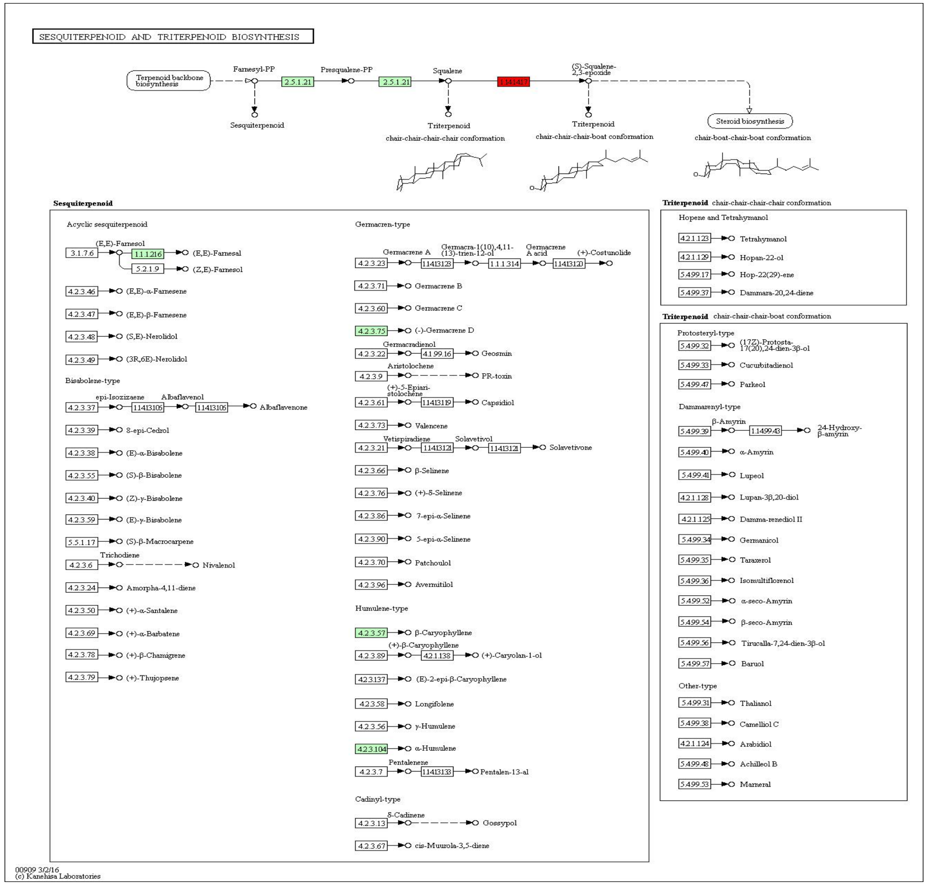

SULFUR METABOLISM
Sulfate (extracellular)
Taurine (extracellular)
Alkanesulfonate (extracellular)
Tetrathionate
Thiosulfate
Trithionate
Sulfite
Sulfide
Sulfate
APS
PAPS
PAP
L-Serine
O-Acetyl-L-serine
L-Cysteine
Acetate
L-Homocysteine
O-Succinyl-L-homoserine
Succinate
L-Homoserine
Methyl-mercaptan
Methyl thioether
Dimethylsulfone
DMSO
DMSP
Methane metabolism
Carbon fixation pathways in prokaryotes
Cysteine and methionine metabolism
Glycine, serine and threonine metabolism
Oxidation state +6 +4 +2 -2
Assimilatory sulfate reduction
PAPSS
Sat
CysND
CysC
CysH
CysJI
Sir
Dissimilatory sulfate reduction and oxidation
AprAB
DsrAB
SOX system
SoxB
SoxYZ
SoxAX
SoxCD
00920 6/25/18
(c) Kanehisa Laboratories
a
SULFUR RELAY SYSTEM
Ubiquitin pathway
Sulfur-relay pathway
2-thiouridine biosynthesis (Saccharomyces cerevisiae)
Molybdenum cofactor (Moco) biosynthesis (Mammals)
Sulfur transfer
tRNA thiolation
Protein modification
2-thiouridine biosynthesis
Eukaryote
Prokaryote
NFS1
Tum1
NCS6
NCS2
Urm1
Uba4
Ahp1
IscS
TusA
TusD
TusC
TusB
TusE
MnmA
Moco biosynthesis
MOCS2A
MOCS3
MOCS2B
MOCS1
Molybdopterin
Moco
YnjE
MoaD
MoeB
MoaE
MoaA
MoaC
MogA
Folate biosynthesis
Thiamine biosynthesis
ThiS
ThiF
ThiI
Thiamine
Cysteine biosynthesis
CysO
MoeZR
CysM
Mec
Cysteine
04122 2/2/17
(c) Kanehisa Laboratories
b


SESQUITERPENOID AND TRITERPENOID BIOSYNTHESIS
Terpenoid backbone biosynthesis
Farnesyl-PP
2.5.1.21
Presqualene-PP
2.5.1.21
Squalene
1.14.14.17
(S)-Squalene-2,3-epoxide
Steroid biosynthesis
Sesquiterpenoid
Triterpenoid chair-chair-chair conformation
Triterpenoid chair-chair-boat conformation
chair-boat-chair-boat conformation
Sesquiterpenoid
Acyclic sesquiterpenoid
(E,E)-Farnesol
(Z,E)-Farnesol
(E,E)-α-Farnesene
(E)-β-Farnesene
(S,E)-Nerolidol
(3R,6E)-Nerolidol
Bisabolene-type
epi-Isozizaene
Albaflavenol
Albaflavenone
8-epi-Cedrol
(E)-α-Bisabolene
(S)-β-Bisabolene
(Z)-γ-Bisabolene
(E)-γ-Bisabolene
(S)-β-Macrocarpene
Trichodiene
Nivalenol
Amorpha-4,11-diene
(+)-α-Santalene
(+)-α-Barbatene
(+)-β-Chamigrene
(+)-Thujopsene
Germacren-type
Germacrene A
Germacra-1(10),4,11-(13)-trien-12-ol
Germacrene A acid
(+)-Costunolide
Germacrene B
Germacrene C
(-)-Germacrene D
Germacradienol
Geosmin
Aristolochene
PR-toxin
(+)-5-Epiaristolochene
Capsidiol
Valencene
Vetispiradiene
Solavetivol
Solavetivone
β-Selinene
(+)-δ-Selinene
7-epi-α-Selinene
5-epi-α-Selinene
Patchoulol
Avermitilol
Humulene-type
β-Caryophyllene
(+)-β-Caryophyllene
(+)-Caryolan-1-ol
(E)-2-epi-β-Caryophyllene
Longifolene
γ-Humulene
α-Humulene
Pentalenene
Pentalen-13-al
Cadinyl-type
δ-Cadinene
Gossypol
cis-Muurola-3,5-diene
Triterpenoid chair-chair-chair conformation
Hopene and Tetrahymanol
Tetrahymanol
Hopan-22-ol
Hop-22(29)-ene
Dammara-20,24-diene
Triterpenoid chair-chair-boat conformation
Protosteryl-type
(17Z)-Protosta-17(20),24-dien-3β-ol
Cucurbitadienol
Parkeol
Dammarenyl-type
β-Amyrin
24-Hydroxy-β-amyrin
α-Amyrin
Lupeol
Lupan-3β,20-diol
Damma-renediol II
Germanicol
Taraxerol
Isomultiflorenol
α-seco-Amyrin
β-seco-Amyrin
Tirucalla-7,24-dien-3β-ol
Baruol
Other-type
Thalianol
Camelliol C
Arabidiol
Achilleol B
Marneral
00909 3/2/16
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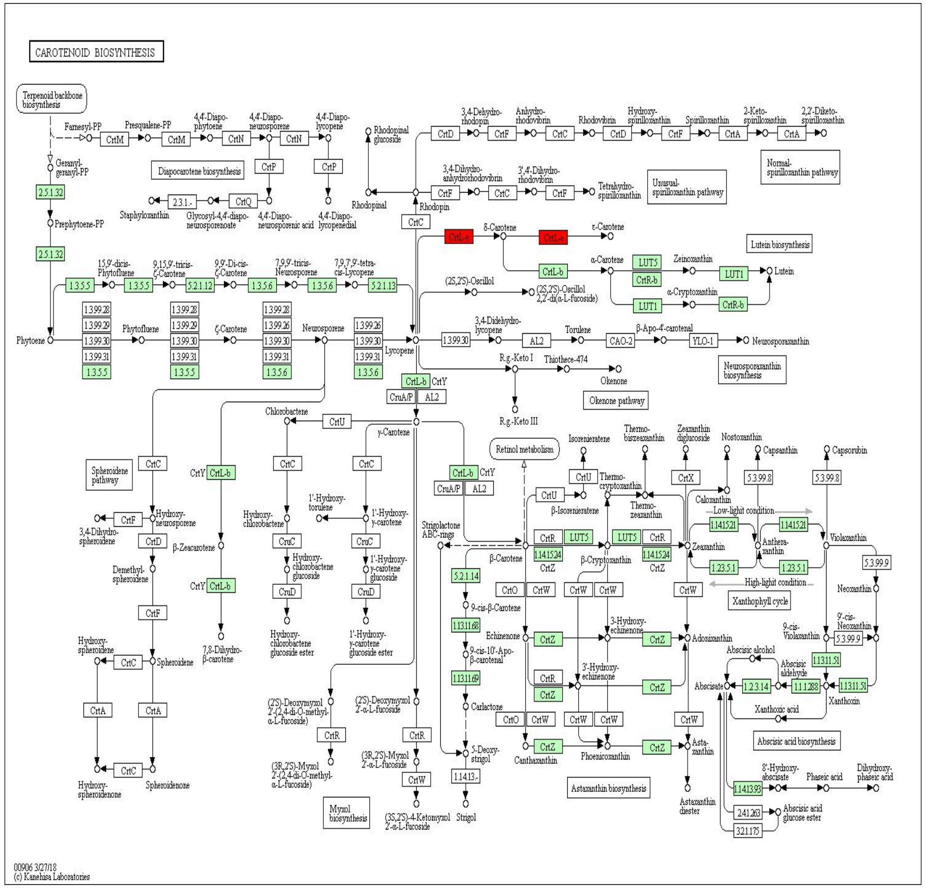
c


CAROTENOID BIOSYNTHESIS
Terpenoid backbone biosynthesis
Farnesyl-PP
Presqualene-PP
4,4'-Diapophytoene
4,4'-Diaponeurosporene
4,4'-Diapolycopene
CrtM
CrtN
CrtP
Diapocarotene biosynthesis
Staphyloxanthin
Glycosyl-4,4'-diaponeurosporenoate
4,4'-Diaponeurosporenic acid
4,4'-Diapolycopenedial
Geranylgeranyl-PP
2.5.1.32
Prephytoene-PP
Phytoene
15,9'-dicis-Phytofluene
9,15,9'-tricis-ζ-Carotene
9,9'-Di-cis-ζ-Carotene
7,9,9'-tricis-Neurosporene
7,9,7',9'-tetra-cis-Lycopene
1.3.5.5
5.2.1.12
1.3.5.6
5.2.1.13
Phytofluene
ζ-Carotene
Neurosporene
Lycopene
Rhodopinal glucoside
Rhodopinal
Rhodopin
3,4-Dehydrorhodopin
Anhydrorhodovibrin
Rhodovibrin
Hydroxyspirilloxanthin
Spirilloxanthin
2-Keto-spirilloxanthin
2,2'-Diketo-spirilloxanthin
CrtD
CrtF
CrtC
CrtA
Normal spirilloxanthin pathway
3,4-Didehydro-anhydrorhodovibrin
3,4'-Didehydro-rhodovibrin
Tetrahydro-spirilloxanthin
Unusual spirilloxanthin pathway
CrtL-e
δ-Carotene
ε-Carotene
Lutein biosynthesis
CrtL-b
α-Carotene
LUT5
Zeinoxanthin
LUT1
Lutein
CrtR-b
α-Cryptoxanthin
(2S,2'S)-Oscillol
(2S,2'S)-Oscillol 2,2'-di(α-L-fucoside)
3,4-Didehydrolycopene
Torulene
β-Apo-4'-carotenal
Neurosporaxanthin
AL2
CAO-2
YLO-1
Neurosporaxanthin biosynthesis
R.g.-Keto I
Thiothece-474
Okenone
Okenone pathway
R.g.-Keto III
CrtY
CruA/P
Chlorobactene
CrtU
γ-Carotene
Spheroidene pathway
Hydroxyneurosporene
Hydroxychlorobactene
1'-Hydroxytorulene
1'-Hydroxy-γ-carotene
3,4-Dihydrospheroidene
β-Zeacarotene
Demethylspheroidene
Hydroxychlorobactene glucoside
1'-Hydroxy-γ-carotene glucoside
Hydroxychlorobactene glucoside ester
1'-Hydroxy-γ-carotene glucoside ester
7,8-Dihydro-β-carotene
Hydroxyspheroidene
Spheroidene
Hydroxyspheroidenone
Spheroidenone
CrtA
CrtC
CrtD
CrtF
Retinol metabolism
Strigolactone ABC-rings
β-Carotene
5.2.1.14
9-cis-β-Carotene
1.13.11.68
9-cis-10'-Apo-β-carotenal
1.13.11.69
Carlactone
5-Deoxystrigol
1.14.13.-
Strigol
(2'S)-Deoxymyxol 2'-(2,4-di-O-methyl-α-L-fucoside)
(2'S)-Deoxymyxol 2'-α-L-fucoside
(3R,2'S)-Myxol 2'-(2,4-di-O-methyl-α-L-fucoside)
(3R,2'S)-Myxol 2'-α-L-fucoside
(3S,2'S)-4-Ketomyxol 2'-α-L-fucoside
Myxol biosynthesis
CrtR
CrtW
Isorenieratene
β-Isorenieratene
Thermobiszeaxanthin
Thermocryptoxanthin
Thermozeaxanthin
Zeaxanthin diglucoside
Nostoxanthin
Caloxanthin
Capsanthin
Capsorubin
5.3.99.8
CrtX
CrtU
CrtZ
1.14.15.24
β-Cryptoxanthin
Zeaxanthin
1.14.15.21
Low-light condition
Antheraxanthin
1.23.5.1
Violaxanthin
High-light condition
Xanthophyll cycle
5.3.99.9
Neoxanthin
9-cis-Violaxanthin
9'-cis-Neoxanthin
1.13.11.51
Echinenone
3-Hydroxyechinenone
3'-Hydroxyechinenone
Adonixanthin
Abscisic alcohol
Abscisic aldehyde
Abscisate
1.2.3.14
1.1.1.288
Xanthoxin
Xanthoxic acid
CrtO
Canthaxanthin
Phoenicoxanthin
Astaxanthin
Astaxanthin diester
Astaxanthin biosynthesis
Abscisic acid biosynthesis
8'-Hydroxyabscisate
Phaseic acid
Dihydrophaseic acid
1.14.13.93
2.4.1.263
3.2.1.175
Abscisic acid glucose ester
00906 3/27/18
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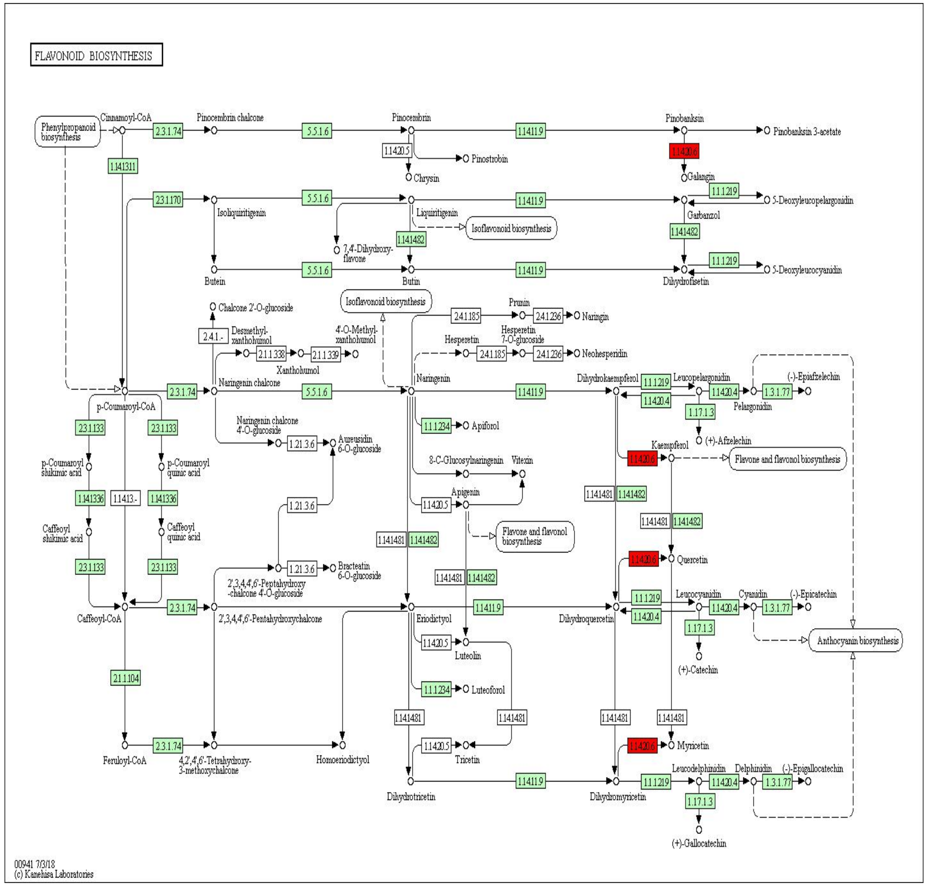
d


FLAVONOID BIOSYNTHESIS
Phenylpropanoid biosynthesis
Cinnamoyl-CoA
Pinocembrin chalcone
Pinocembrin
Pinobanksin
Pinobanksin 3-acetate
Pinostrobin
Chrysin
Galangin
Isoliquiritigenin
Liquiritigenin
Isoflavonoid biosynthesis
7,4'-Dihydroxy-flavone
Garbanzol
5-Deoxyleucopelargonidin
Butein
Butin
Dihydrofisetin
5-Deoxyleucocyanidin
Chalcone 2'-O-glucoside
Desmethyl-xanthohumol
4'-O-Methyl-xanthohumol
Xanthohumol
Prunin
Naringin
Hesperetin
Hesperetin 7-O-glucoside
Neohesperidin
p-Coumaroyl-CoA
Naringenin chalcone
Naringenin
Dihydrokaempferol
Leucopelargonidin
Pelargonidin
(-)-Epiafzelechin
(+)-Afzelechin
Naringenin chalcone 4'-O-glucoside
Aureusidin 6-O-glucoside
Apiforol
Kaempferol
Flavone and flavonol biosynthesis
p-Coumaroyl shikimic acid
p-Coumaroyl quinic acid
8-C-Glucosylnaringenin
Vitexin
Apigenin
Caffeoyl shikimic acid
Caffeoyl quinic acid
Bracteatin 6-O-glucoside
Quercetin
2',3,4,4',6'-Peptahydroxy-chalcone 4'-O-glucoside
Caffeoyl-CoA
2',3,4,4',6'-Pentahydroxychalcone
Eriodictyol
Dihydroquercetin
Leucocyanidin
Cyanidin
(-)-Epicatechin
Anthocyanin biosynthesis
Luteolin
(+)-Catechin
Luteoforol
Feruloyl-CoA
2',4',6'-Trihydroxy-3-methoxychalcone
Homoeriodictyol
Tricetin
Myricetin
Dihydrotricetin
Dihydromyricetin
Leucodelphinidin
Delphinidin
(-)-Epigallocatechin
(+)-Gallocatechin
00941 7/3/18
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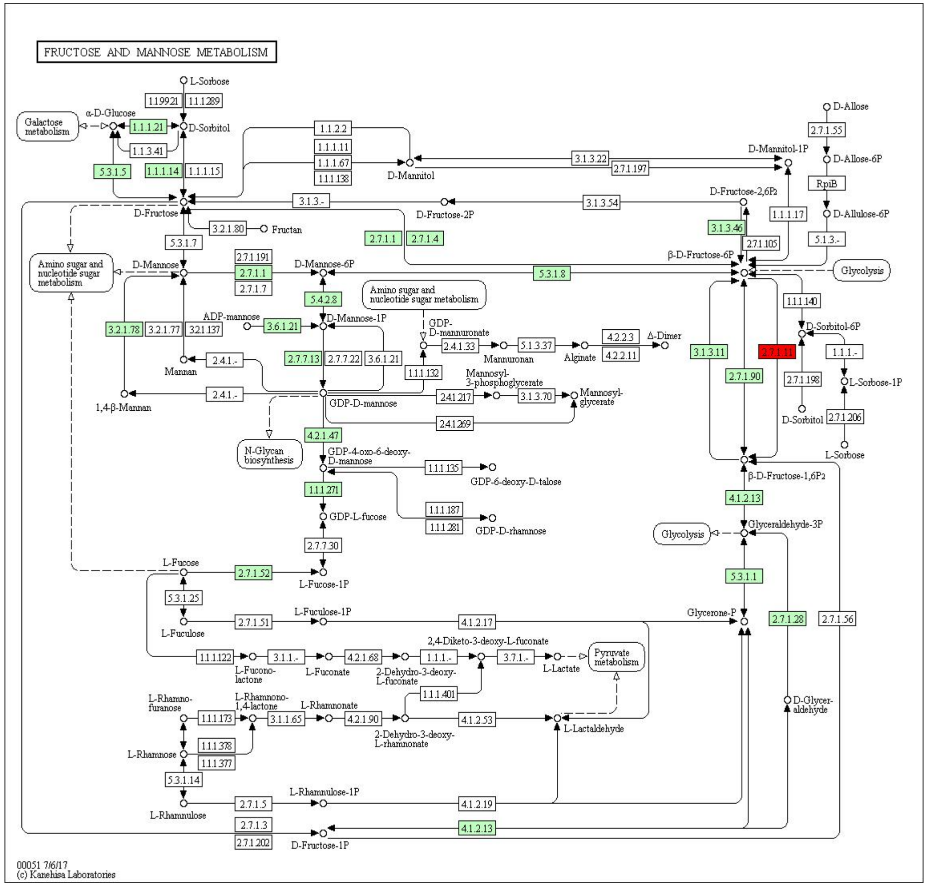
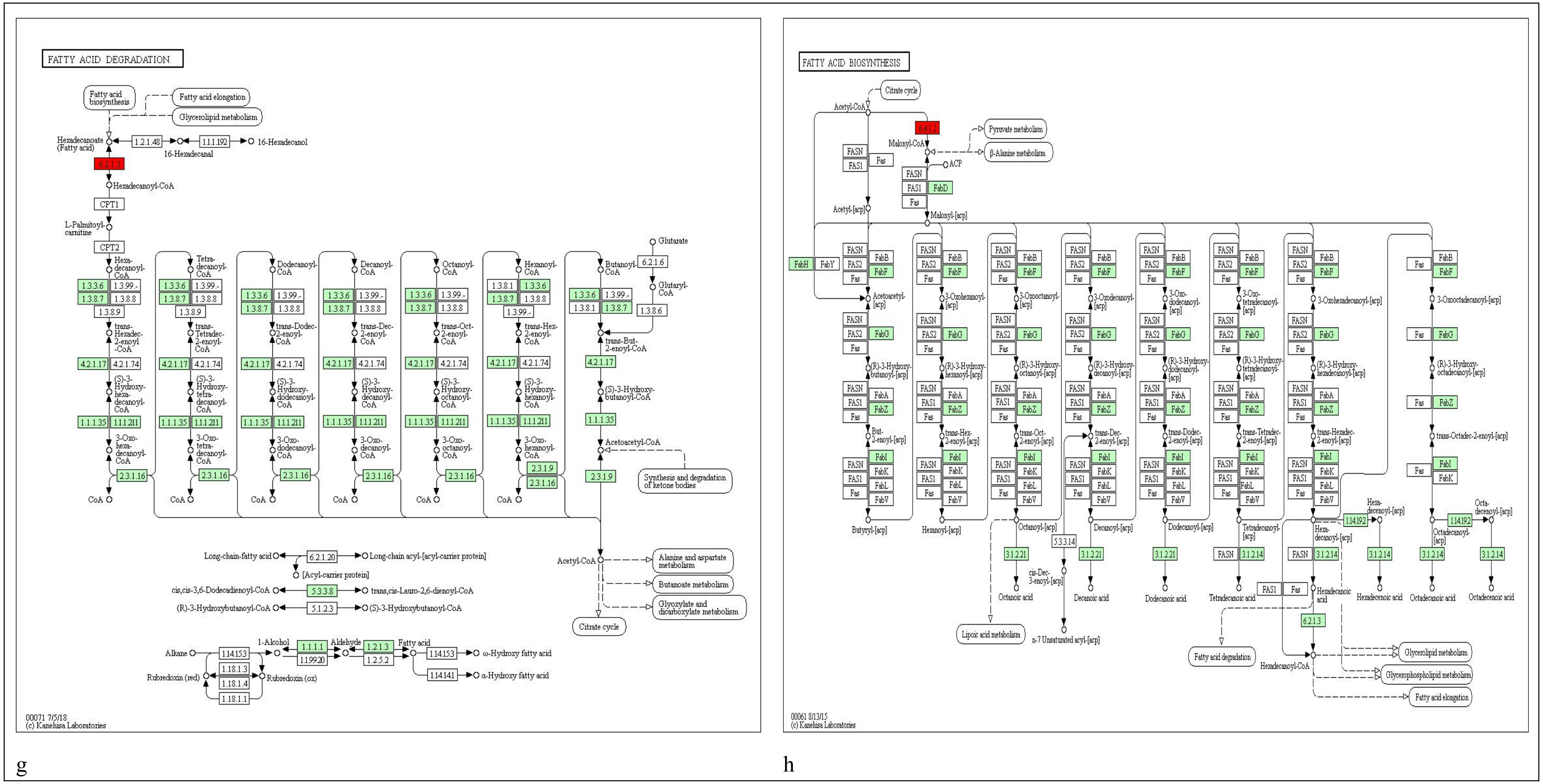
e


FRUCTOSE AND MANNOSE METABOLISM
L-Sorbose
α-D-Glucose
D-Sorbitol
Galactose metabolism
D-Mannitol
D-Mannitol-1P
D-Allose
D-Allose-6P
D-Allulose-6P
D-Fructose
D-Fructose-2P
D-Fructose-2,6P2
Fructan
Amino sugar and nucleotide sugar metabolism
D-Mannose
D-Mannose-6P
β-D-Fructose-6P
Glycolysis
ADP-mannose
D-Mannose-1P
GDP-D-mannuronate
Mannuronan
Alginate
Δ-Dimer
D-Sorbitol-6P
Mannan
1,4-β-Mannan
GDP-D-mannose
Mannosyl-3-phosphoglycerate
Mannosyl-glycerate
D-Sorbitol
L-Sorbose-1P
N-Glycan biosynthesis
GDP-4-oxo-6-deoxy-D-mannose
GDP-6-deoxy-D-talose
L-Sorbose
β-D-Fructose-1,6P2
GDP-L-fucose
GDP-D-rhamnose
Glyceraldehyde-3P
L-Fucose
L-Fucose-1P
L-Fuculose
L-Fuculose-1P
Glycerone-P
L-Fucono-lactone
L-Fuconate
2-Dehydro-3-deoxy-L-fuconate
2,4-Diketo-3-deoxy-L-fuconate
L-Lactate
Pyruvate metabolism
L-Rhamno-furanose
L-Rhamnono-1,4-lactone
L-Rhamnonate
2-Dehydro-3-deoxy-L-rhamnonate
L-Lactaldehyde
D-Glycer-aldehyde
L-Rhamnose
L-Rhamnulose
L-Rhamnulose-1P
D-Fructose-1P
00051 7/6/17
(c) Kanehisa Laboratories

f


FATTY ACID DEGRADATION
Fatty acid biosynthesis
Fatty acid elongation
Glycerolipid metabolism
Hexadecanoate (Fatty acid)
1.2.1.48
16-Hexadecanal
1.1.1.192
16-Hexadecanol
6.2.1.3
Hexadecanoyl-CoA
CPT1
L-Palmitoyl-carnitine
CPT2
Hexadecanoyl-CoA
Tetradecanoyl-CoA
Dodecanoyl-CoA
Decanoyl-CoA
Octanoyl-CoA
Hexanoyl-CoA
Butanoyl-CoA
Glutarate
6.2.1.6
Glutaryl-CoA
1.3.8.6
1.3.3.6
1.3.99.-
1.3.8.7
1.3.8.8
1.3.8.9
1.3.8.1
trans-Hexadec-2-enoyl-CoA
trans-Tetradec-2-enoyl-CoA
trans-Dodec-2-enoyl-CoA
trans-Dec-2-enoyl-CoA
trans-Oct-2-enoyl-CoA
trans-Hex-2-enoyl-CoA
trans-But-2-enoyl-CoA
4.2.1.17
4.2.1.74
(S)-3-Hydroxyhexadecanoyl-CoA
(S)-3-Hydroxytetradecanoyl-CoA
(S)-3-Hydroxydodecanoyl-CoA
(S)-3-Hydroxydecanoyl-CoA
(S)-3-Hydroxyoctanoyl-CoA
(S)-3-Hydroxyhexanoyl-CoA
(S)-3-Hydroxybutanoyl-CoA
1.1.1.35
1.1.1.211
3-Oxohexadecanoyl-CoA
3-Oxotetradecanoyl-CoA
3-Oxododecanoyl-CoA
3-Oxodecanoyl-CoA
3-Oxooctanoyl-CoA
3-Oxohexanoyl-CoA
Acetoacetyl-CoA
2.3.1.16
2.3.1.9
CoA
Synthesis and degradation of ketone bodies
Acetyl-CoA
Alanine and aspartate metabolism
Butanoate metabolism
Glyoxylate and dicarboxylate metabolism
Citrate cycle
Long-chain-fatty acid
6.2.1.20
Long-chain acyl-[acyl-carrier protein]
[Acyl-carrier protein]
cis,cis-3,6-Dodecadienoyl-CoA
5.3.3.8
trans,cis-Lauro-2,6-dienoyl-CoA
(R)-3-Hydroxybutanoyl-CoA
5.1.2.3
(S)-3-Hydroxybutanoyl-CoA
Alkane
1.14.15.3
1-Alcohol
1.1.1.1
1.1.99.20
Aldehyde
1.2.1.3
1.2.5.2
Fatty acid
1.14.15.3
ω-Hydroxy fatty acid
1.14.14.1
α-Hydroxy fatty acid
1.18.1.3
1.18.1.4
1.18.1.1
Rubredoxin (red)
Rubredoxin (ox)
00071 7/5/18
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g
FATTY ACID BIOSYNTHESIS
Citrate cycle
Acetyl-CoA
6.4.1.2
Pyruvate metabolism
Malonyl-CoA
β-Alanine metabolism
ACP
FASN
FAS1
Fas
FabD
Acetyl-[acp]
Malonyl-[acp]
FabH
FabY
FAS2
FabB
FabF
FabG
FabA
FabZ
FabI
FabK
FabL
FabV
Acetoacetyl-[acp]
3-Oxohexanoyl-[acp]
3-Oxooctanoyl-[acp]
3-Oxodecanoyl-[acp]
3-Oxododecanoyl-[acp]
3-Oxotetradecanoyl-[acp]
3-Oxohexadecanoyl-[acp]
3-Oxooctadecanoyl-[acp]
(R)-3-Hydroxybutanoyl-[acp]
(R)-3-Hydroxyhexanoyl-[acp]
(R)-3-Hydroxyoctanoyl-[acp]
(R)-3-Hydroxydecanoyl-[acp]
(R)-3-Hydroxydodecanoyl-[acp]
(R)-3-Hydroxytetradecanoyl-[acp]
(R)-3-Hydroxyhexadecanoyl-[acp]
(R)-3-Hydroxyoctadecanoyl-[acp]
But-2-enoyl-[acp]
trans-Hex-2-enoyl-[acp]
trans-Oct-2-enoyl-[acp]
trans-Dec-2-enoyl-[acp]
trans-Dodec-2-enoyl-[acp]
trans-Tetradec-2-enoyl-[acp]
trans-Hexadec-2-enoyl-[acp]
trans-Octadec-2-enoyl-[acp]
Butyryl-[acp]
Hexanoyl-[acp]
Octanoyl-[acp]
Decanoyl-[acp]
Dodecanoyl-[acp]
Tetradecanoyl-[acp]
Hexadecanoyl-[acp]
Octadecanoyl-[acp]
Hexadecenoyl-[acp]
Octadecenoyl-[acp]
1.14.19.2
5.3.3.14
cis-Dec-3-enoyl-[acp]
n-7 Unsaturated acyl-[acp]
3.1.2.21
3.1.2.14
Octanoic acid
Decanoic acid
Dodecanoic acid
Tetradecanoic acid
Hexadecanoic acid
Hexadecenoic acid
Octadecanoic acid
Octadecenoic acid
6.2.1.3
Hexadecanoyl-CoA
Lipoic acid metabolism
Fatty acid degradation
Glycerolipid metabolism
Glycerophospholipid metabolism
Fatty acid elongation
00061 8/13/15
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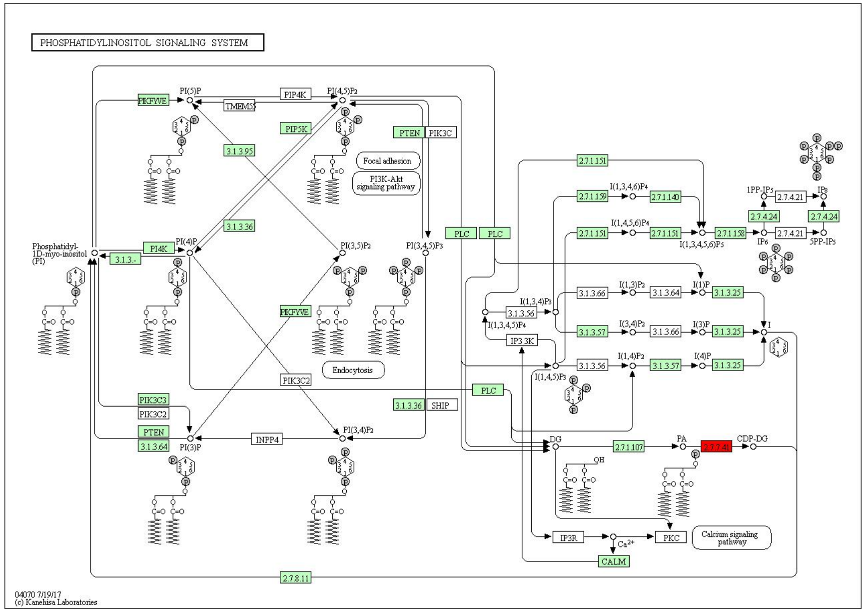
h



i

Additional file 18 Figure S6 The targets for DE miRNAs enriched in the top 20 KEGG pathway. a: sulfur metabolism in L4 *vs* L0, and the other five groups also in the top 20 pathway; b: sulfur relay system in L4 *vs* L0, the L4 *vs* L13, L0 *vs* L13 and L0 *vs* L28 also in the top 20 pathway; c: sesquiterpenoid and triterpenoid biosynthesis in L4 *vs* L28, the L4 *vs* L13 and L13 *vs* L28 also in the top 20 pathway; d: carotenoid biosynthesis in L4 *vs* L28, and the L0 *vs* L28 also in the top 20 pathway; e: flavonoid biosynthesis in L4 *vs* L0, and also in the L4 *vs* L28, L0 *vs* L13 and L13 *vs* L28 (not at the top 20 pathway); f: fructose and mannose metabolism in L0 *vs* L13; g: fatty acid degradation in L4 *vs* L0; h: fatty acid biosynthesis in L4 *vs* L28; i: phosphatidylinositol signaling system in L0 *vs* L13. The nodes are marked in red background color indicating the DEGs is up-regulated expression, and the nodes are marked in green background color indicating the DEGs is down-regulated expression. On the other side, the white nodes indicated the genes are DEGs, but there is no distinguishment of the DEGs about the up- / down-regulated expression.