LEGENDS TO SUPPLEMENTARY FIGURES

Fig S1: Signal distribution plots (A) and Principal component analysis (PCA, B) of all intensity values achieved in the study (three samples for each egg type AM, RE and E0).

Fig S2: Enriched GO biological process terms in amictic eggs (AM), resting eggs (RE) and resting eggs before hatching (E0).

Fig S3: Enriched KEGG pathways in AM (blue), RE (red) and E0 (green). For each pathway, the nominator in the bar labels shows the number of proteins displayed in each egg type and the denominator shows the total number of proteins (KOs) in the translated reference transcriptome that were associated with the pathway.

Fig S4: Enriched GO biological processes of the proteins with significant differences in their abundance in the comparisons of AM vs. RE (blue) and AM vs. E0 (red).

Fig S5: A heat-map showing the abundance level of proteins in Fatty acid degradation pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. Two vertical bars to the left of the heat map indicate whether the abundance of a protein significantly differed in the comparison of AM vs RE (left) or AM vs E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p-value<0.05, FC>3). An orange box indicates that the protein was identified in one egg type but not in the other. A while box indicates there were no statistically significant differences in the abundance of the protein, in the compared groups.

Fig S6: A KEGG map displaying the proteins in association with Valine, leucine and isoleucine degradation pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S7: A KEGG map displaying the proteins in association with the Glycolysis/Gluconeogenesis pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show

proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S8: A heat-map showing the abundance level of proteins in the Glycolysis/Gluconeogenesis pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

Fig S9: A heat-map showing the abundance level of proteins in the Citrate cycle (TCA) pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

Fig S10: A KEGG map displaying the proteins in association with the Pyruvate metabolism pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S11: A heat-map showing the abundance level of proteins in the Pyruvate metabolism pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein

showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

Fig S12: A KEGG map displaying the proteins in association with the Cell cycle pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S13: A KEGG map displaying the proteins in association with the Spliceosome pathway. Boxes in grey show he proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S14: A KEGG map displaying the proteins in association with the mRNA surveillance pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S15: A KEGG map displaying the proteins in association with the Proteasome pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

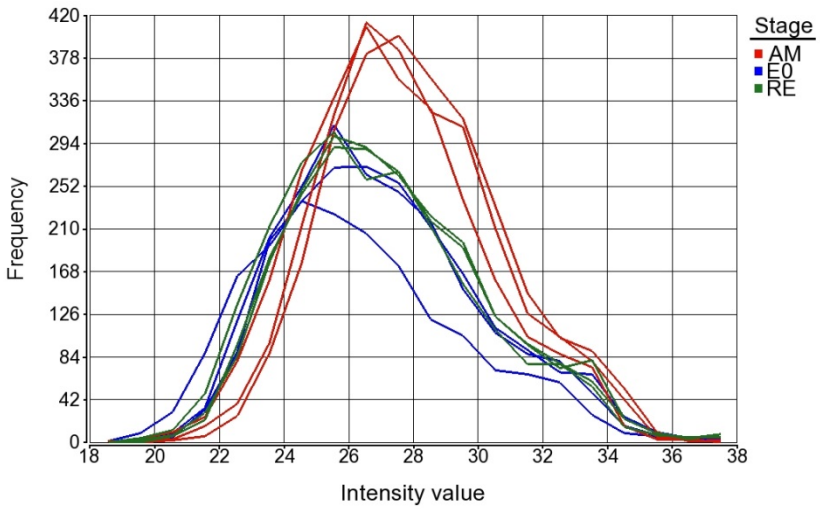
Fig S16: A heat-map showing the abundance level of proteins in the Oxidative phosphorylation pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

Fig S17: A KEGG map displaying the proteins in association with the Pentose phosphate pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

Fig S18: A heat-map showing the abundance level of proteins in the Pentose phosphate pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

Fig S19: A KEGG map displaying the proteins in association with the Protein processing in endoplasmic reticulum pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

A


Frequency
420
378
336
294
252
210
168
126
84
42
0
18
20
22
24
26
28
30
32
34
36
38
Intensity value
Stage
AM
E0
RE

B

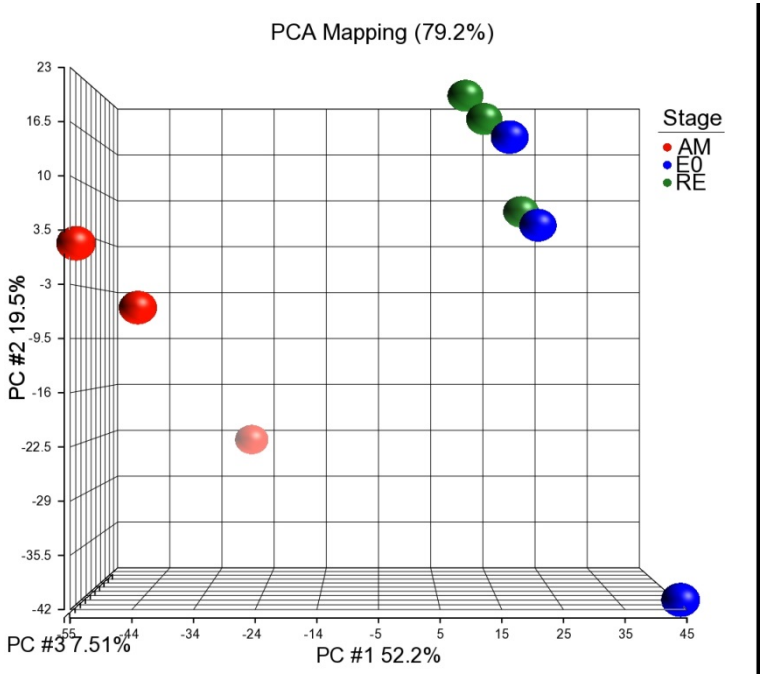

PCA Mapping (79.2%)
23
16.5
10
3.5
-3
-9.5
-16
-22.5
-29
-35.5
-42
PC #2 19.5%
-55
-44
-34
-24
-14
-5
5
15
25
35
45
PC #3 7.51%
PC #1 52.2%
Stage
AM
E0
RE

Fig S1

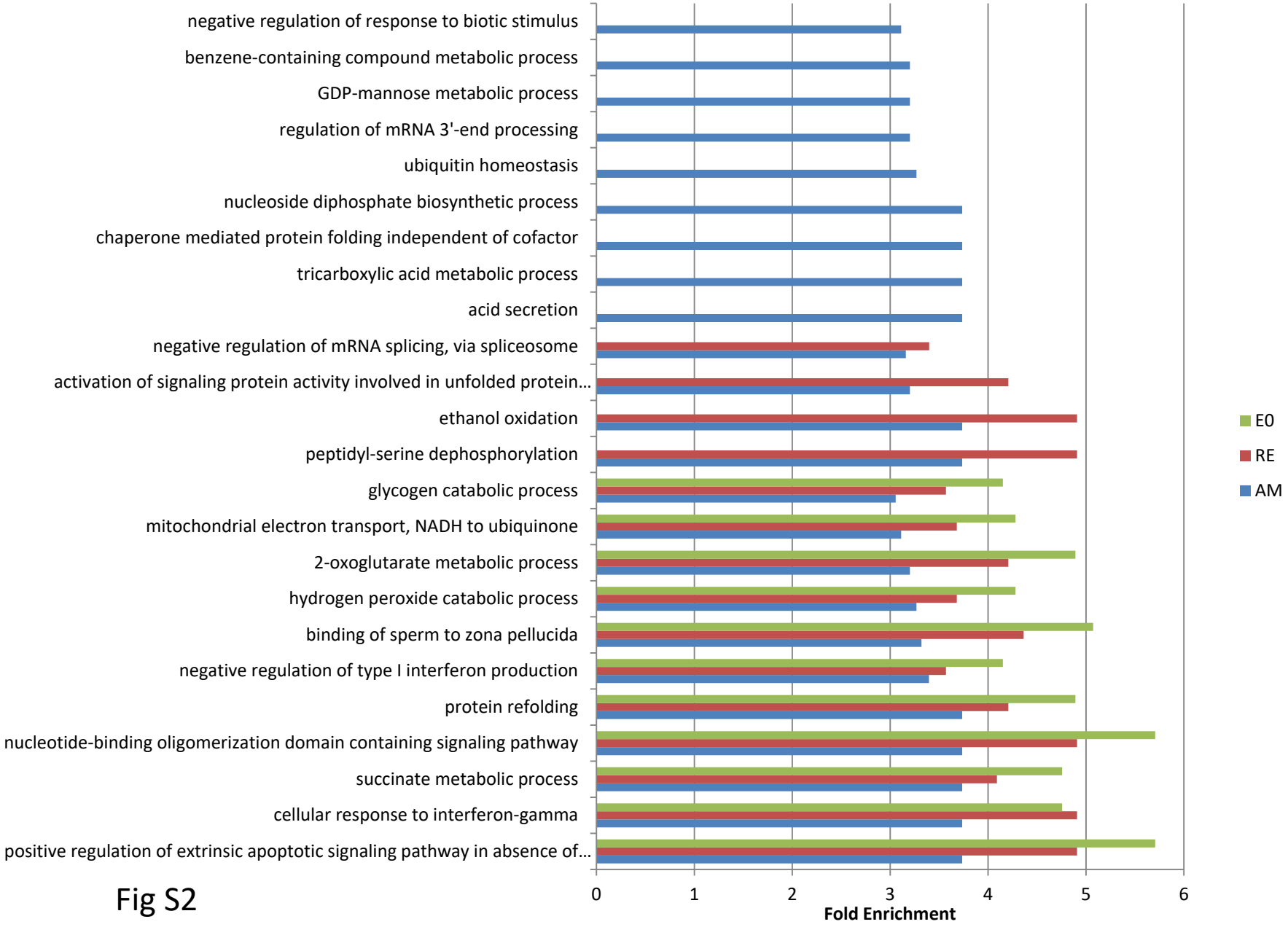

negative regulation of response to biotic stimulus
benzene-containing compound metabolic process
GDP-mannose metabolic process
regulation of mRNA 3'-end processing
ubiquitin homeostasis
nucleoside diphosphate biosynthetic process
chaperone mediated protein folding independent of cofactor
tricarboxylic acid metabolic process
acid secretion
negative regulation of mRNA splicing, via spliceosome
activation of signaling protein activity involved in unfolded protein...
ethanol oxidation
peptidyl-serine dephosphorylation
glycogen catabolic process
mitochondrial electron transport, NADH to ubiquinone
2-oxoglutarate metabolic process
hydrogen peroxide catabolic process
binding of sperm to zona pellucida
negative regulation of type I interferon production
protein refolding
nucleotide-binding oligomerization domain containing signaling pathway
succinate metabolic process
cellular response to interferon-gamma
positive regulation of extrinsic apoptotic signaling pathway in absence of...
0
1
2
3
4
5
6
Fold Enrichment
E0
RE
AM

Fig S2

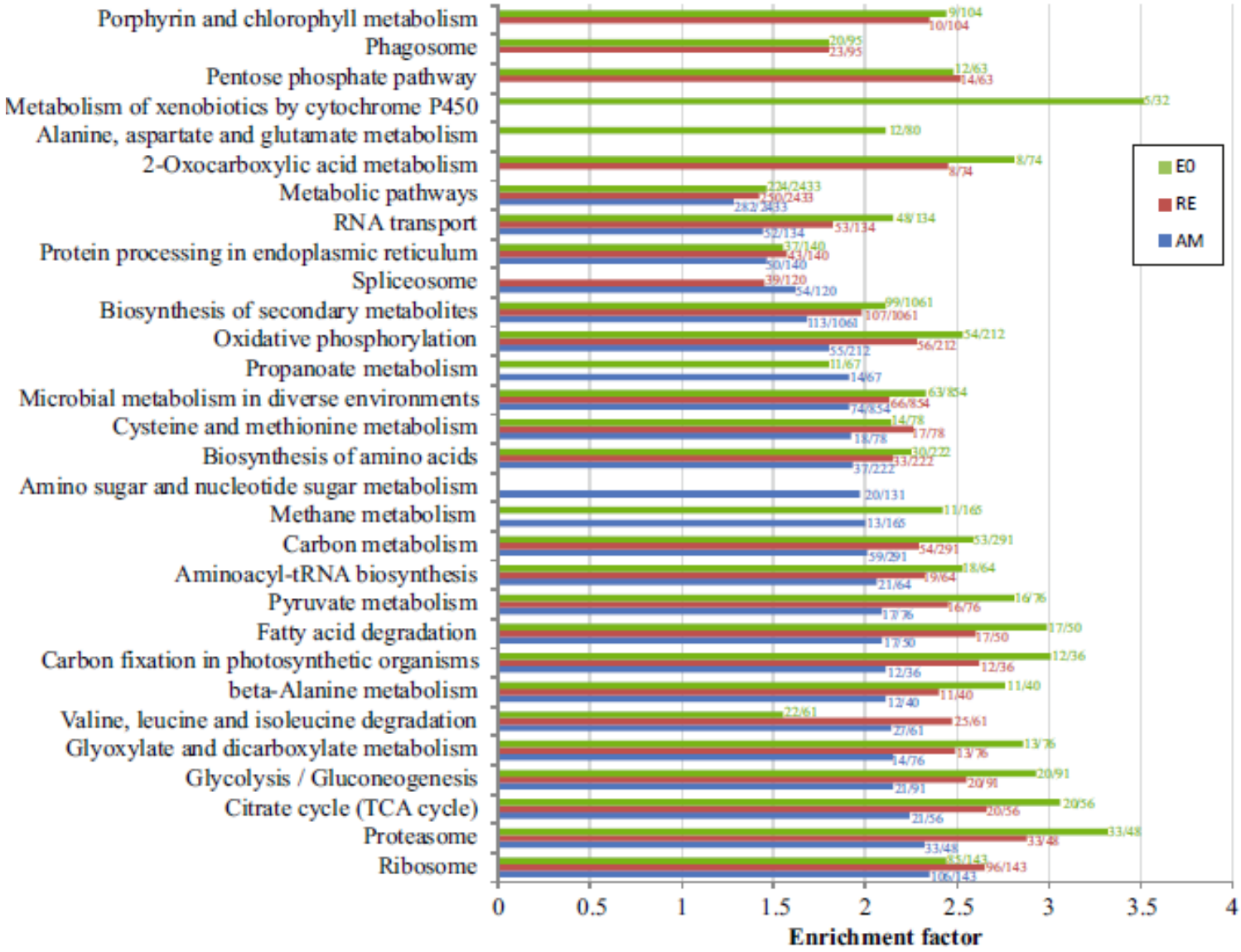

Porphyrin and chlorophyll metabolism
Phagosome
Pentose phosphate pathway
Metabolism of xenobiotics by cytochrome P450
Alanine, aspartate and glutamate metabolism
2-Oxocarboxylic acid metabolism
Metabolic pathways
RNA transport
Protein processing in endoplasmic reticulum
Spliceosome
Biosynthesis of secondary metabolites
Oxidative phosphorylation
Propanoate metabolism
Microbial metabolism in diverse environments
Cysteine and methionine metabolism
Biosynthesis of amino acids
Amino sugar and nucleotide sugar metabolism
Methane metabolism
Carbon metabolism
Aminoacyl-tRNA biosynthesis
Pyruvate metabolism
Fatty acid degradation
Carbon fixation in photosynthetic organisms
beta-Alanine metabolism
Valine, leucine and isoleucine degradation
Glyoxylate and dicarboxylate metabolism
Glycolysis / Gluconeogenesis
Citrate cycle (TCA cycle)
Proteasome
Ribosome
9/104
10/104
20/95
23/95
12/63
14/63
5/32
12/80
8/74
8/74
224/2433
250/2433
282/2433
48/134
53/134
52/134
37/140
43/140
50/140
39/120
54/120
99/1061
107/1061
113/1061
54/212
56/212
55/212
11/67
14/67
63/854
66/854
74/854
14/78
17/78
18/78
30/222
33/222
37/222
20/131
11/165
13/165
53/291
54/291
59/291
18/64
19/64
21/64
16/76
16/76
17/76
17/50
17/50
17/50
12/36
12/36
12/36
11/40
11/40
12/40
22/61
25/61
27/61
13/76
13/76
14/76
20/91
20/91
21/91
20/56
20/56
21/56
33/48
33/48
33/48
85/143
96/143
106/143
EO
RE
AM
0
0.5
1
1.5
2
2.5
3
3.5
4
Enrichment factor

Fig S3

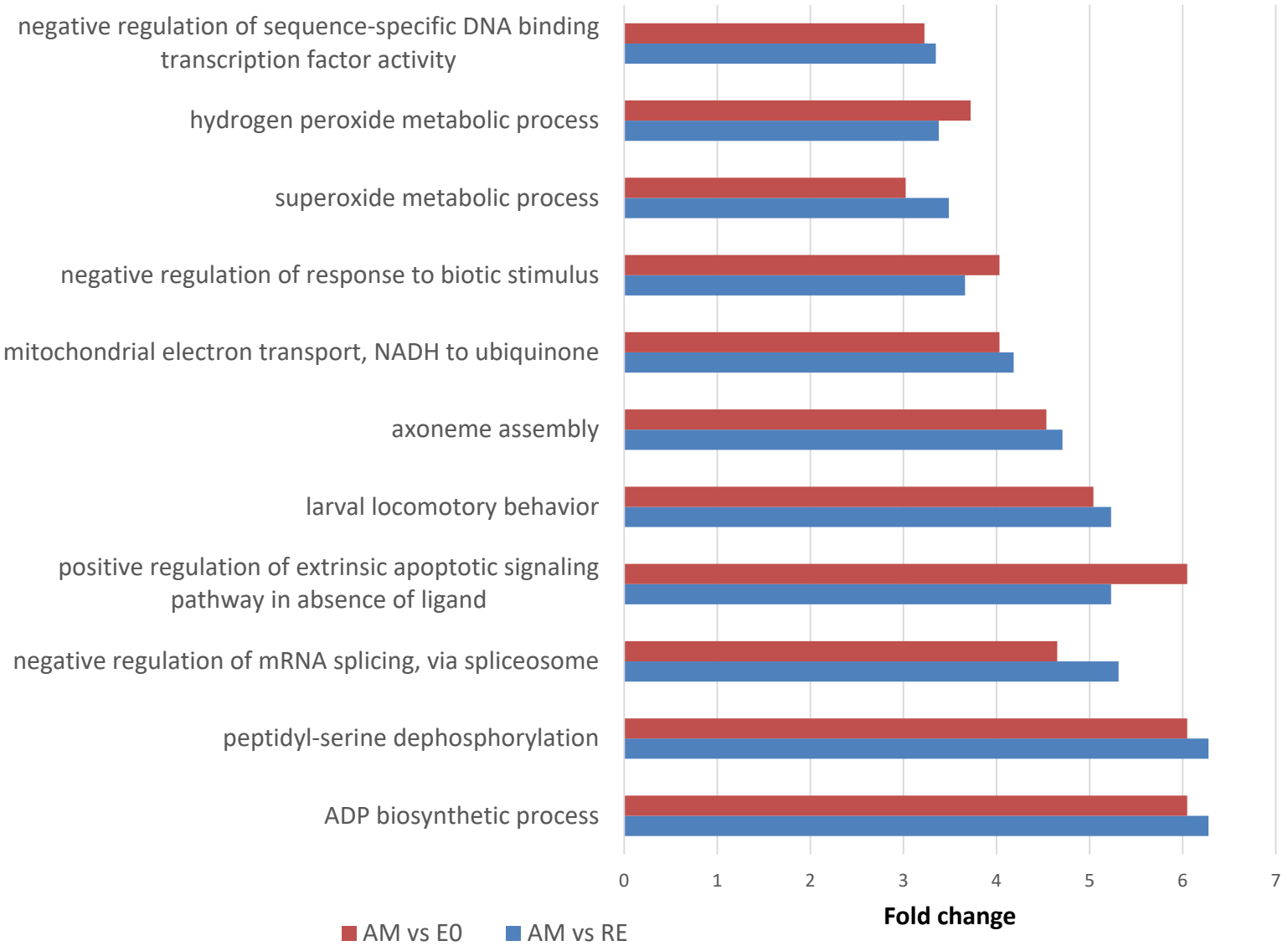

negative regulation of sequence-specific DNA binding transcription factor activity
hydrogen peroxide metabolic process
superoxide metabolic process
negative regulation of response to biotic stimulus
mitochondrial electron transport, NADH to ubiquinone
axoneme assembly
larval locomotory behavior
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand
negative regulation of mRNA splicing, via spliceosome
peptidyl-serine dephosphorylation
ADP biosynthetic process
0
1
2
3
4
5
6
7
Fold change
AM vs E0
AM vs RE

Fig S4

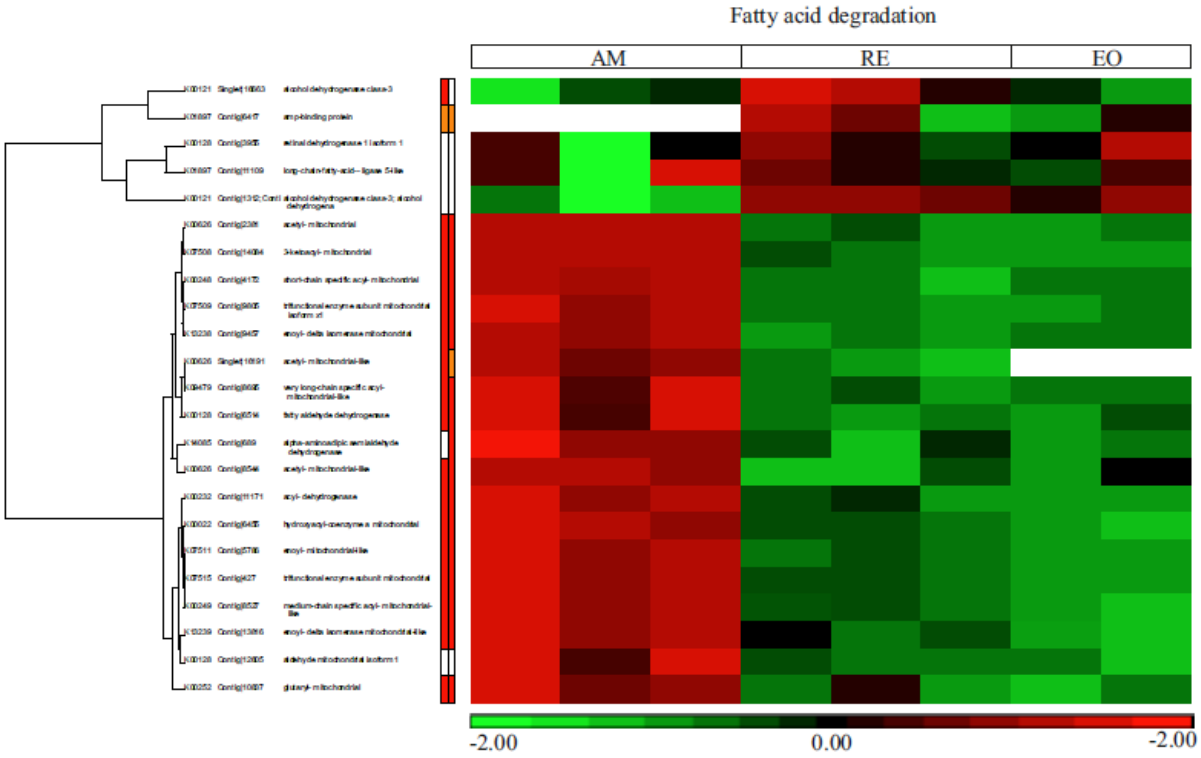


Fig S5

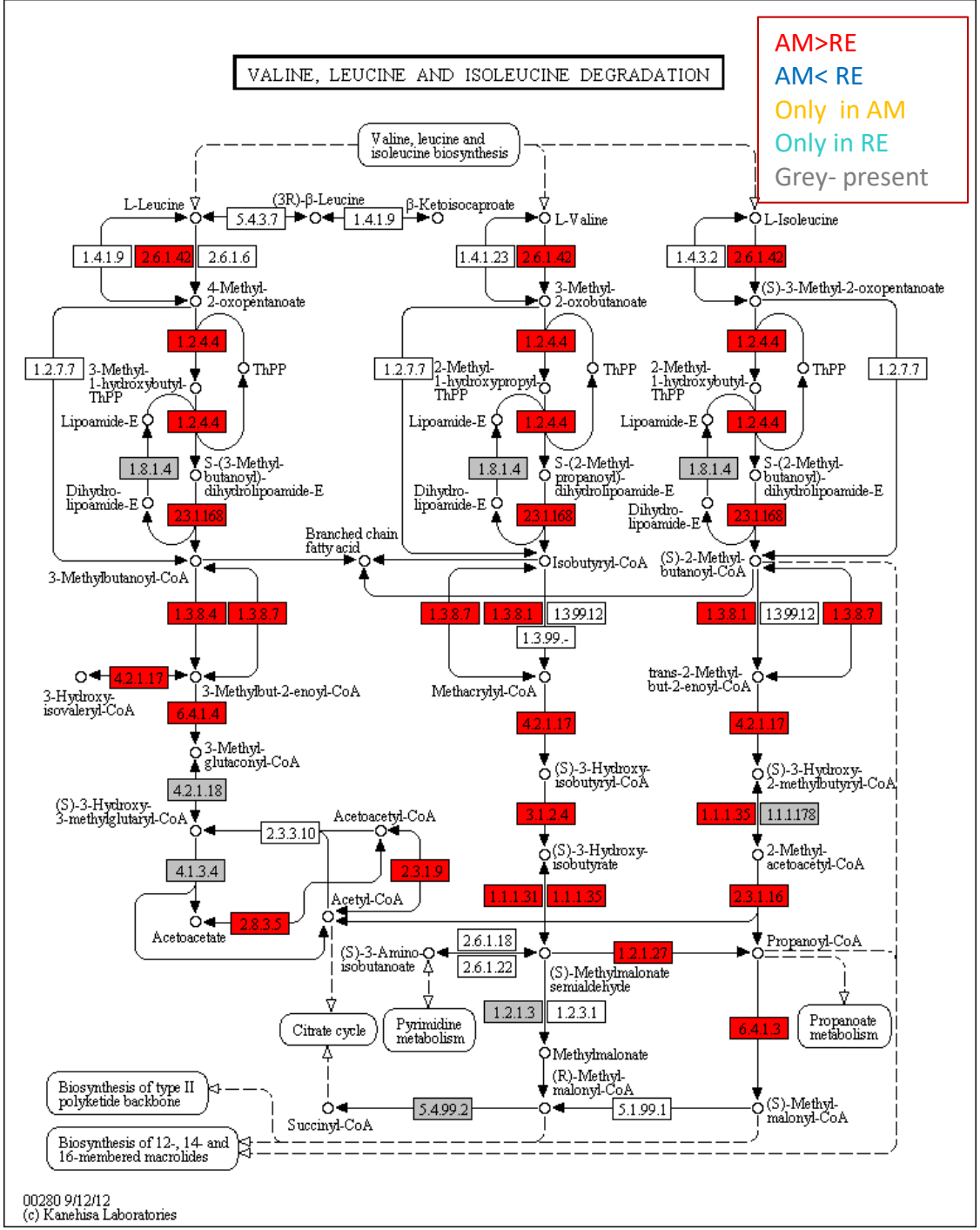

AM>RE
AM< RE
Only in AM
Only in RE
Grey- present
VALINE, LEUCINE AND ISOLEUCINE DEGRADATION
Valine, leucine and isoleucine biosynthesis
L-Leucine
(3R)-β-Leucine
β-Ketoisocaproate
L-Valine
L-Isoleucine
5.4.3.7
1.4.1.9
1.4.1.23
1.4.3.2
2.6.1.42
2.6.1.6
4-Methyl-2-oxopentanoate
3-Methyl-2-oxobutanoate
(S)-3-Methyl-2-oxopentanoate
1.2.4.4
1.2.7.7
3-Methyl-1-hydroxybutyl-ThPP
2-Methyl-1-hydroxypropyl-ThPP
2-Methyl-1-hydroxybutyl-ThPP
ThPP
Lipoamide-E
1.8.1.4
S-(3-Methyl-butanoyl)-dihydrolipoamide-E
S-(2-Methyl-propanoyl)-dihydrolipoamide-E
S-(2-Methyl-butanoyl)-dihydrolipoamide-E
Dihydro-lipoamide-E
2.3.1.168
Branched chain fatty acid
3-Methylbutanoyl-CoA
Isobutyryl-CoA
(S)-2-Methyl-butanoyl-CoA
1.3.8.4
1.3.8.7
1.3.8.1
1.3.99.12
1.3.99.-
4.2.1.17
3-Hydroxy-isovaleryl-CoA
3-Methylbut-2-enoyl-CoA
Methacrylyl-CoA
trans-2-Methyl-but-2-enoyl-CoA
6.4.1.4
3-Methyl-glutaconyl-CoA
(S)-3-Hydroxy-isobutyryl-CoA
(S)-3-Hydroxy-2-methylbutyryl-CoA
4.2.1.18
3.1.2.4
1.1.1.35
1.1.1.178
(S)-3-Hydroxy-3-methylglutaryl-CoA
2.3.3.10
Acetoacetyl-CoA
(S)-3-Hydroxy-isobutyrate
2-Methyl-acetoacetyl-CoA
4.1.3.4
2.3.1.9
1.1.1.31
2.3.1.16
Acetyl-CoA
Acetoacetate
2.8.3.5
2.6.1.18
2.6.1.22
(S)-3-Amino-isobutanoate
1.2.1.27
(S)-Methylmalonate semialdehyde
Propanoyl-CoA
Citrate cycle
Pyrimidine metabolism
1.2.1.3
1.2.3.1
6.4.1.3
Propanoate metabolism
Methylmalonate
(R)-Methyl-malonyl-CoA
Biosynthesis of type II polyketide backbone
5.4.99.2
5.1.99.1
(S)-Methyl-malonyl-CoA
Succinyl-CoA
Biosynthesis of 12-, 14- and 16-membered macrolides
00280 9/12/12
(c) Kanehisa Laboratories

Fig S6

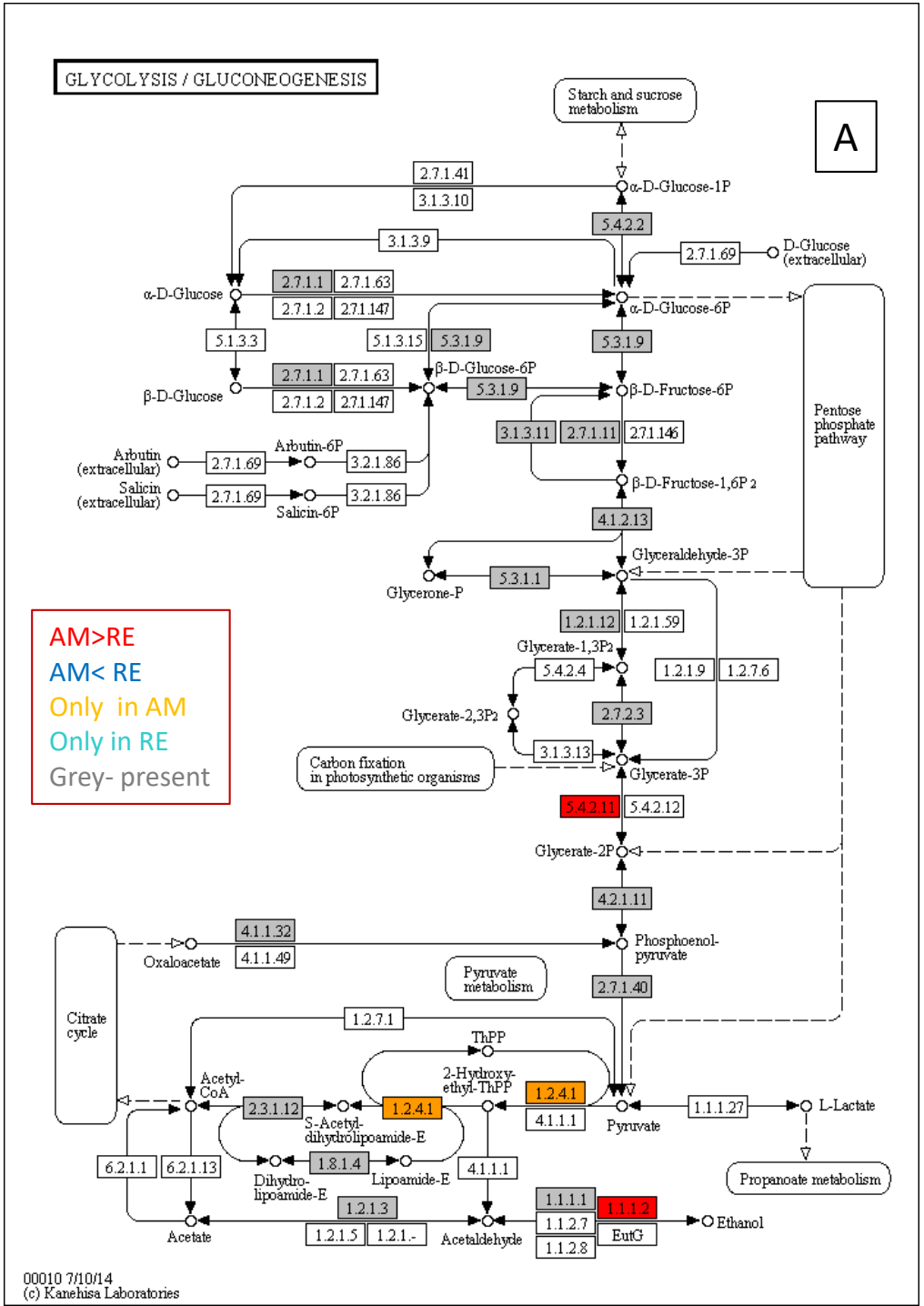
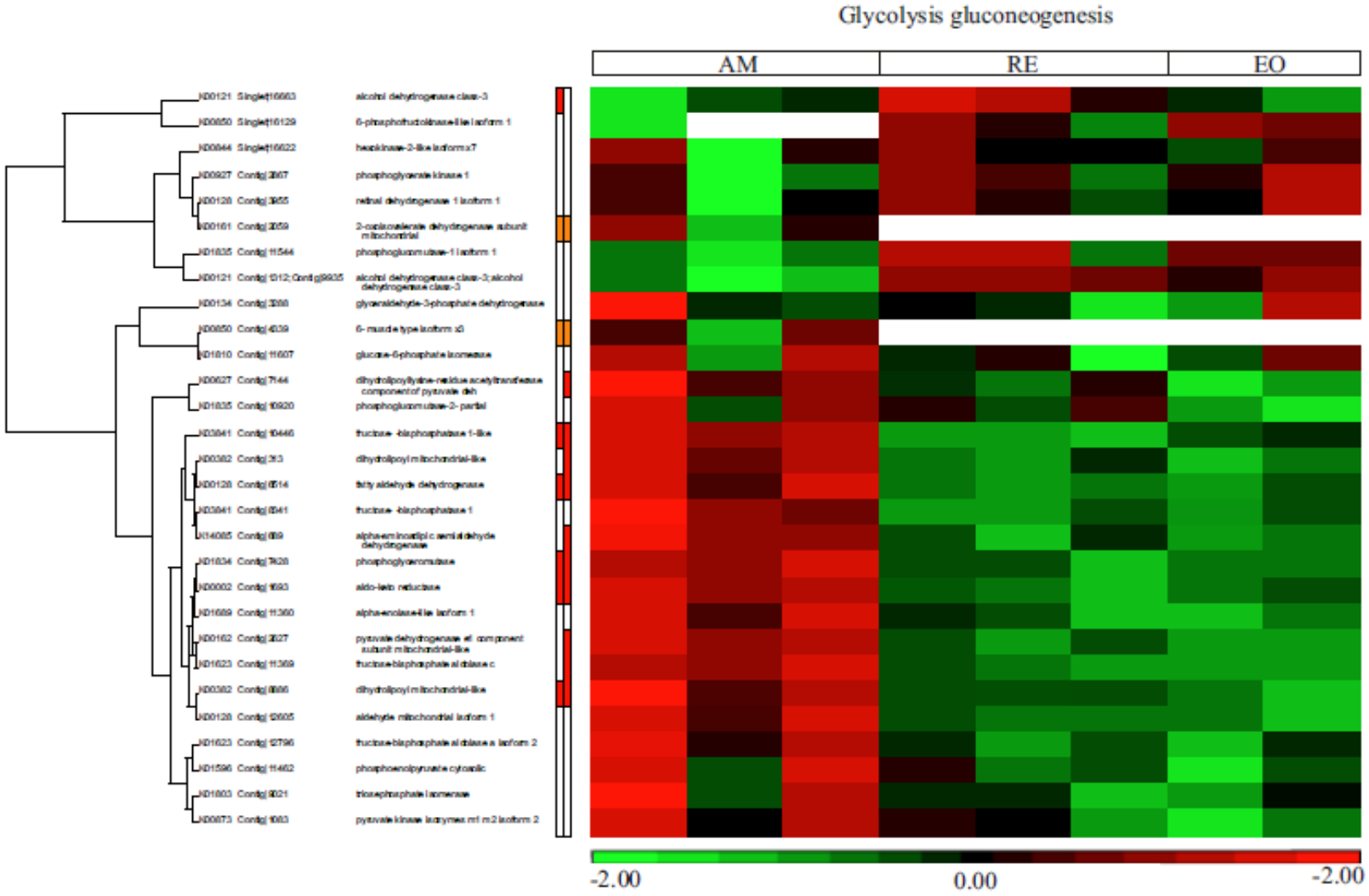

GLYCOLYSIS / GLUCONEOGENESIS
A
Starch and sucrose metabolism
α-D-Glucose-1P
D-Glucose (extracellular)
α-D-Glucose
α-D-Glucose-6P
β-D-Glucose-6P
β-D-Glucose
β-D-Fructose-6P
Pentose phosphate pathway
Arbutin (extracellular)
Arbutin-6P
Salicin (extracellular)
Salicin-6P
β-D-Fructose-1,6P2
Glyceraldehyde-3P
Glycerone-P
AM>RE
AM< RE
Only in AM
Only in RE
Grey- present
Glycerate-1,3P2
Glycerate-2,3P2
Carbon fixation in photosynthetic organisms
Glycerate-3P
Glycerate-2P
Phosphoenol-pyruvate
Oxaloacetate
Pyruvate metabolism
Citrate cycle
ThPP
2-Hydroxy-ethyl-ThPP
Acetyl-CoA
S-Acetyl-dihydrolipoamide-E
Dihydro-lipoamide-E
Lipoamide-E
Pyruvate
L-Lactate
Propanoate metabolism
Acetate
Acetaldehyde
Ethanol
EutG
00010 7/10/14
(c) Kanehisa Laboratories

Fig S7



Fog S8

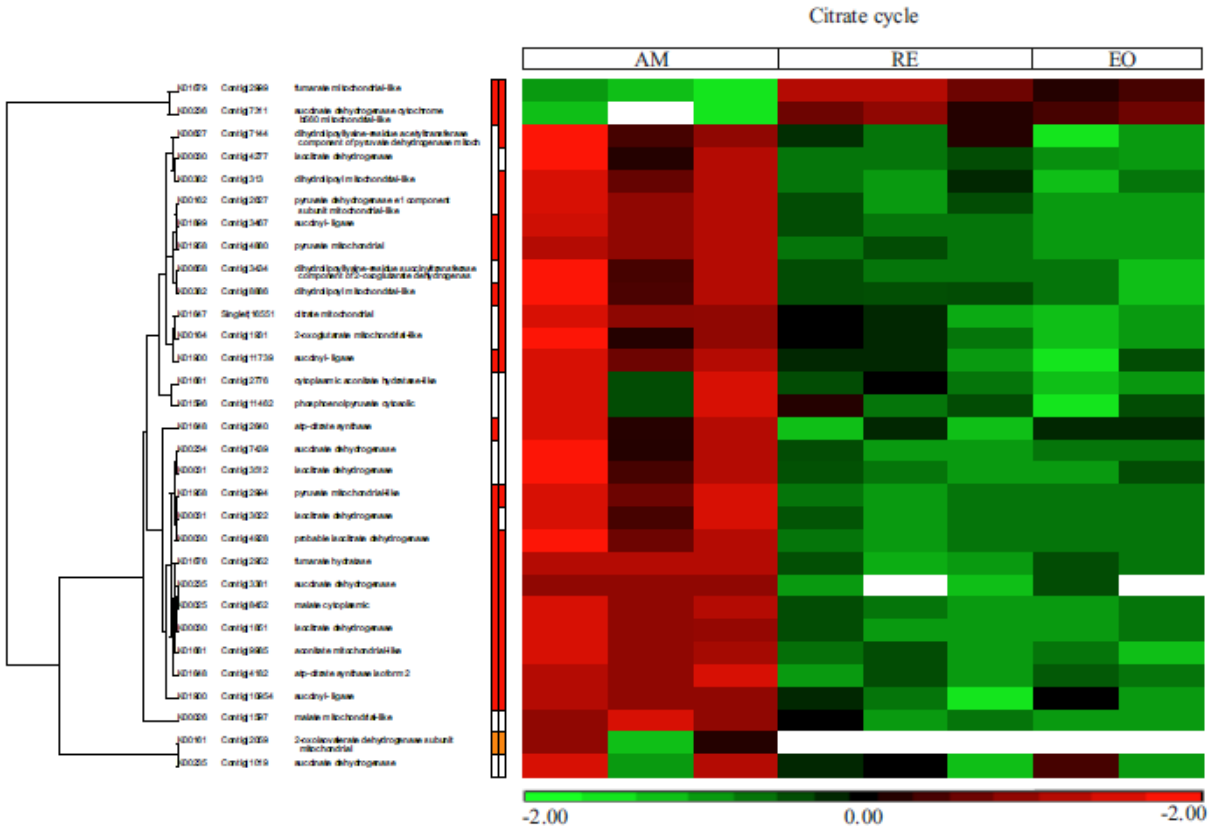


Fig S9

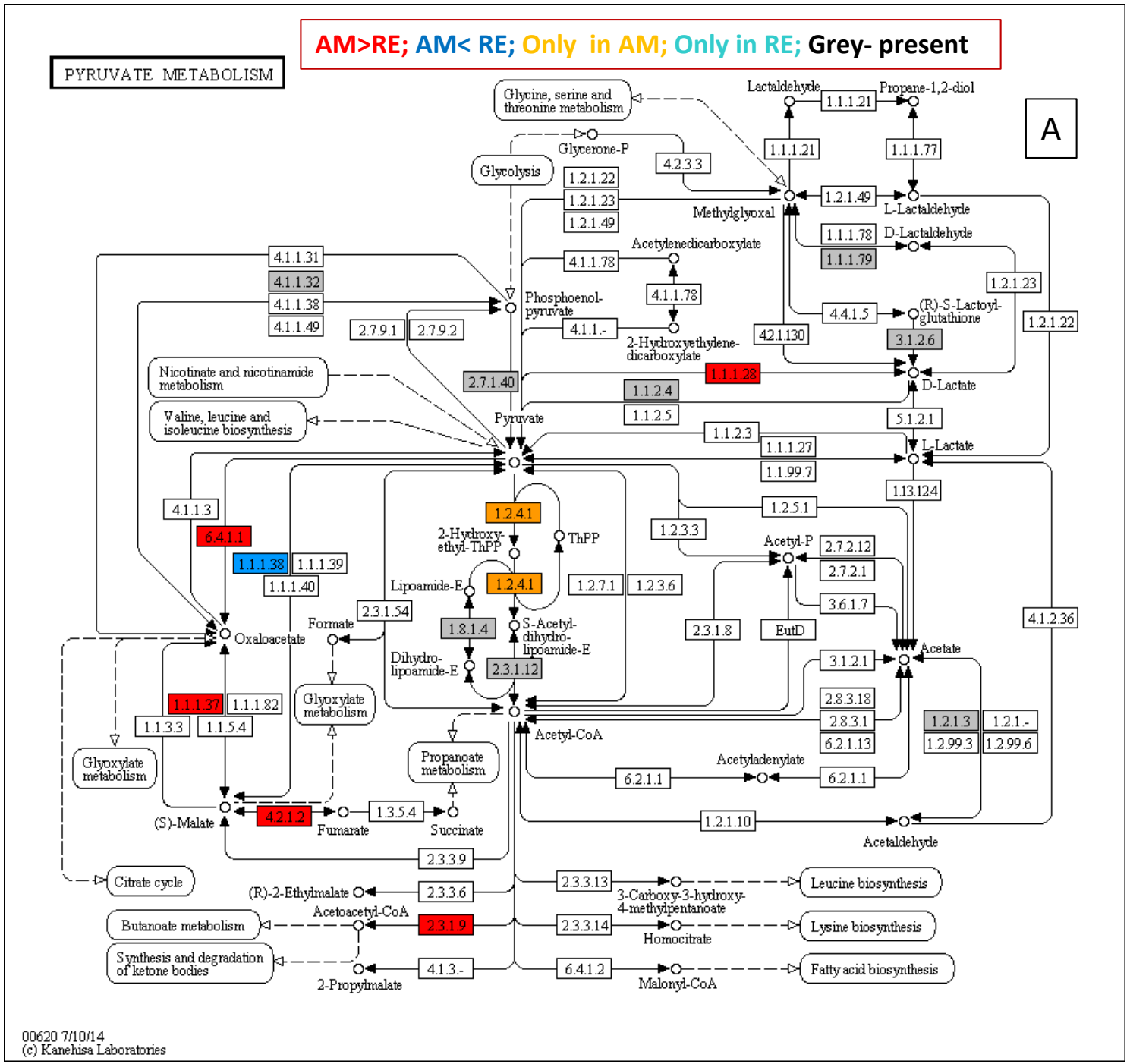

AM>RE; AM< RE; Only in AM; Only in RE; Grey- present
PYRUVATE METABOLISM
A
Glycine, serine and threonine metabolism
Glycerone-P
Glycolysis
Methylglyoxal
Lactaldehyde
Propane-1,2-diol
L-Lactaldehyde
D-Lactaldehyde
Acetylenedicarboxylate
Phosphoenol-pyruvate
2-Hydroxyethylene-dicarboxylate
(R)-S-Lactoyl-glutathione
Nicotinate and nicotinamide metabolism
Valine, leucine and isoleucine biosynthesis
Pyruvate
D-Lactate
L-Lactate
2-Hydroxy-ethyl-ThPP
ThPP
Lipoamide-E
S-Acetyl-dihydro-lipoamide-E
Dihydro-lipoamide-E
Acetyl-P
EutD
Acetate
Oxaloacetate
Formate
Glyoxylate metabolism
Acetyl-CoA
Propanoate metabolism
Acetyladenylate
(S)-Malate
Fumarate
Succinate
Acetaldehyde
Citrate cycle
(R)-2-Ethylmalate
Acetoacetyl-CoA
Butanoate metabolism
Synthesis and degradation of ketone bodies
2-Propylmalate
3-Carboxy-3-hydroxy-4-methylpentanoate
Homocitrate
Malonyl-CoA
Leucine biosynthesis
Lysine biosynthesis
Fatty acid biosynthesis
00620 7/10/14
(c) Kanehisa Laboratories

Fig S10

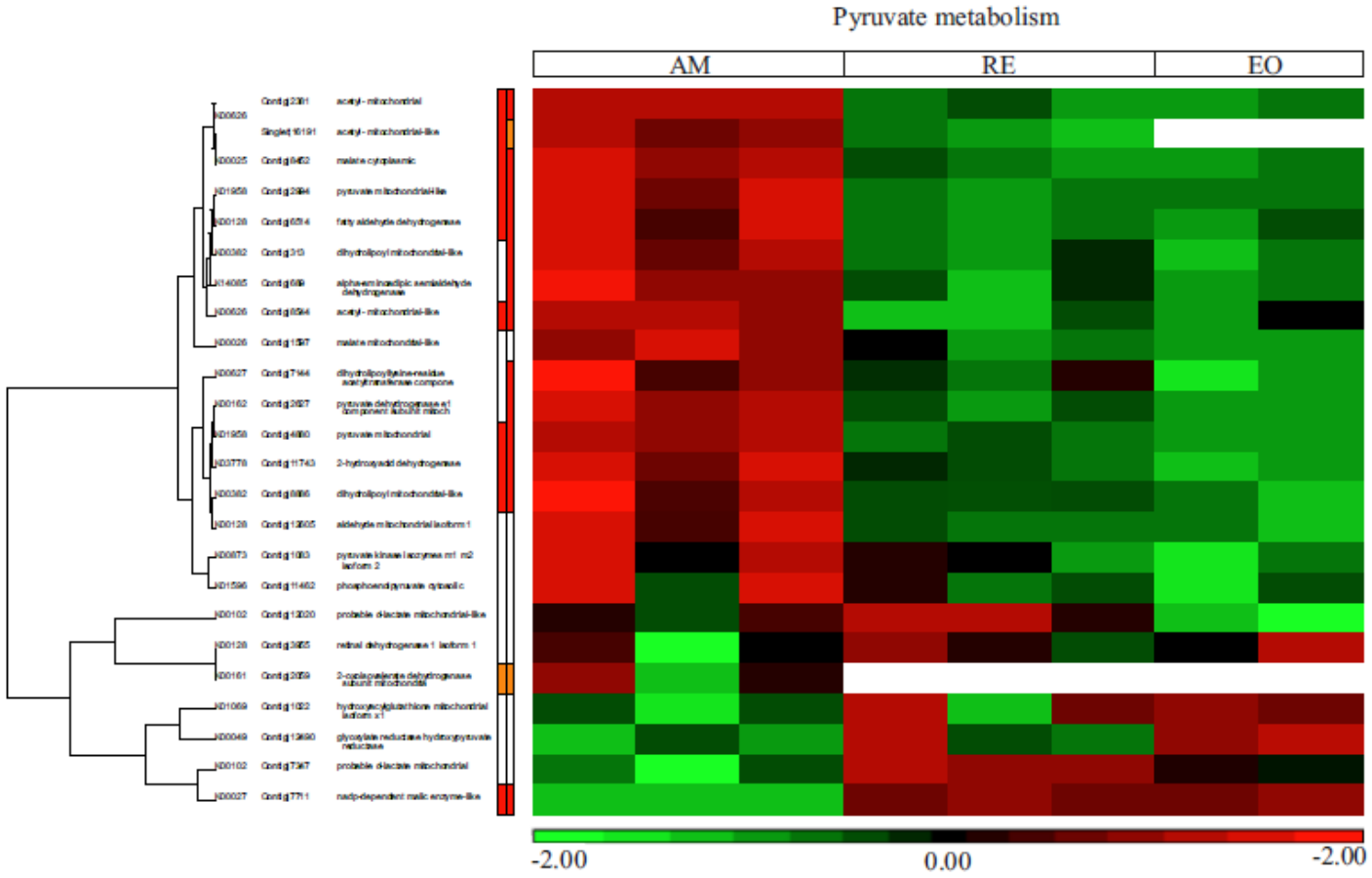


Fig S11

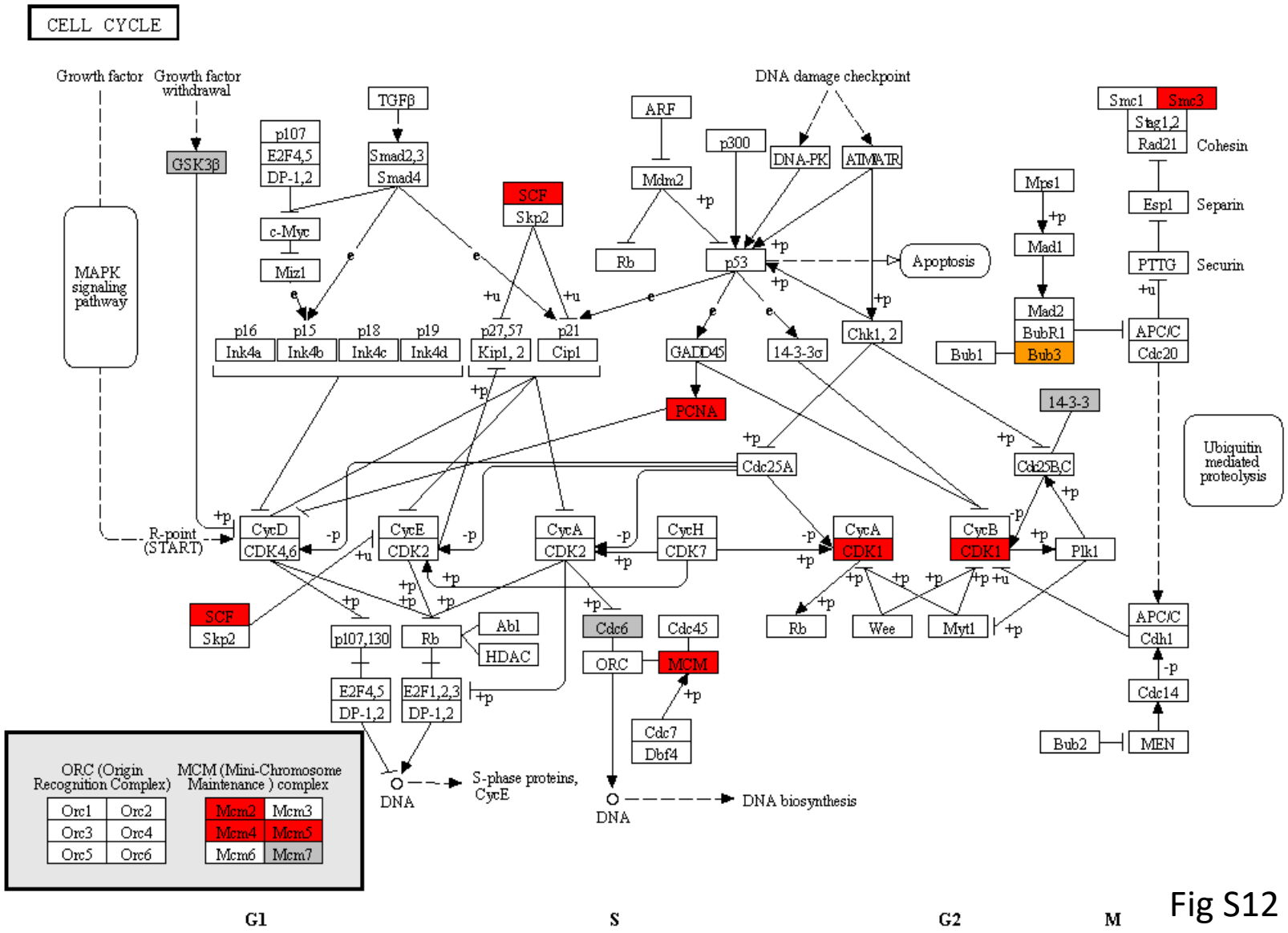

CELL CYCLE
Growth factor
Growth factor withdrawal
GSK3β
MAPK signaling pathway
TGFβ
Smad2,3
Smad4
p107
E2F4,5
DP-1,2
c-Myc
Miz1
SCF
Skp2
ARF
Mdm2
p300
DNA-PK
ATM/ATR
DNA damage checkpoint
Rb
p53
Apoptosis
p16 Ink4a
p15 Ink4b
p18 Ink4c
p19 Ink4d
p27,57 Kip1, 2
p21 Cip1
GADD45
14-3-3σ
Chk1, 2
PCNA
Mps1
Mad1
Mad2
BubR1
Bub3
Bub1
Smc1
Smc3
Stag1,2
Rad21
Cohesin
Esp1
Separin
PTTG
Securin
APC/C
Cdc20
14-3-3
Ubiquitin mediated proteolysis
Cdc25A
Cdc25B,C
R-point (START)
CycD
CDK4,6
CycE
CDK2
CycA
CDK2
CycH
CDK7
CycA
CDK1
CycB
CDK1
Plk1
SCF
Skp2
p107,130
Rb
Abl
HDAC
Cdc6
Cdc45
ORC
MCM
Cdc7
Dbf4
E2F4,5
DP-1,2
E2F1,2,3
DP-1,2
Rb
Wee
Myt1
APC/C
Cdh1
Cdc14
Bub2
MEN
DNA
S-phase proteins, CycE
DNA
DNA biosynthesis
ORC (Origin Recognition Complex)
Orc1
Orc2
Orc3
Orc4
Orc5
Orc6
MCM (Mini-Chromosome Maintenance) complex
Mcm2
Mcm3
Mcm4
Mcm5
Mcm6
Mcm7
G1
S
G2
M
04110 8/7/13
(c) Kanehisa Laboratories

Fig S12

AM>RE; AM< RE; Only in AM; Only in RE; Grey- present

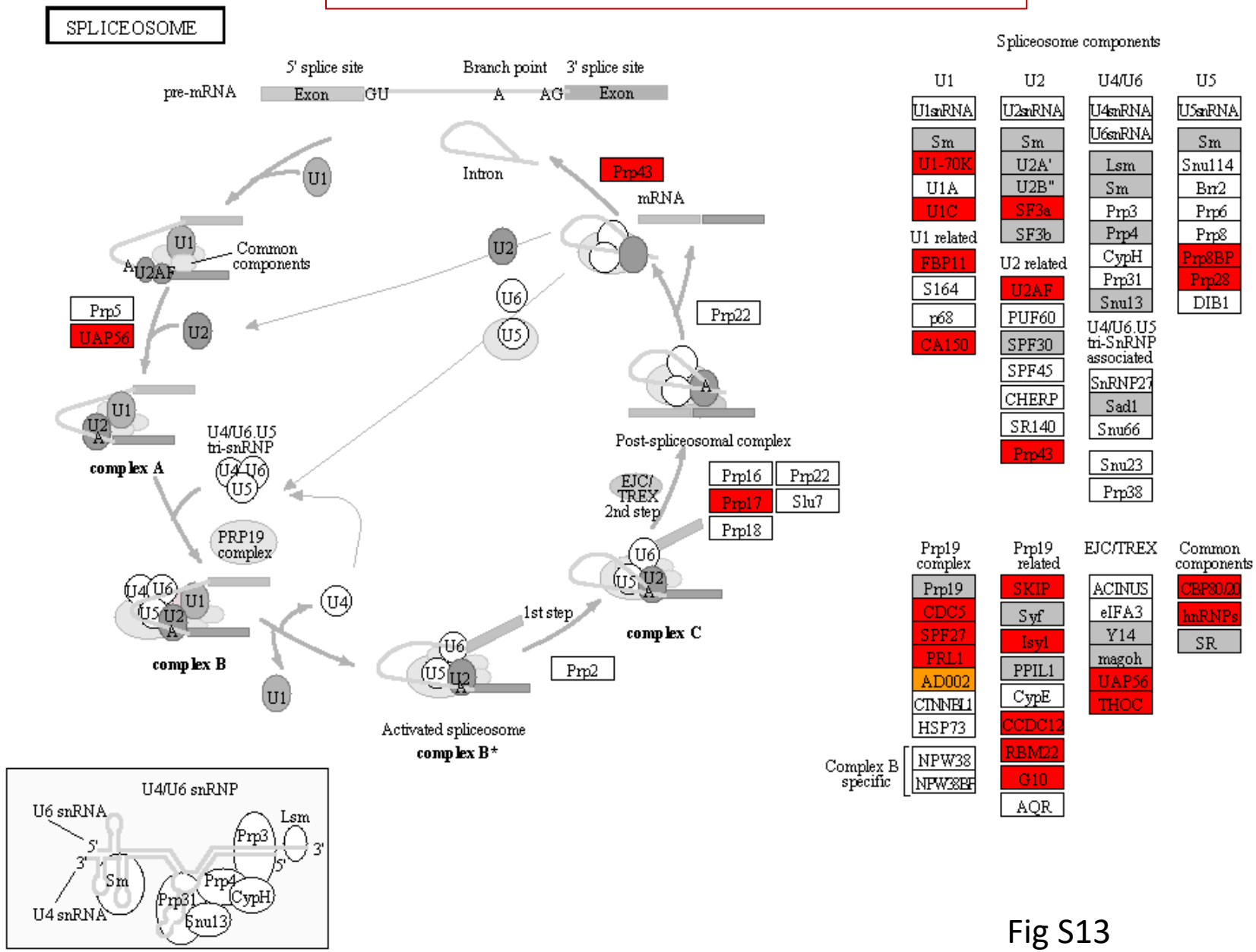


Fig S13

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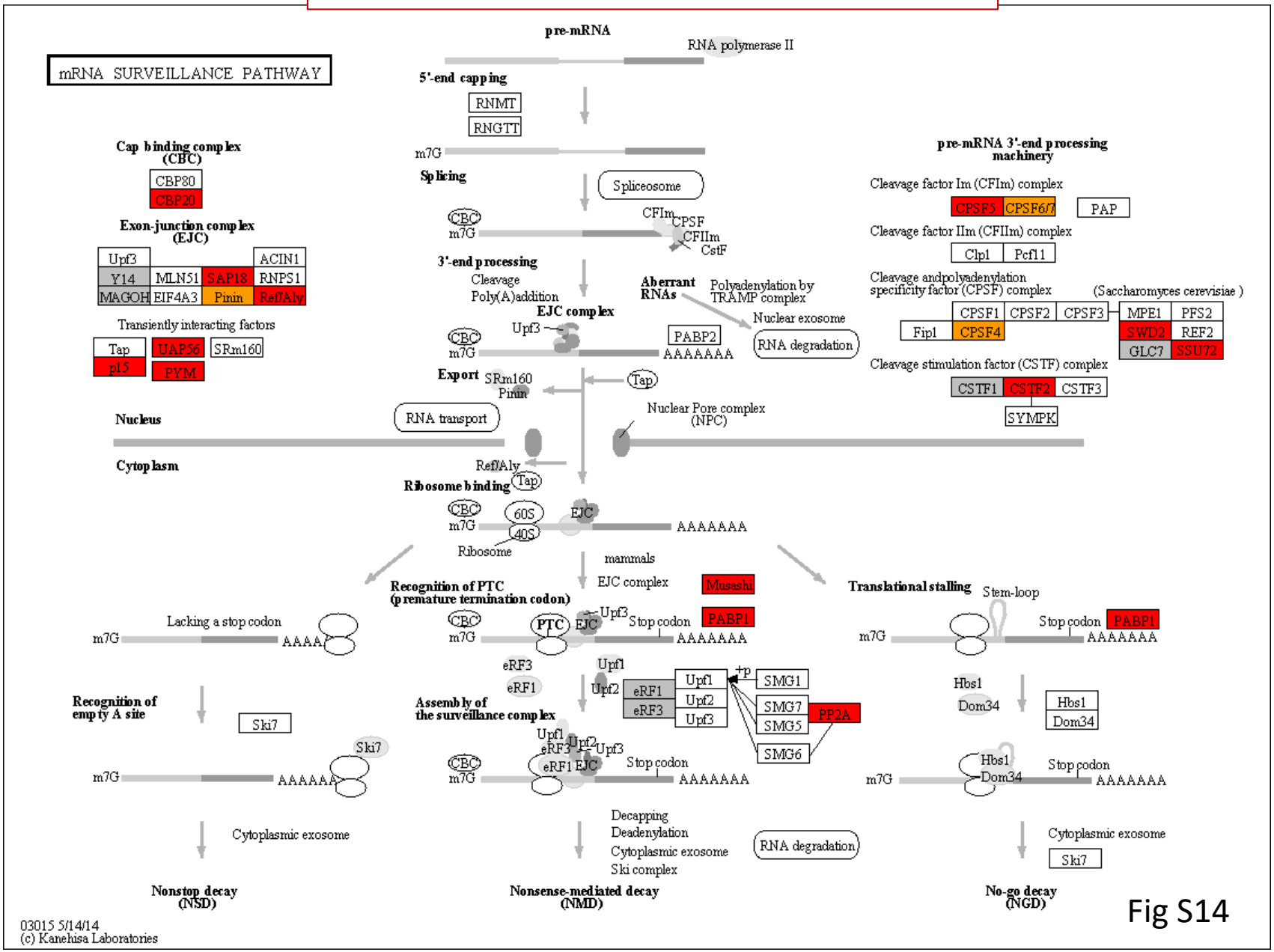

Fig S14

AM>RE; AM< RE; Only in AM; Only in RE; Grey- present

A

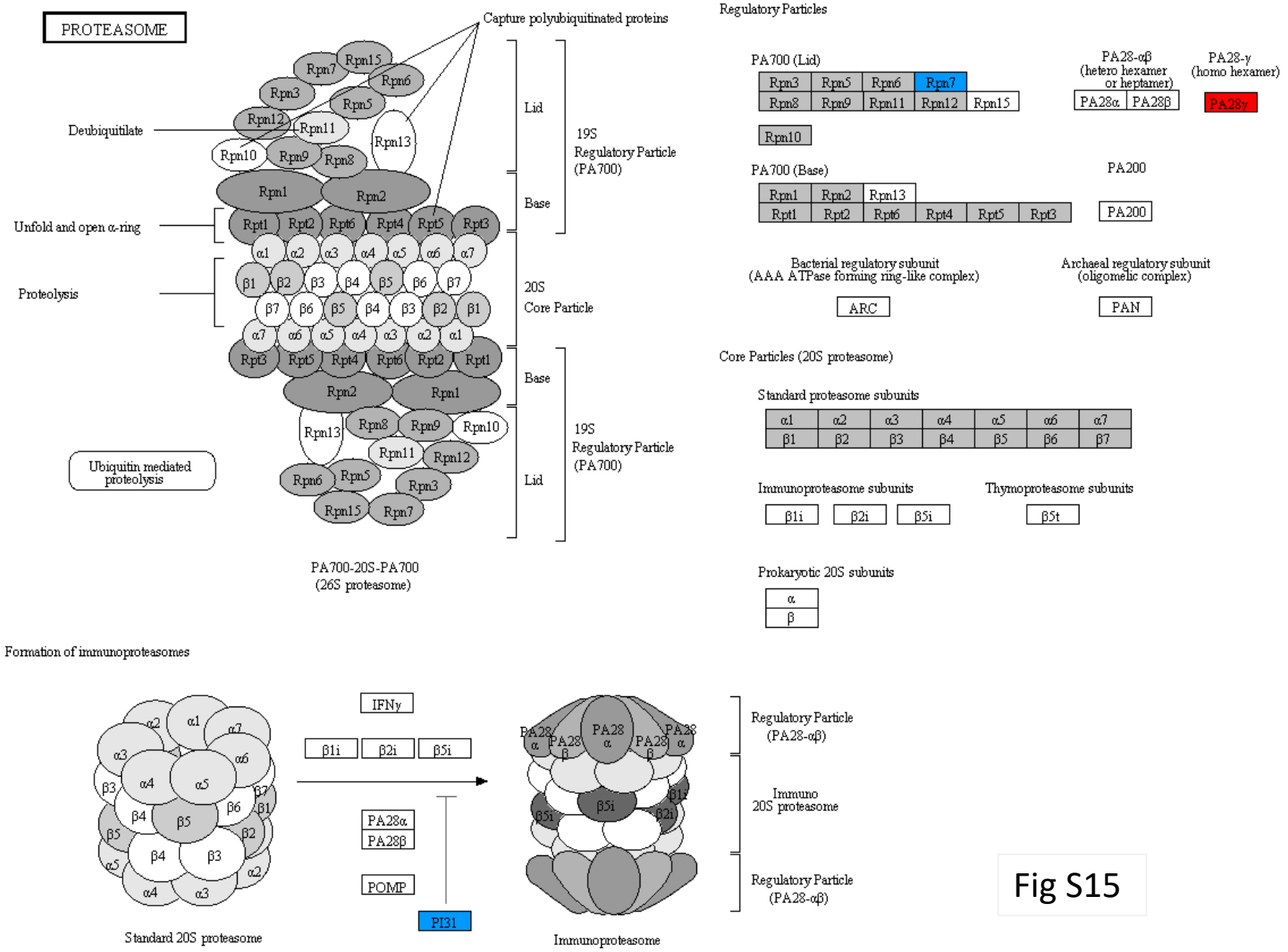

Fig S15

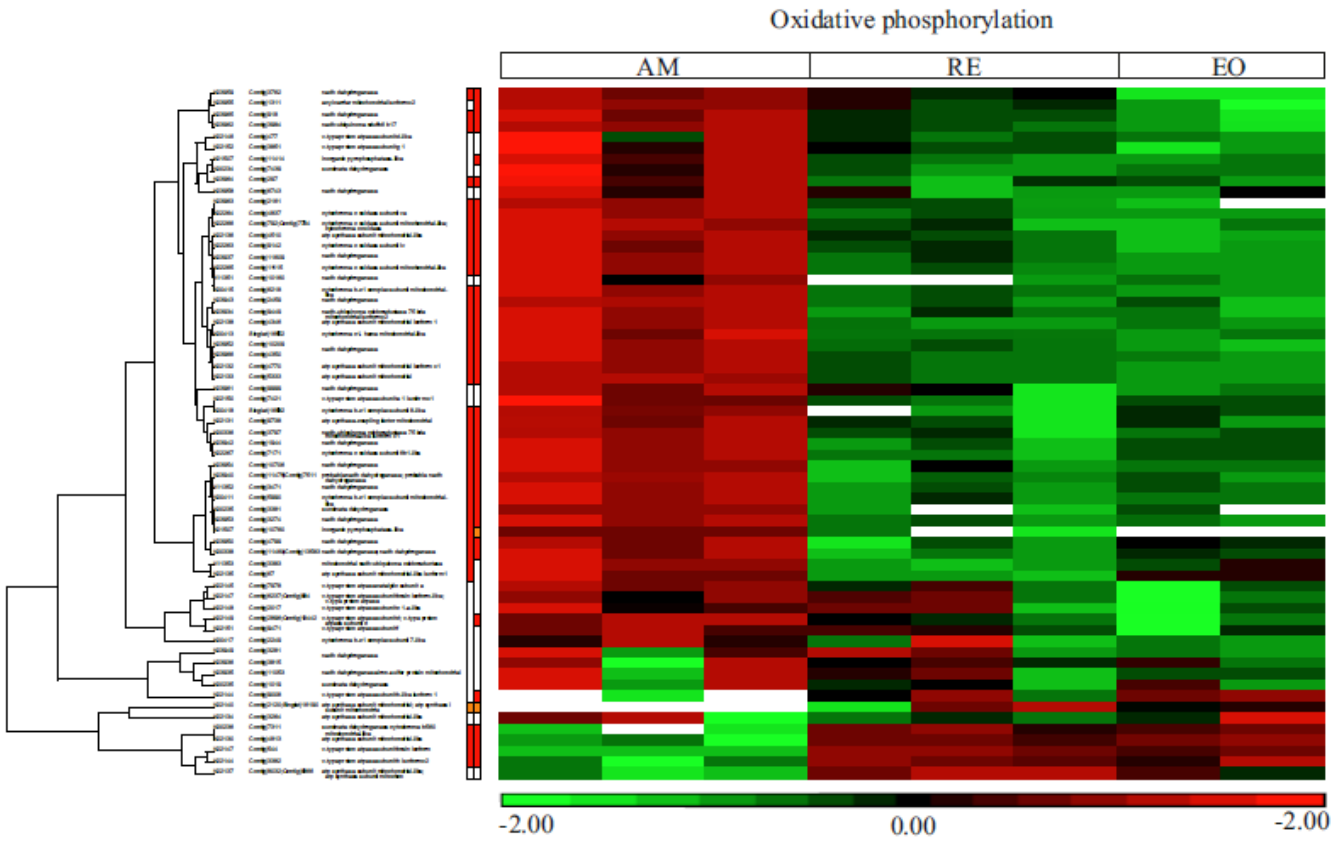

Fig S16

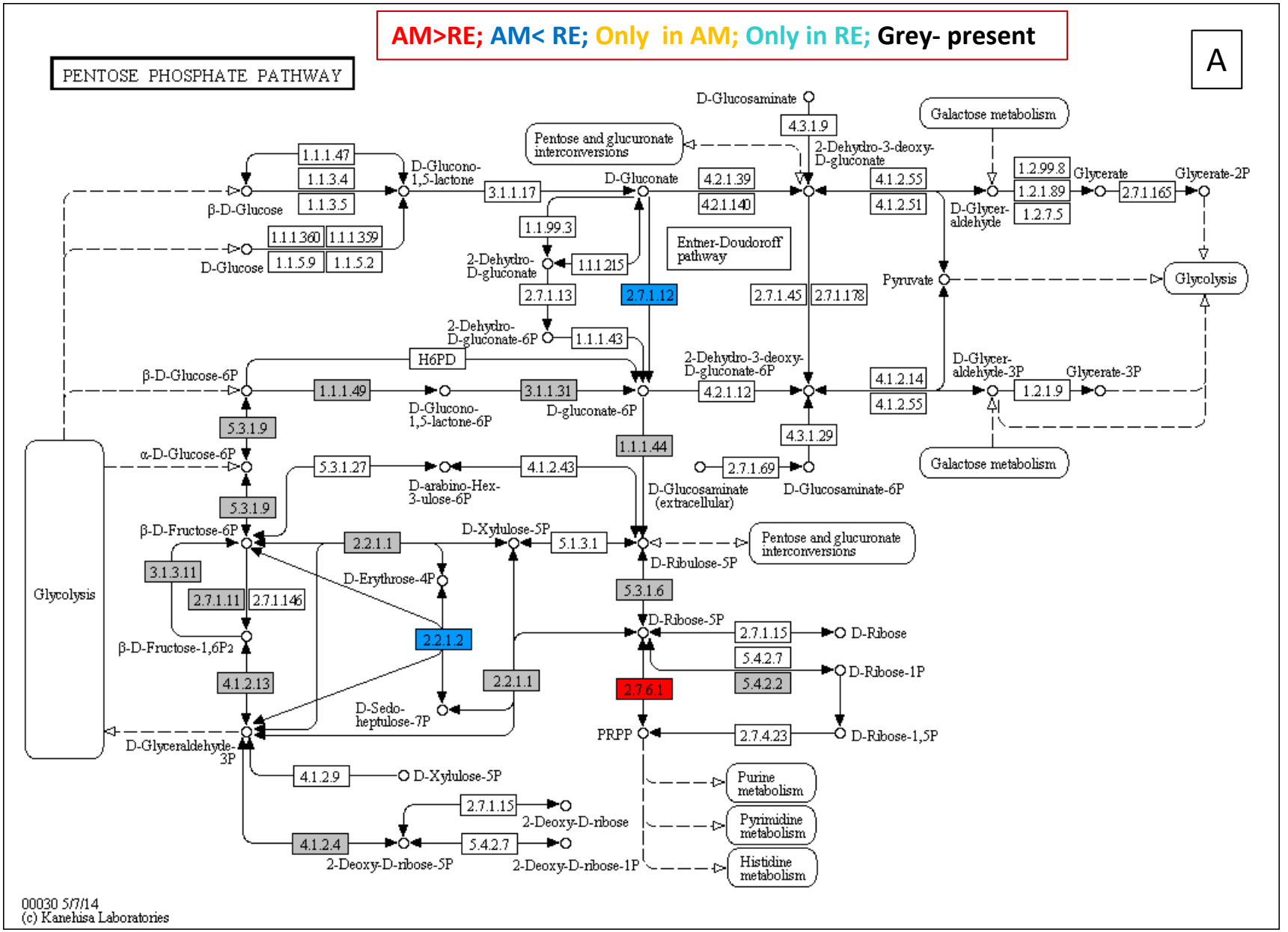
AM>RE; AM< RE; Only in AM; Only in RE; Grey- present
A
PENTOSE PHOSPHATE PATHWAY
D-Glucosaminate
4.3.1.9
Galactose metabolism
Pentose and glucuronate interconversions
2-Dehydro-3-deoxy-D-gluconate
1.1.1.47
1.1.3.4
1.1.3.5
D-Glucono-1,5-lactone
3.1.1.17
D-Gluconate
4.2.1.39
4.2.1.140
4.1.2.55
4.1.2.51
1.2.99.8
1.2.1.89
1.2.7.5
Glycerate
2.7.1.165
Glycerate-2P
β-D-Glucose
D-Glycer-aldehyde
1.1.1.360
1.1.1.359
1.1.5.9
1.1.5.2
D-Glucose
1.1.99.3
1.1.1.215
2-Dehydro-D-gluconate
Entner-Doudoroff pathway
Pyruvate
Glycolysis
2.7.1.13
2.7.1.12
2.7.1.45
2.7.1.178
2-Dehydro-D-gluconate-6P
1.1.1.43
H6PD
β-D-Glucose-6P
1.1.1.49
3.1.1.31
2-Dehydro-3-deoxy-D-gluconate-6P
4.2.1.12
4.1.2.14
4.1.2.55
D-Glycer-aldehyde-3P
1.2.1.9
Glycerate-3P
D-Glucono-1,5-lactone-6P
D-gluconate-6P
5.3.1.9
4.3.1.29
1.1.1.44
α-D-Glucose-6P
5.3.1.27
4.1.2.43
2.7.1.69
Galactose metabolism
D-arabino-Hex-3-ulose-6P
D-Glucosaminate (extracellular)
D-Glucosaminate-6P
5.3.1.9
β-D-Fructose-6P
2.2.1.1
D-Xylulose-5P
5.1.3.1
Pentose and glucuronate interconversions
D-Ribulose-5P
3.1.3.11
D-Erythrose-4P
5.3.1.6
Glycolysis
2.7.1.11
2.7.1.146
D-Ribose-5P
2.7.1.15
D-Ribose
β-D-Fructose-1,6P2
2.2.1.2
5.4.2.7
D-Ribose-1P
4.1.2.13
2.2.1.1
5.4.2.2
2.7.6.1
D-Sedo-heptulose-7P
PRPP
2.7.4.23
D-Ribose-1,5P
D-Glyceraldehyde-3P
4.1.2.9
D-Xylulose-5P
Purine metabolism
2.7.1.15
2-Deoxy-D-ribose
Pyrimidine metabolism
4.1.2.4
5.4.2.7
2-Deoxy-D-ribose-5P
2-Deoxy-D-ribose-1P
Histidine metabolism
00030 5/7/14
(c) Kanehisa Laboratories

Fig S17

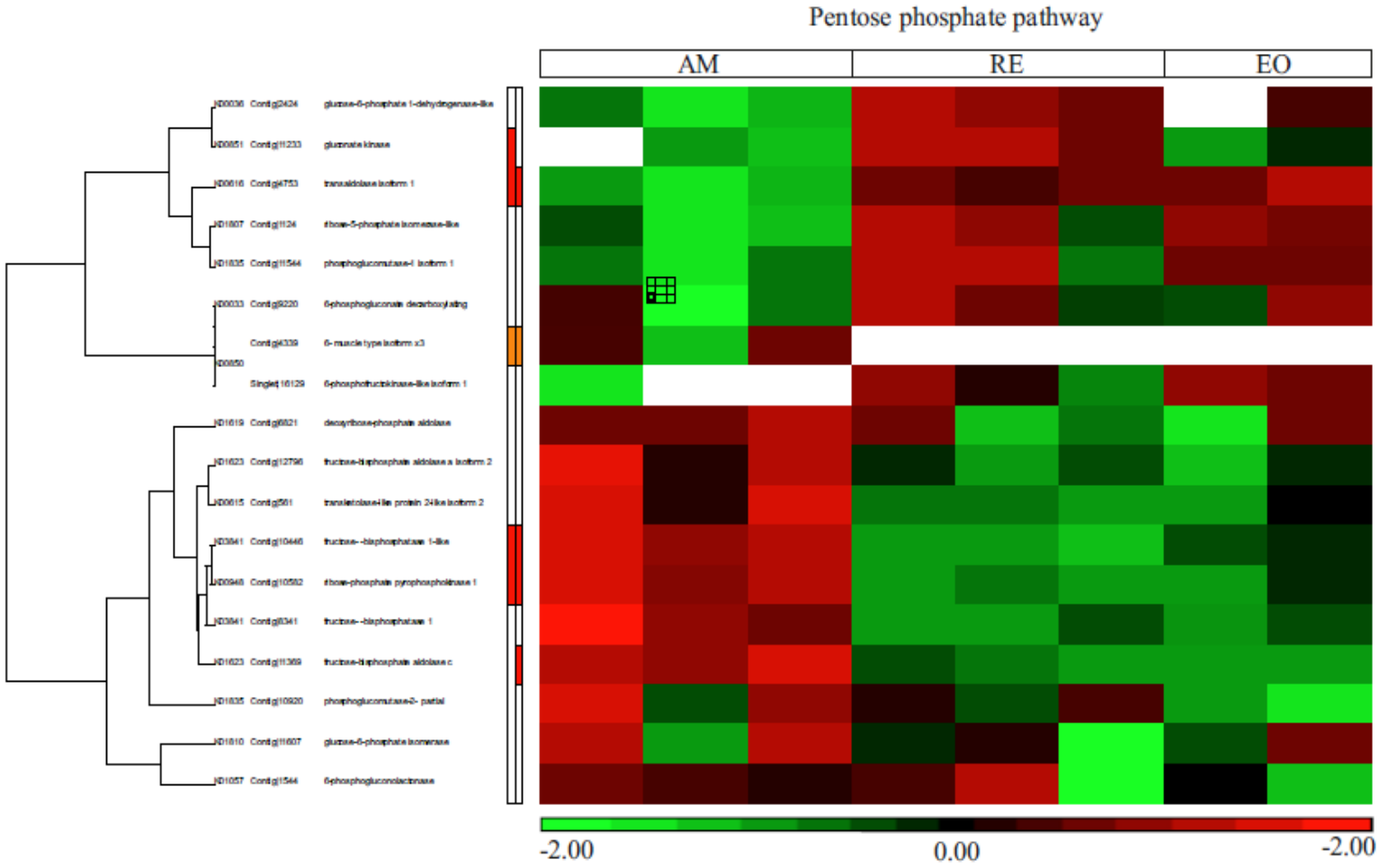

Fig S18

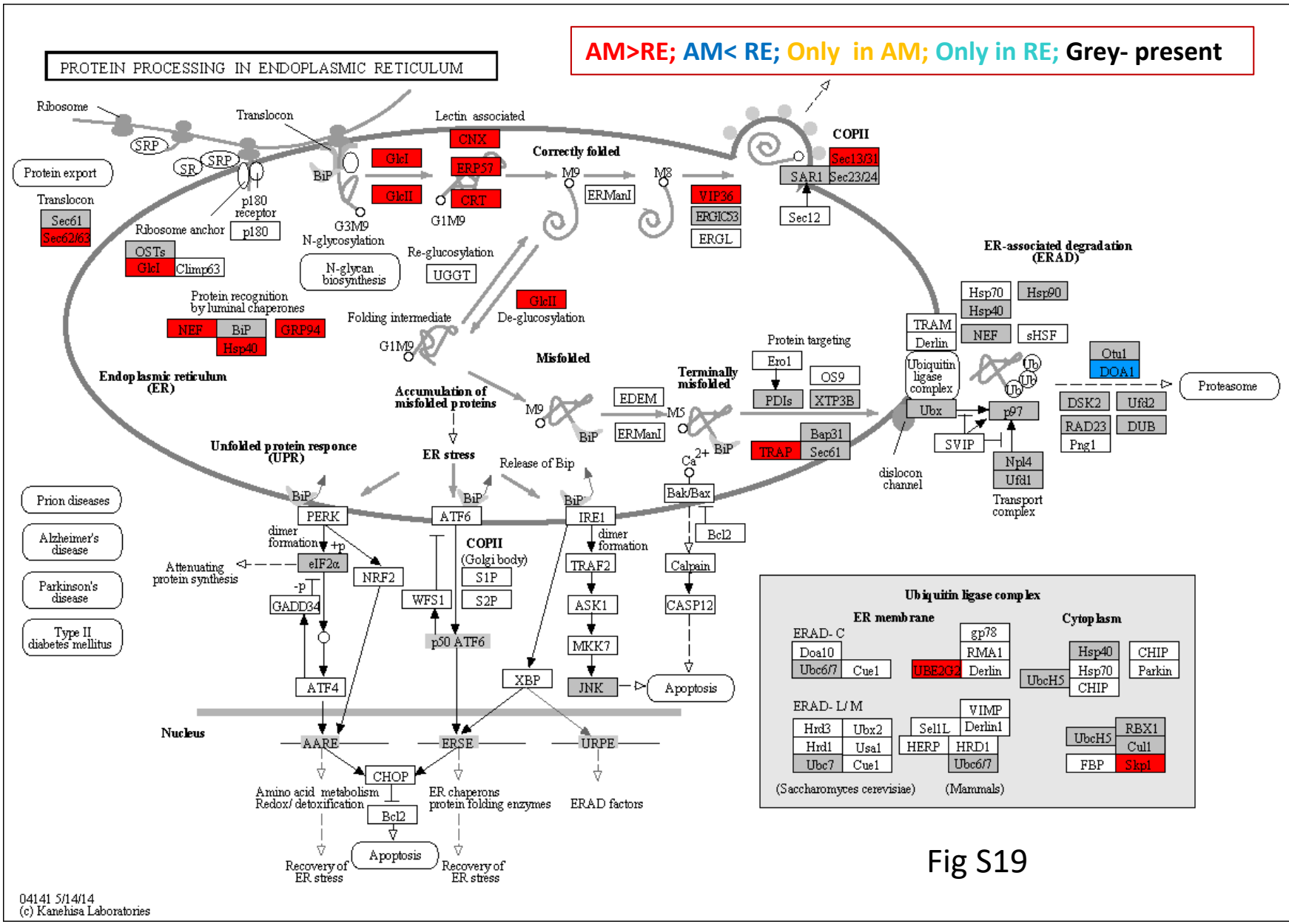
AM>RE; AM< RE; Only in AM; Only in RE; Grey- present
PROTEIN PROCESSING IN ENDOPLASMIC RETICULUM
Ribosome
Translocon
Lectin associated
CNX
GlcI
GlcII
ERP57
CRT
Correctly folded
M9
M8
ERManI
VIP36
ERGIC53
ERGL
COPII
Sec13/31
SAR1
Sec23/24
Sec12
Protein export
Translocon
Sec61
Sec62/63
SRP
SR
p180 receptor
p180
Ribosome anchor
OSTs
Climp63
BiP
G3M9
N-glycosylation
N-glycan biosynthesis
Re-glucosylation
UGGT
G1M9
Protein recognition by luminal chaperones
NEF
BiP
Hsp40
GRP94
Folding intermediate
De-glucosylation
Endoplasmic reticulum (ER)
Misfolded
Accumulation of misfolded proteins
Terminally misfolded
EDEM
ERManI
Protein targeting
Ero1
PDIs
OS9
XTP3B
Bap31
TRAP
Sec61
ER-associated degradation (ERAD)
Hsp70
Hsp90
Hsp40
TRAM
Derlin
NEF
sHSF
Ubiquitin ligase complex
Ub
Ubx
p97
SVIP
dislocon channel
Npl4
Ufd1
Transport complex
Otu1
DOA1
DSK2
Ufd2
RAD23
DUB
Png1
Proteasome
Unfolded protein responce (UPR)
ER stress
Release of Bip
Ca2+
Bak/Bax
Bcl2
Calpain
CASP12
PERK
dimer formation
+p
eIF2α
Attenuating protein synthesis
-p
GADD34
NRF2
ATF4
ATF6
COPII
(Golgi body)
S1P
S2P
WFS1
p50 ATF6
IRE1
dimer formation
TRAF2
ASK1
MKK7
JNK
Apoptosis
XBP
Nucleus
AARE
ERSE
URPE
CHOP
Amino acid metabolism
Redox/ detoxification
ER chaperons
protein folding enzymes
ERAD factors
Bcl2
Apoptosis
Recovery of ER stress
Recovery of ER stress
Prion diseases
Alzheimer's disease
Parkinson's disease
Type II diabetes mellitus
Ubiquitin ligase complex
ER membrane
Cytoplasm
ERAD- C
Doa10
Ubc6/7
Cue1
gp78
RMA1
UBE2G2
Derlin
Hsp40
Hsp70
CHIP
UbcH5
CHIP
Parkin
ERAD- L/ M
Hrd3
Hrd1
Ubc7
Ubx2
Usa1
Cue1
Sel1L
HERP
VIMP
Derlin1
HRD1
Ubc6/7
UbcH5
RBX1
Cul1
FBP
Skp1
(Saccharomyces cerevisiae)
(Mammals)
04141 5/14/14
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Fig S19