Electronic Supplementary Material (ESI) for Environmental Science: Processes & Impacts.

Supplementary Material

Porphyrin metabolism and carbon fixation responding to mixed emerging PFASs with environmental concentrations in *Skeletonema costatum* at different growth phases

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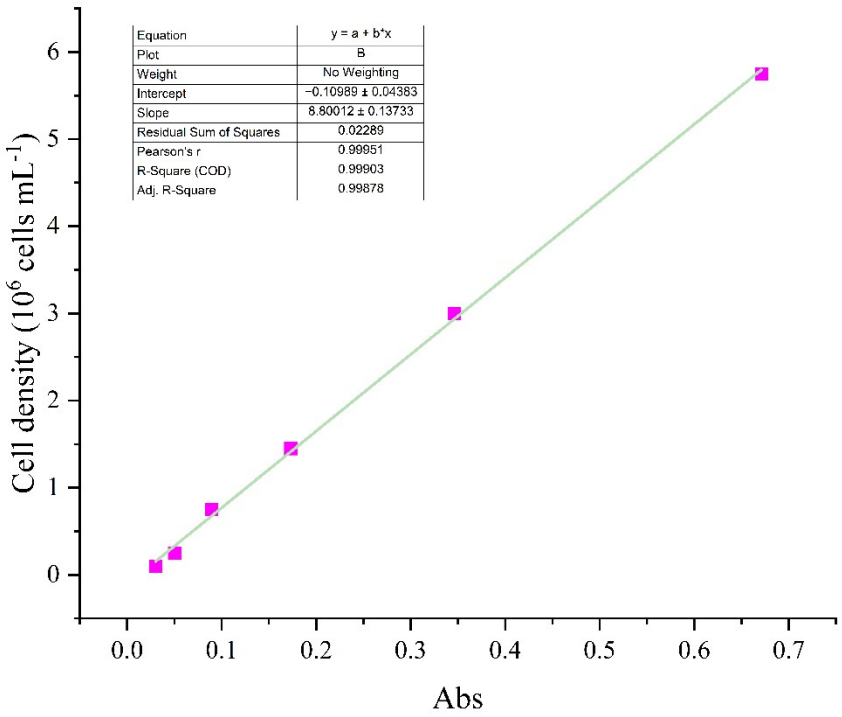
2. Materials and methods

TEXT S1: ANALYSIS OF POPULLATION AND CELLULAR LEVELS

Linear relation between the cell density and the OD



$$Y = 8.8x - 0.11$$

Determination of enzymatic activities

The algal suspensions (20 mL) from different samples were centrifuged at 5000 rpm for 10 min at 4°C. The cellular precipitates were resuspended with 2.5 mL PBS (0.1 M, pH 7.4) and freeze-thawed for three times. The samples were broken with ultrasonic cell disruptor (FS-900N, Shanghai Shengyang Ultrasonic Instrument Co., Ltd, China) in 270W for 20 min (work 5s, stop 5s) at ice-bath condition. The mixtures were centrifuged at 12000 rpm for 10 min at 4°C. The extractive was used for determination, stored at 4°C.

Mensuration of the content of total proteins: The stock solution of Coomassie brilliant blue (CBB) was diluted in a ratio of 1:4. The 50 μL of distilled water, protein standard, and samples were added to the Coomassie bright blue color solution (3 mL), respectively. The mixtures were placed for 10 min and measured in absorbance value (A_0) with ultraviolet-visible spectrophotometer (Hash DR-6000, Hash Corporation, USA) at 595 nm. The concentrations of samples (C_{pr}) were calculated as follow:

$$C_{pr}\,(g\,L^{-1}) = (A_{0\,sample} - A_{0\,blank}) / (A_{0\,standard} - A_{0\,blank}) \times C_{st1} \times N \quad (1)$$

where $C_{st\,1}$ ($C_{standard}$) is 0.524 g L^{-1}, the N represent dilution multiple of the sample before testing.

Mensuration of T-SOD activity: The solution was prepared and added in turn according to the instruction. The final mixtures were placed for 10 min at room temperature and determined in absorbance value (A_2) with ultraviolet-visible spectrophotometer at 550 nm. The vitalities (VI) of samples were calculated as follow:

$$VI_{sample}\,(U\,mgprot^{-1}) = (A_{2\,control} - A_{2\,sample}) / A_{2\,control} / 50\% \times (V_1 / V_2) / C_{pr} \quad (3)$$

where the V_{1}, V_{2} and C_{pr} represent total volumes of solution, volumes of sample, and the corresponding to concentration of proteins. The "mgprot" is the abbreviation of "milligrams of protein".

Mensuration of the content of GSH: The solution was prepared and added in turn according to the instruction. The final mixtures were measured in absorbance value (A_3) with ultraviolet-visible spectrophotometer at 420 nm. The contents of GSH (CG) in samples were calculated as follow:

$$CG_{sample}\,(gGSH\,prot^{-1}) = (A_{3\,sample} - A_{3\,blank}) / (A_{3\,standard} - A_{3\,blank}) \times C_{st3} / C_{pr} \quad (4)$$

where C_{st3} is 20×10^{-6} mol L^{-1} and Mr (GSH) is 307 g mol^{-1}.

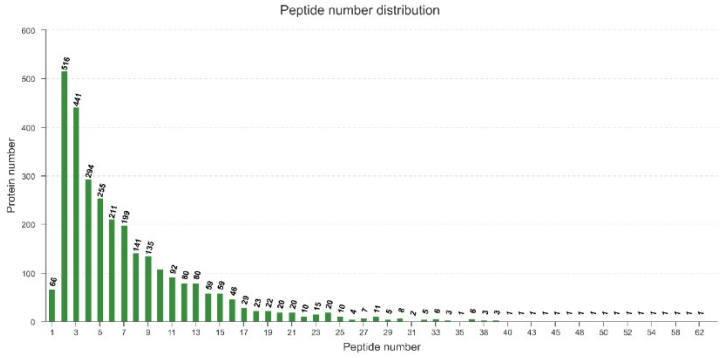
TEXT S2: ANALYSIS OF MULTI-OMICS

The data background of transcriptome

The quality control of sequencing data statistic. The clean data of each sample reached 6.29 Gb. The Q30 base percentages were above 94.9%.

The data background of proteome

The quality control of sequencing data statistic as follows:


Peptide number distribution
Protein number
Peptide number
516
441
294
256
211
159
141
135
92
80
80
59
59
46
29
23
22
20
20
10
15
20
10
4
7
11
5
8
2
5
6
3
1
6
3
3
1
1
1
1
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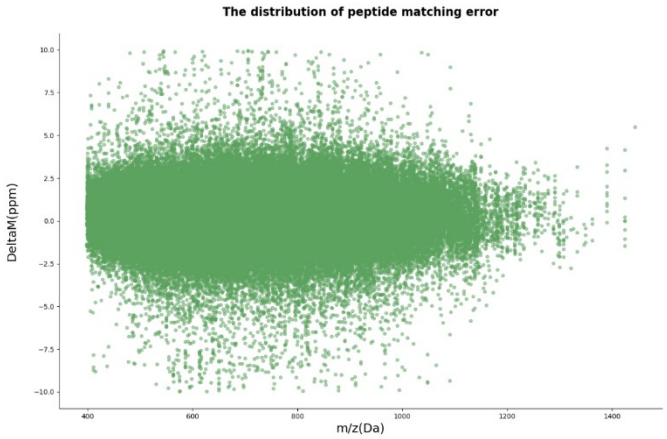
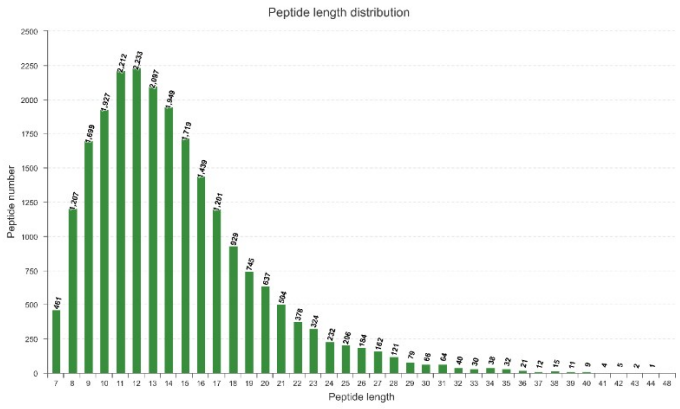
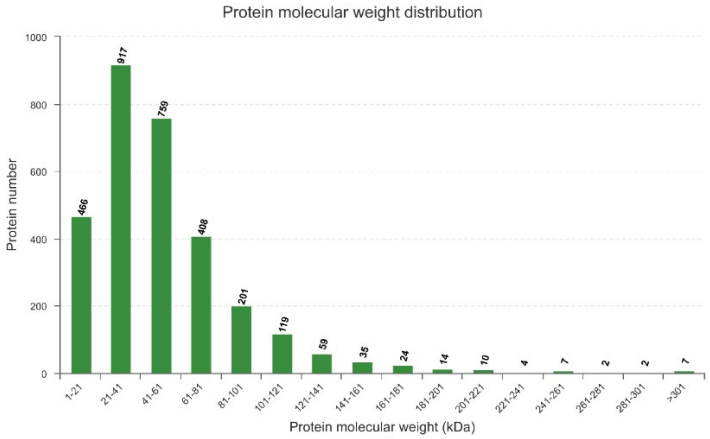
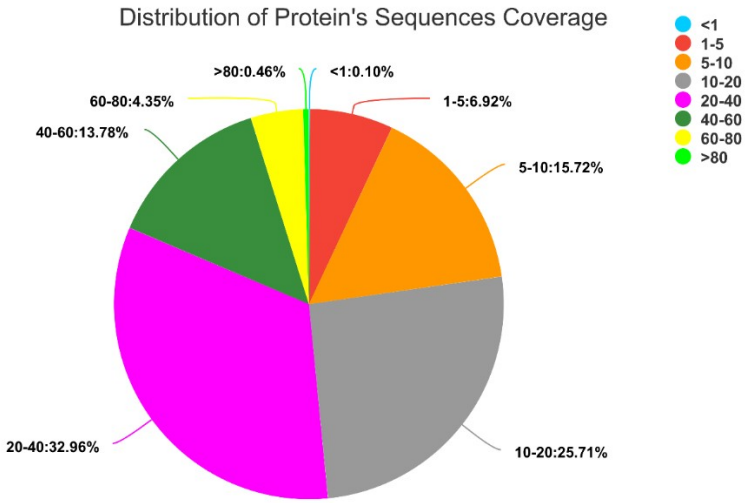
1
1
1
1
1
1
1
1
1
1


The distribution of peptide matching error
DeltaM(ppm)
m/z(Da)


Peptide length distribution
Peptide number
Peptide length
461
1207
1689
1927
2212
2233
1967
1549
1119
1439
1081
829
745
637
504
378
324
232
206
184
162
121
79
68
64
40
30
30
32
21
12
15
11
9
4
5
2
1


Protein molecular weight distribution
Protein number
Protein molecular weight (kDa)
466
917
759
408
201
119
59
35
24
14
10
4
7
2
2
7
1-21
21-41
41-61
61-81
81-101
101-121
121-141
141-161
161-181
181-201
201-221
221-241
241-261
261-281
281-301
>301


Distribution of Protein's Sequences Coverage
<1
1-5
5-10
10-20
20-40
40-60
60-80
>80
>80:0.46%
<1:0.10%
60-80:4.35%
1-5:6.92%
40-60:13.78%
5-10:15.72%
20-40:32.96%
10-20:25.71%

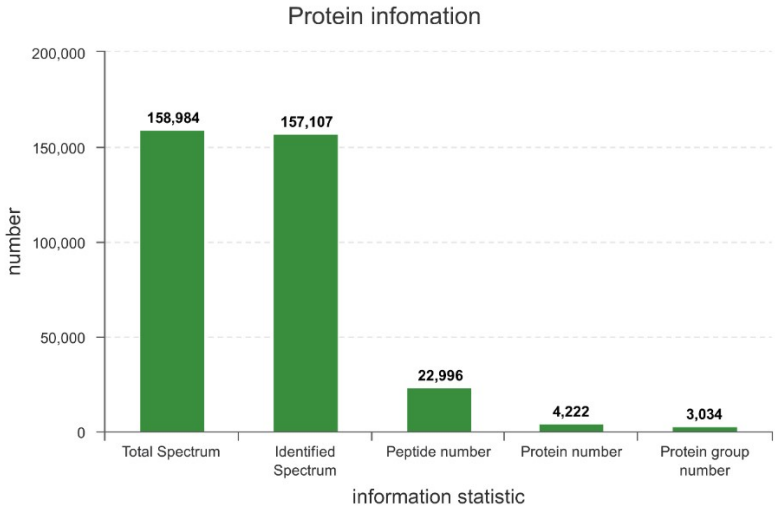
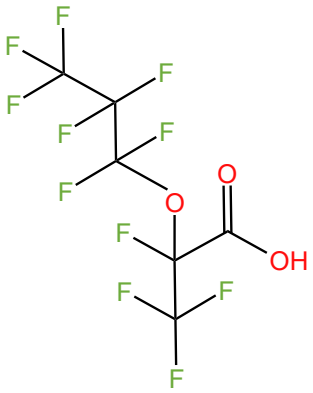
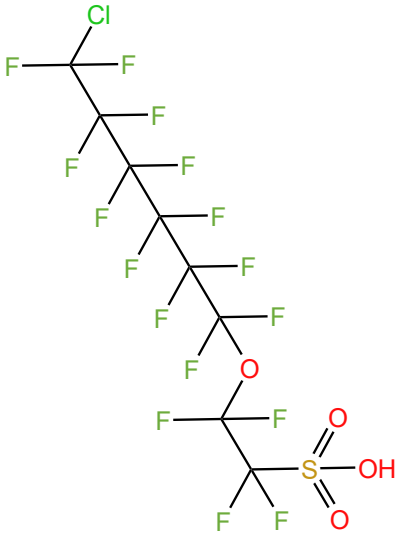
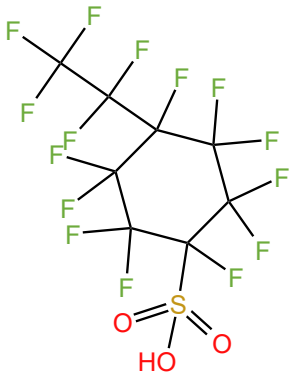

Protein infomation
200,000
150,000
100,000
50,000
0
number
158,984
157,107
22,996
4,222
3,034
Total Spectrum
Identified Spectrum
Peptide number
Protein number
Protein group number
information statistic

Table S1

The physiochemical characteristics of hexafluoropropylene oxide dimer acid (HFPO-DA), 6:2 chlorinated polyfluorinated ether sulphonate (6:2 Cl-PFAES), and perfluoroethylcyclohexane sulphonate (PFECHS).

Compound	HFPO-DA	6:2 Cl-PFAES	PFECHS	References
CAS #	13252-13-6	756428-58-1	646-83-3	(Mahoney et al., 2022)
Structure				
Molecular mass (g mol^{-1})	330.04	300.10	461.13	(Mahoney et al., 2022)
Water solubility (mol L^{-1})	>2.61	1.15e-3	9.68e-6 to 1.35e-3 [a]	(Mahoney et al., 2022)
Concentrations range [b]	3.9-40000 ng L^{-1}	7.9-7600 ng L^{-1}	0.14-195 ng L^{-1}	(Mahoney et al., 2022; Xiao, 2017)

[a] Prediction.

[b] Concentrations range from the wastewater's (high values) to the marine's (low values).

Table S2

Culture condition of *S. costatum* (GY-11). The level of composition of culture medium is g L^{-1}.

Items	Contents	Concentrations of stock solution (g L^{-1})
Culture medium	F/2 medium	
Composition of culture medium	$NaNO_3$	75.00
	$NaH_2PO_4 \cdot H_2O$	5.00
	$Na_2SiO_3 \cdot 9H2O$	30
	Na_2EDTA	4.36
	$FeCl_3 \cdot 6H_2O$	3.15
	$CoCl_2 \cdot 6H_2O$	10
	$Na_2MoO_4 \cdot 5H_2O$	6.3
	$MnCl_2 \cdot 4H_2O$	180
	$ZnSO_4 \cdot 7H_2O$	23
	$CuSO_4 \cdot 5H_2O$	9.8
	Vitamin B1	0.1
	Vitamin B12	0.0005
	Vitamin H	0.0005
Culture device	Intelligent artificial climate incubator (RXM-168B, Ningbo Jiangnan Instrument Factory Co., Ltd, China)	
Culture light source	white fluorescent light, 80 μmoL·photons $m^{-2} \cdot s^{-1}$ light intensity	
Other materials	Pinhole filter	

Table S3

The results of the one-way ANOVA analysis of variance for the comparison of OD, cell viability, Chl-*a* content, T-SOD activity and GSH content between solvent control (SC) and treatment with 300 ng/L of mixed PFAS (TF). The paired sample T test analysis for comparison between TF 14 and TF 8.

Group	*p*-value				
	OD	Cell Viability	Chl-a Content	T-SOD Activity	GSH Content
TF_8_vs_SC_8 (G1)	--	--	--	--	--
TF_14_vs_SC_14 (G2)	--	--	--	--	< 0.041
TF_14_vs_TF_8 (G3)	< 0.001	< 0.006	< 0.031	--	< 0.001

The "--" represents no significant differences compared to the solvent control, namely $p > 0.05$.

Table S4

The GO function enrichment (top 5 in DEPs) of correlation analysis between transcriptome and proteome.

Comparison group	Upregulated term	Downregulated term
(TF_8_vs_SC_8)	1. chloroplast organization	1. methyltransferase activity
	2. plastid organization	2. nucleotide-excision repair
	3. response to nitrogen compound	3. pyruvate, phosphate dikinase activity
	4. negative gravitropism	4. phosphotransferase activity, paired acceptors
	5. response to ammonium ion	5. spliceosomal complex
(TF_14_vs_SC_14)	1. response to ammonium ion	1. secretion by cell
	2. response to ethylene	2. secretion
	3. negative gravitropism	3. exocyst localization
	4. response to nitrogen compound	4. DNA replication checkpoint
	5. response to cation stress	5. mitotic DNA replication checkpoint
TF_14_vs_TF_8	1. pyruvate, phosphate dikinase activity	1. translation
	2. phosphotransferase activity, paired acceptors	2. amide biosynthetic process
		3. peptide biosynthetic process
	3. oxidoreductase activity	4. structural molecule activity
	4. tricarboxylic acid cycle	5. structural constituent of ribosome
	5. macromolecule biosynthetic process	

References:

Mahoney, H., Xie, Y., Brinkmann, M., Giesy, J.P., 2022. Next generation per- and poly-fluoroalkyl substances: Status and trends, aquatic toxicity, and risk assessment. Eco-Environment & Health 1(2), 117-131.

Xiao, F., 2017. Emerging poly- and perfluoroalkyl substances in the aquatic environment: A review of current literature. Water Res. 124, 482-495.

3. Transcriptomic and proteomic characteristics and function enrichment analysis of DEGs and DEPs of *S. costatum*

Fig. S1. The expressed genes between SC and TF on the 8th and 14th days in the 300 ng L^{-1}.

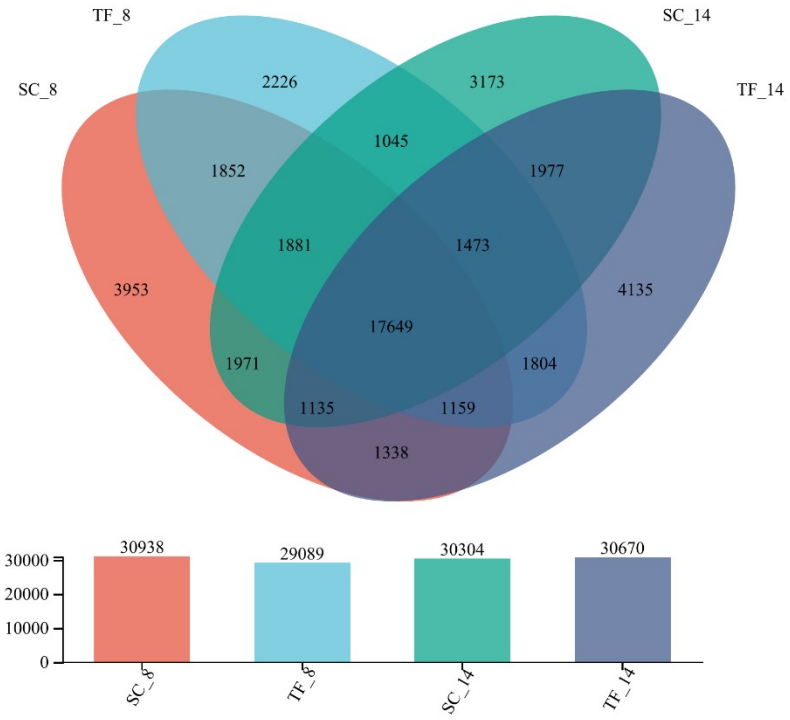
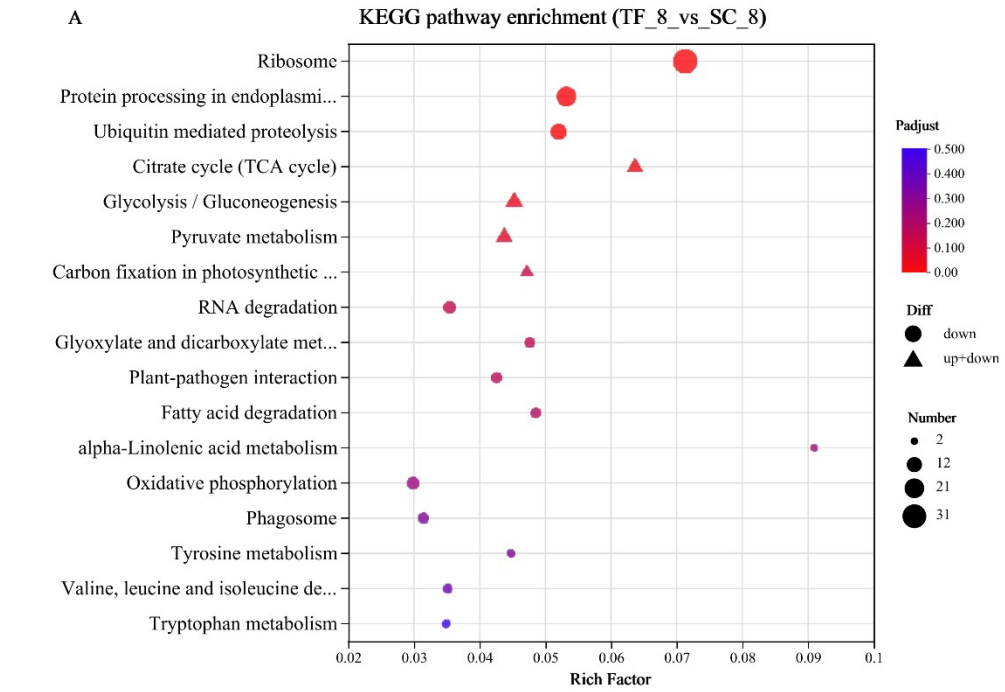
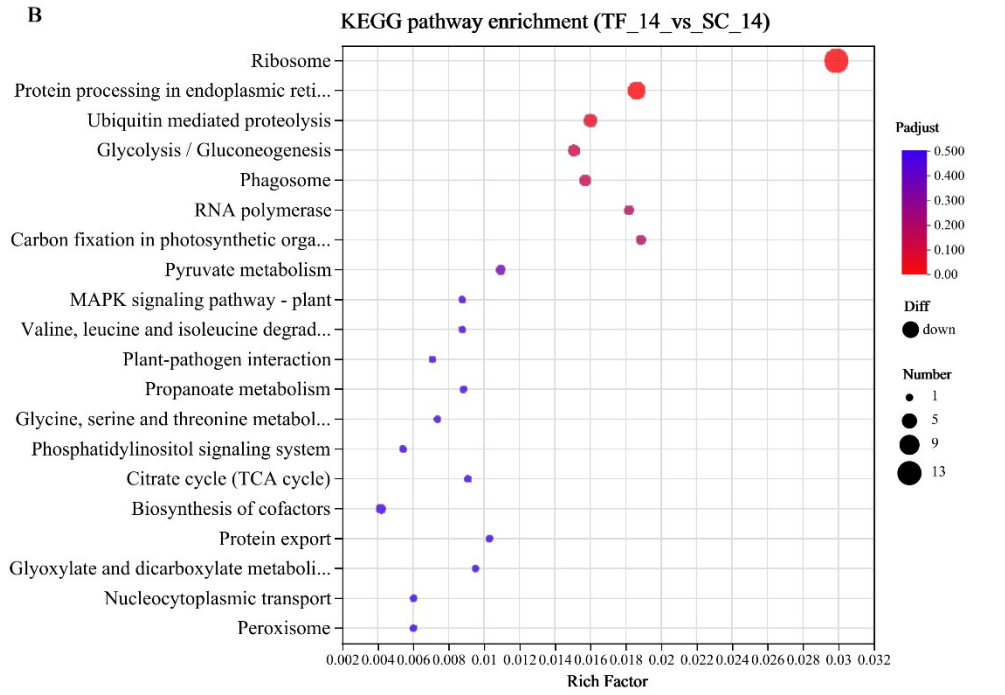


Fig. S2 KEGG pathways enrichment analysis of DEGs in G1, G2, and G3 (Top 20).





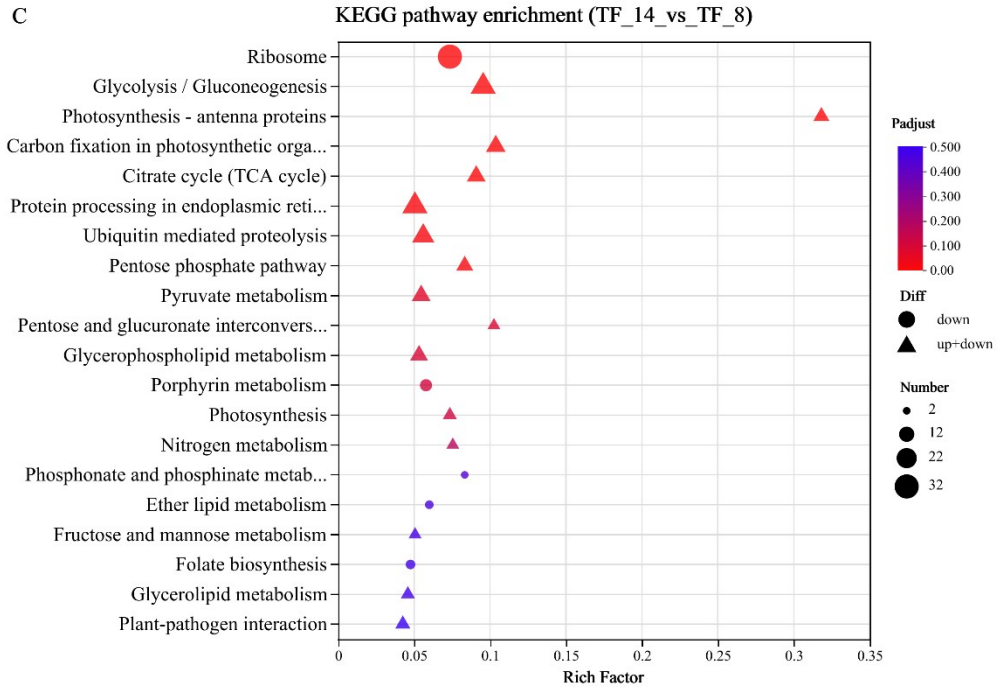


Fig. S3. The expressed proteins between SC and TF on the 8th and 14th days in the 300 ng L^{-1}.

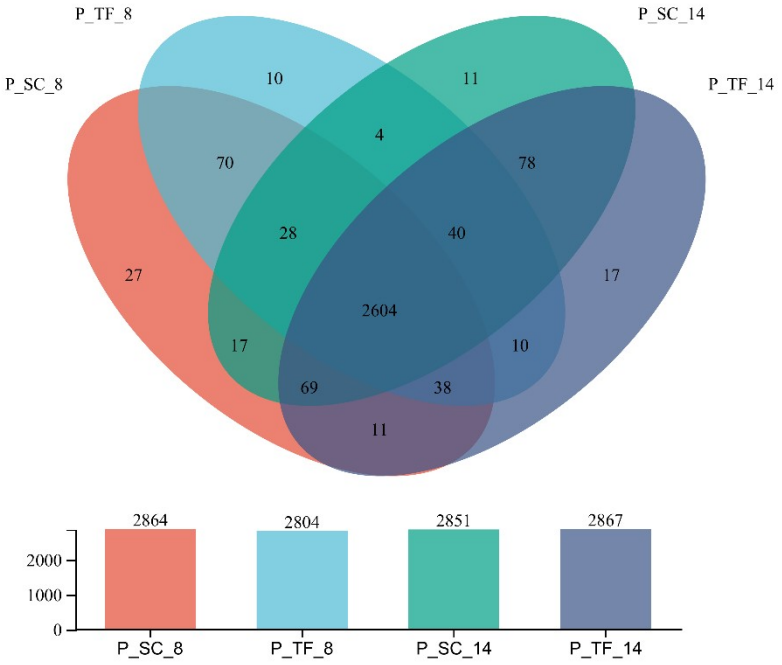
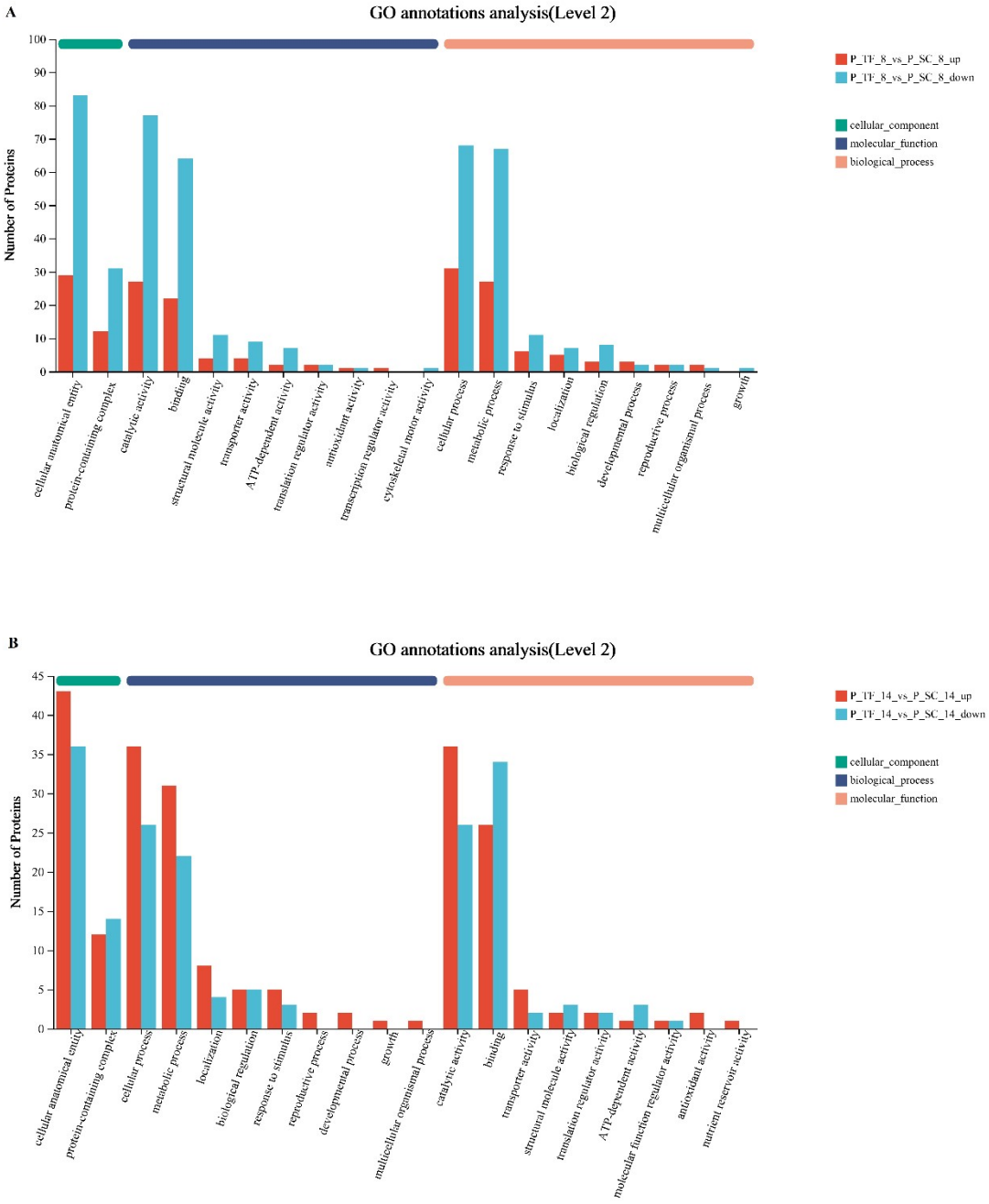


Fig. S4 GO annotations analysis of DEPs in G1, G2, and G3.



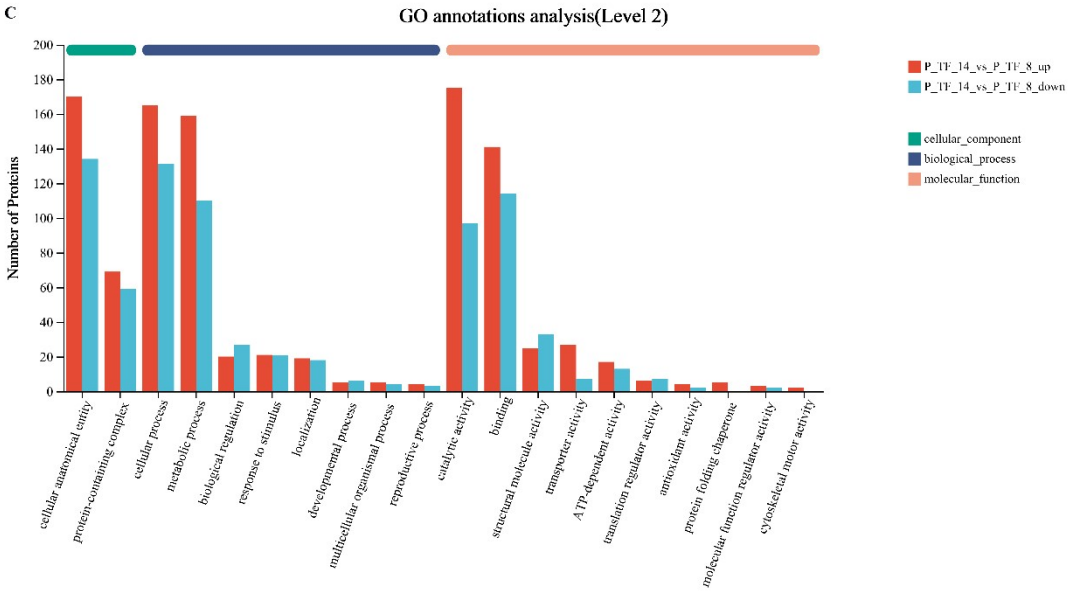
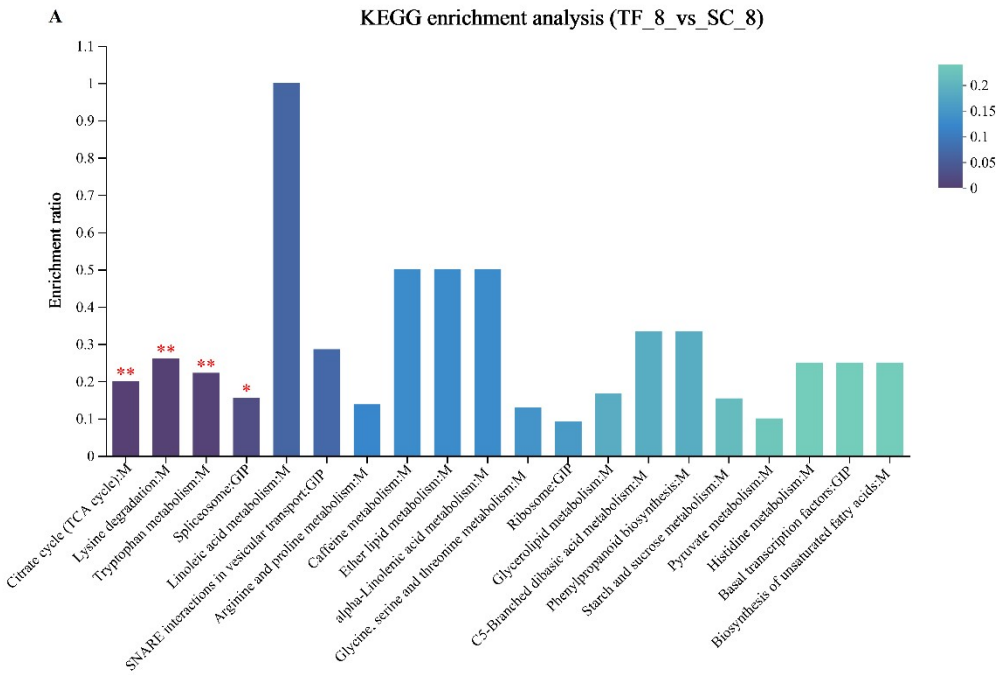
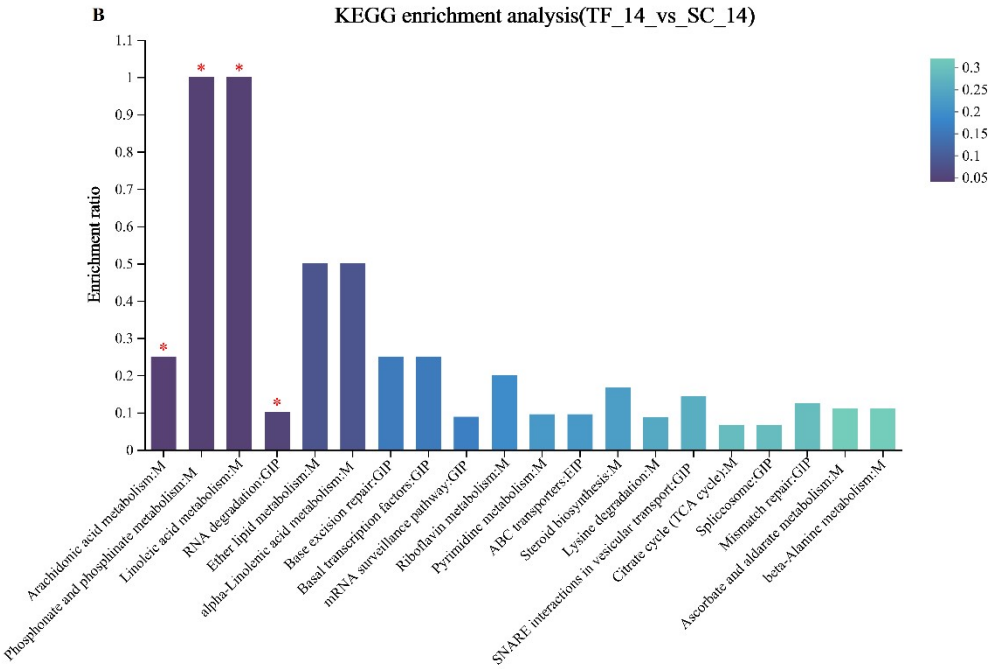


Fig. S5 KEGG pathways enrichment analysis of DEPs in G1, G2, and G3.




B
KEGG enrichment analysis(TF_14_vs_SC_14)
Enrichment ratio
1.1
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.3
0.25
0.2
0.15
0.1
0.05
Arachidonic acid metabolism:M
Phosphonate and phosphinate metabolism:M
Linoleic acid metabolism:M
RNA degradation:GIP
Ether lipid metabolism:M
alpha-Linolenic acid metabolism:M
Base excision repair:GIP
Basal transcription factors:GIP
mRNA surveillance pathway:GIP
Riboflavin metabolism:M
Pyrimidine metabolism:M
ABC transporters:EIP
Steroid biosynthesis:M
Lysine degradation:M
SNARE interactions in vesicular transport:GIP
Citrate cycle (TCA cycle):M
Spliceosome:GIP
Mismatch repair:GIP
Ascorbate and aldarate metabolism:M
beta-Alanine metabolism:M

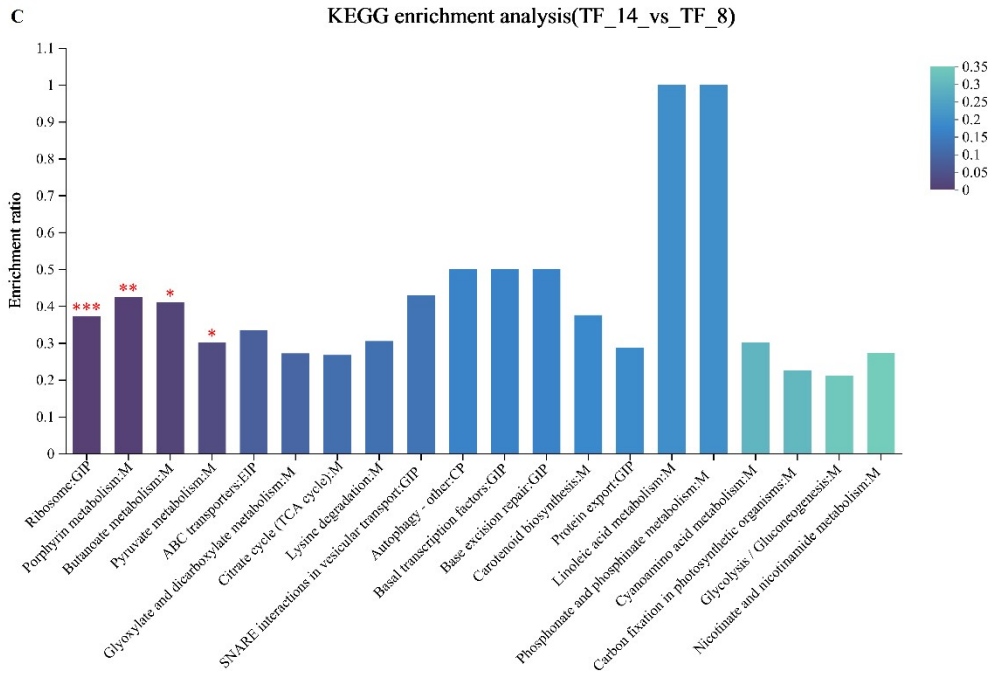

C
KEGG enrichment analysis(TF_14_vs_TF_8)
Enrichment ratio
1.1
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Ribosome:GIP
Porphyrin metabolism:M
Butanoate metabolism:M
Pyruvate metabolism:M
ABC transporters:EIP
Glyoxylate and dicarboxylate metabolism:M
Citrate cycle (TCA cycle):M
Lysine degradation:M
SNARE interactions in vesicular transport:GIP
Autophagy - other:CP
Basal transcription factors:GIP
Base excision repair:GIP
Carotenoid biosynthesis:M
Protein export:GIP
Linoleic acid metabolism:M
Phosphonate and phosphinate metabolism:M
Cyanoamino acid metabolism:M
Carbon fixation in photosynthetic organisms:M
Glycolysis / Gluconeogenesis:M
Nicotinate and nicotinamide metabolism:M

Fig. S6 Relationship between expressed genes and proteins.

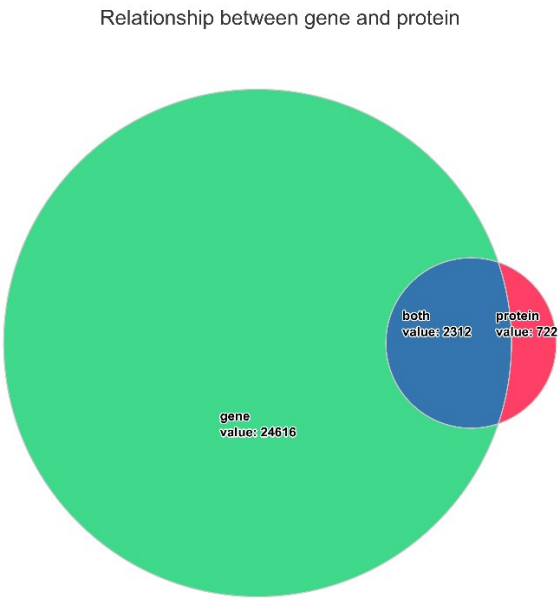
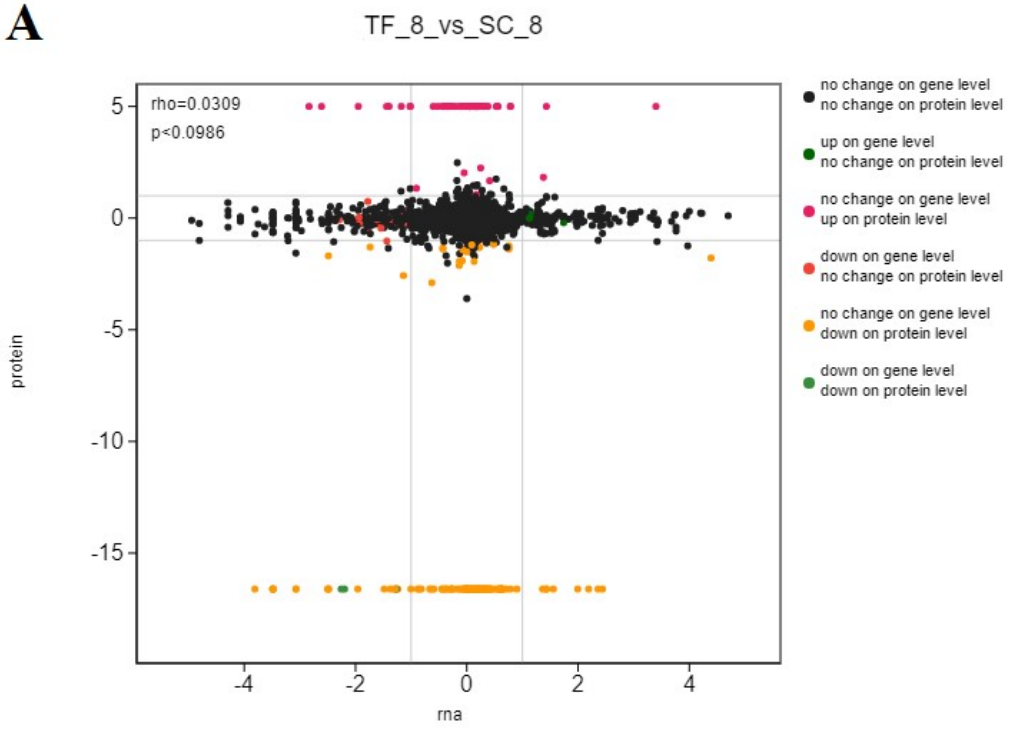
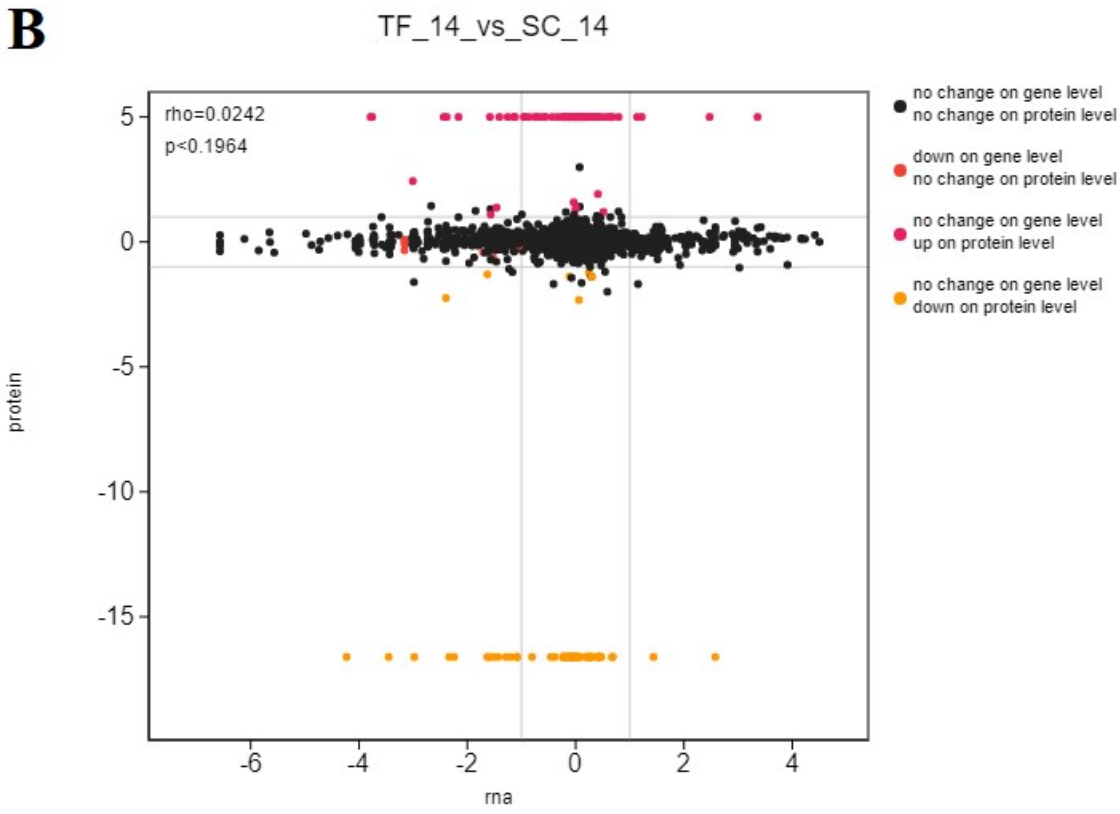


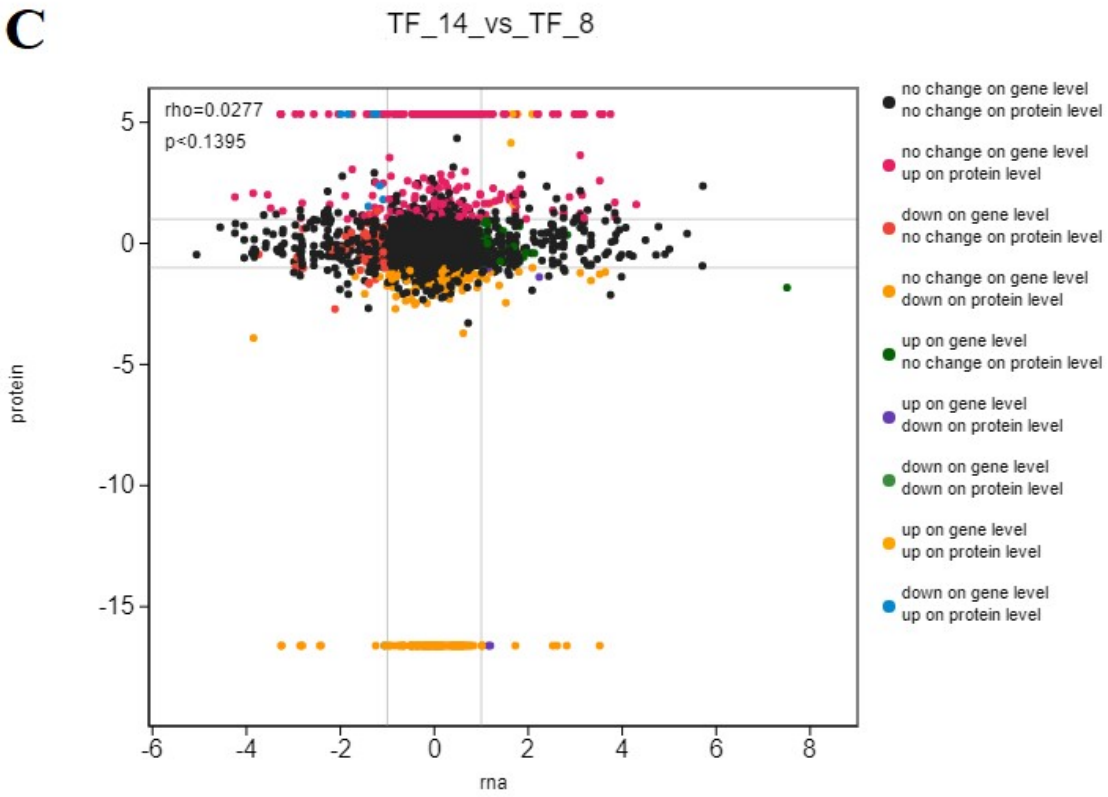
Fig. S7 Differential expression analysis between transcriptome and proteome of G1, G2, and G3 (nine-quadrant diagram).

A


TF_8_vs_SC_8
rho=0.0309
p<0.0986
protein
rna
5
0
-5
-10
-15
-4
-2
0
2
4
no change on gene level
no change on protein level
up on gene level
no change on protein level
no change on gene level
up on protein level
down on gene level
no change on protein level
no change on gene level
down on protein level
down on gene level
down on protein level

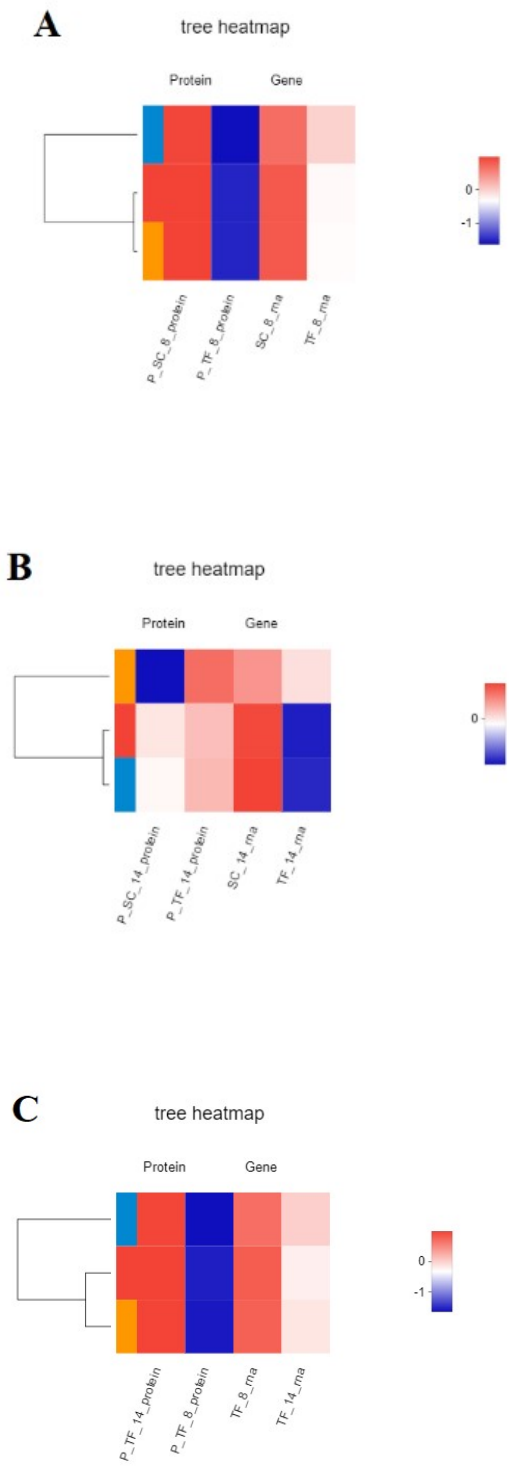
B


TF_14_vs_SC_14
rho=0.0242
p<0.1964
protein
rna
5
0
-5
-10
-15
-6
-4
-2
0
2
4
no change on gene level
no change on protein level
down on gene level
no change on protein level
no change on gene level
up on protein level
no change on gene level
down on protein level



The vertical coordinate represents log2(ratio of protein), and the horizontal coordinate represents log2(ratio of gene), the expression ratio of the corresponding transcript in the comparison group. The rho represents a person relationship between transcriptome and proteome; the p represents the correlation test p value; the greater the absolute value of rho，the greater the correlation between the two omics.

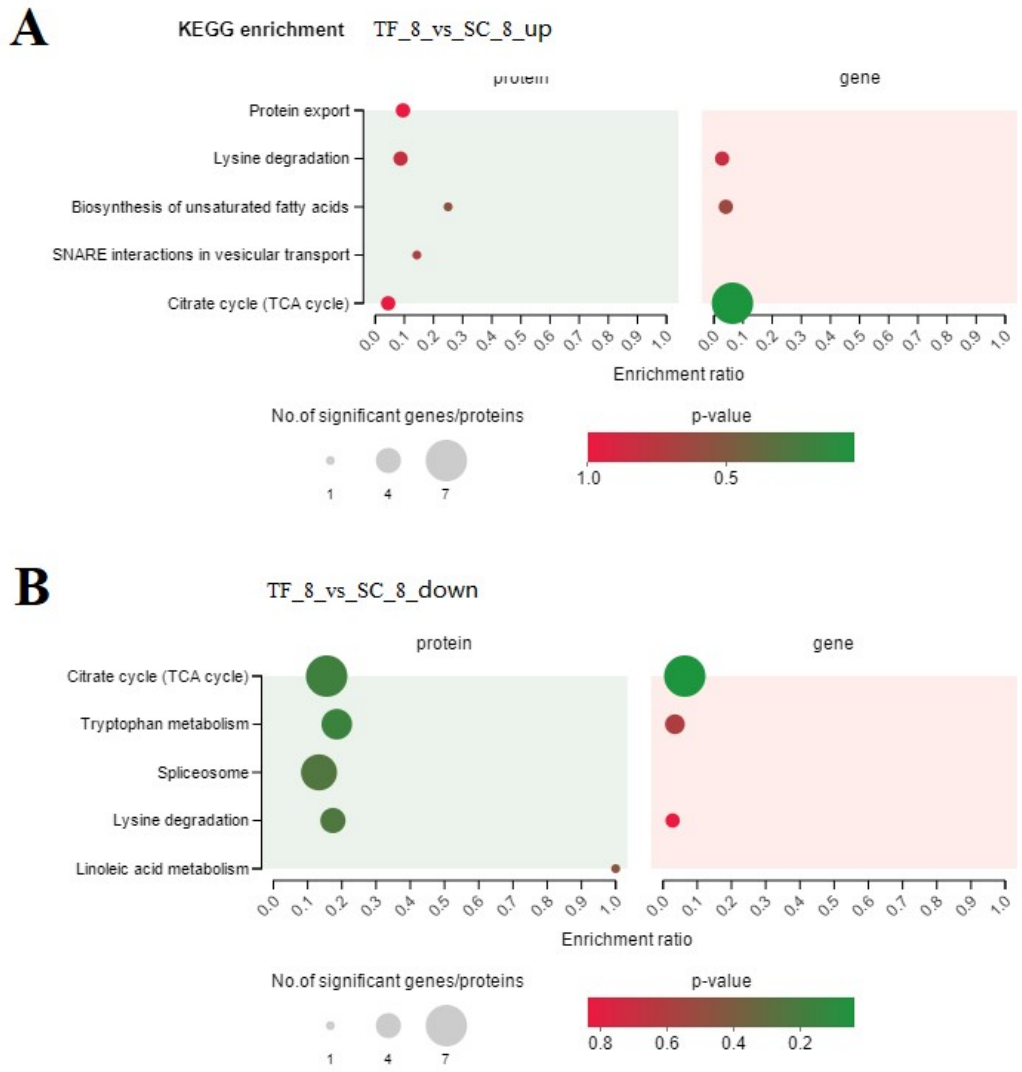
Fig. S8 Differential expression analysis between transcriptome and proteome of G1, G2, and G3 (tree heatmap).



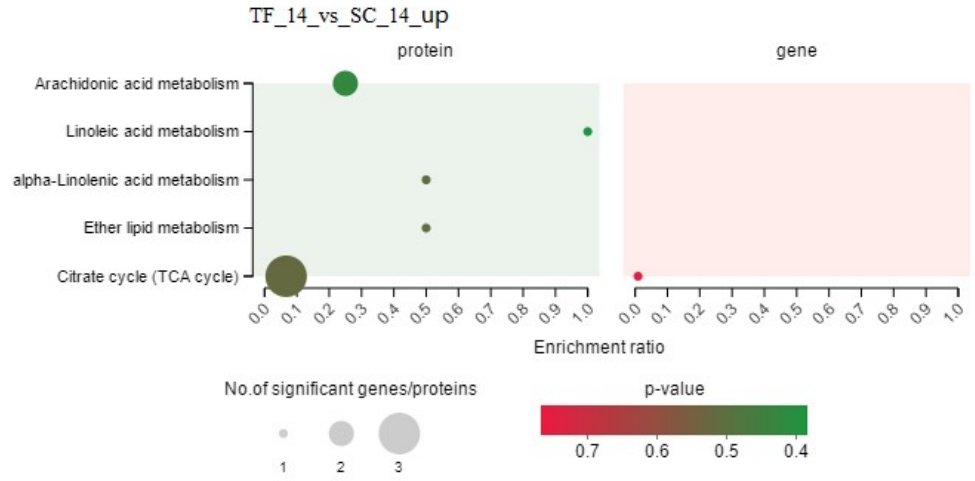
Each column in the figure represents a group or sample, each row represents a protein/gene, and the color in the figure represents the relative expression level of the protein/gene in the group of

samples. For the specific change trend of the expression level, please see the digital label under the color bar on the upper left. On the left is the tree diagram of protein/gene clustering, and on the right is the name of protein/gene. The closer the two protein/gene branches are, the closer their expression levels are. The top is the tree diagram of sample clustering, and the bottom is the name of the sample. The closer the branches of the two samples are, the closer the expression patterns of all proteins/genes in the two samples are, that is, the closer the change trend of expression quantity is.

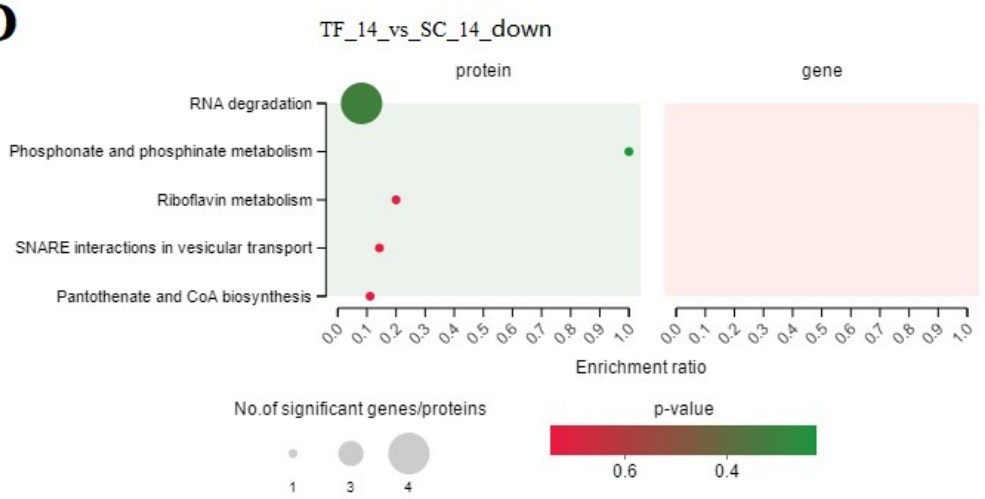
Fig. S9 KEGG pathways enrichment of association analysis between transcriptome and proteome of G1, G2, and G3 (top 5 in DEPs).



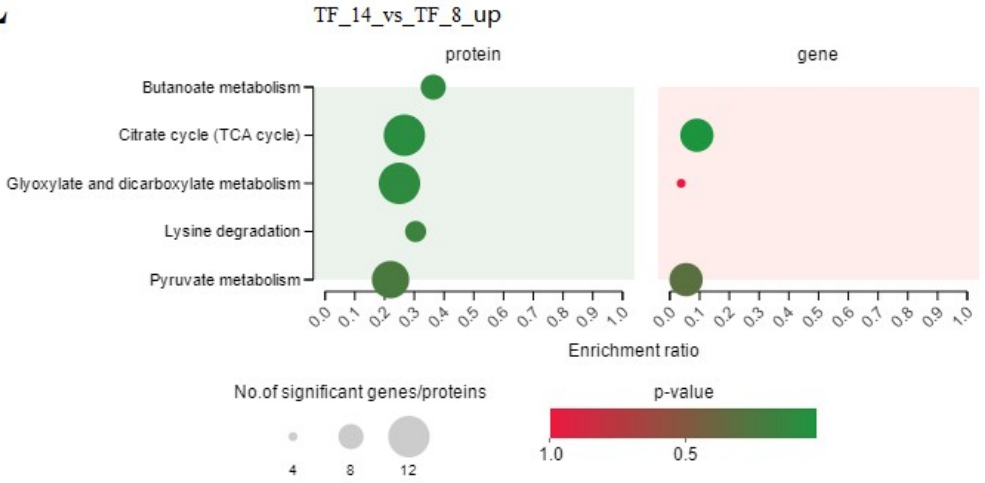
C

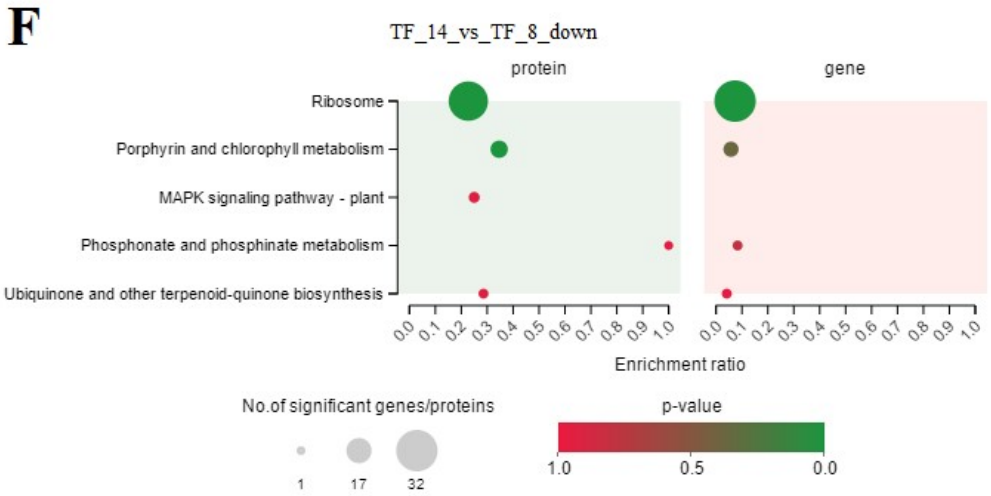

TF_14_vs_SC_14_up
protein
gene
Arachidonic acid metabolism
Linoleic acid metabolism
alpha-Linolenic acid metabolism
Ether lipid metabolism
Citrate cycle (TCA cycle)
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
Enrichment ratio
No.of significant genes/proteins
1 2 3
p-value
0.7 0.6 0.5 0.4

D


TF_14_vs_SC_14_down
protein
gene
RNA degradation
Phosphonate and phosphinate metabolism
Riboflavin metabolism
SNARE interactions in vesicular transport
Pantothenate and CoA biosynthesis
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
Enrichment ratio
No.of significant genes/proteins
1 3 4
p-value
0.6 0.4

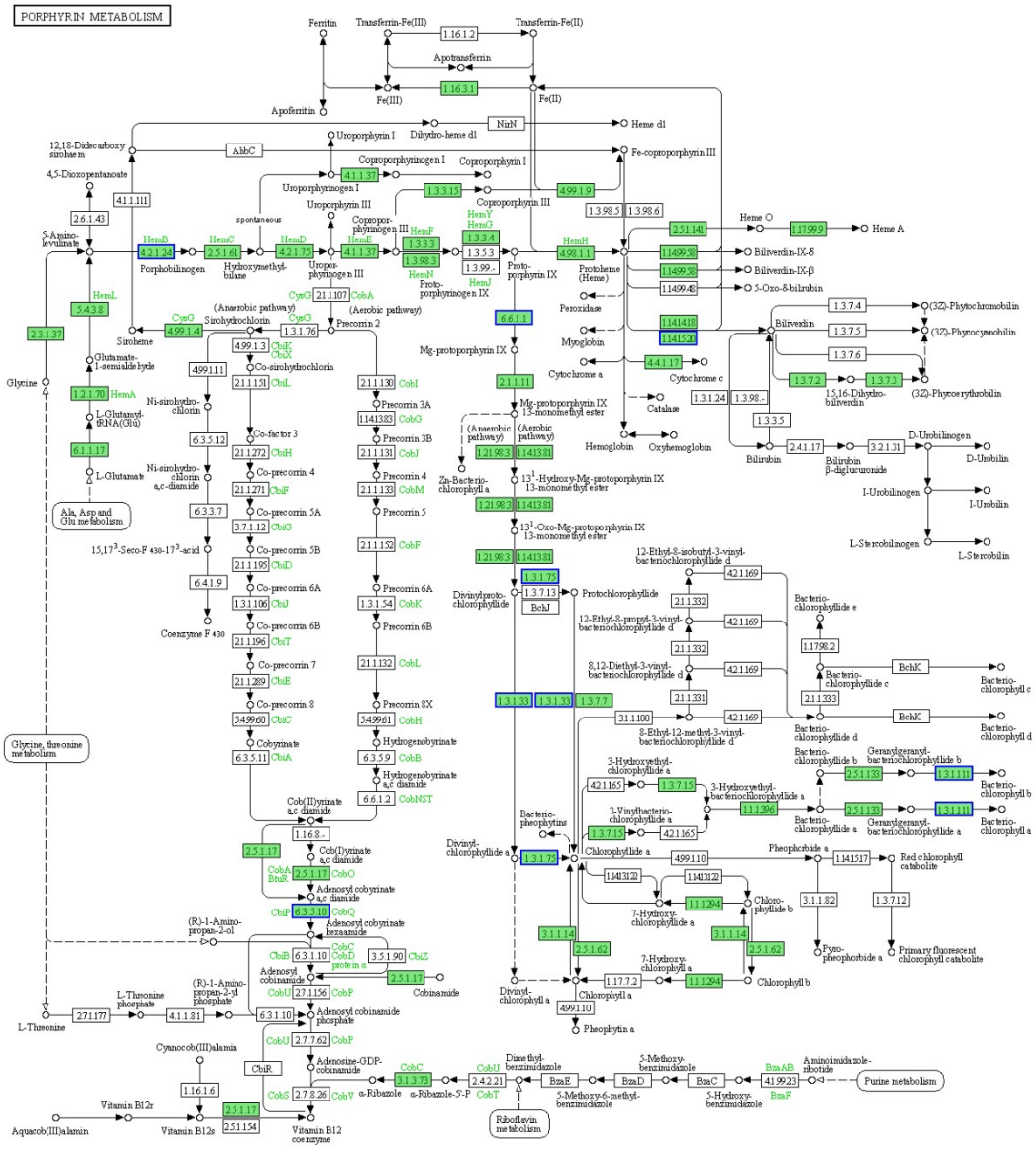
E


TF_14_vs_TF_8_up
protein
gene
Butanoate metabolism
Citrate cycle (TCA cycle)
Glyoxylate and dicarboxylate metabolism
Lysine degradation
Pyruvate metabolism
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
Enrichment ratio
No.of significant genes/proteins
4 8 12
p-value
1.0 0.5



The KEGG pathways enrichment (top 5) of correlation analysis between transcriptome and proteome. The enrichment ratio indicates the ratio of DEGs/DEPs to the total number of annotated genes/proteins in this KEGG pathway. Each bubble represents a KEGG pathway. The different colors of the bubbles represent p-value.

Fig. S10 KEGG pathways enrichment analysis in porphyrin metabolism of DEGs and DEPs in G3 (TF_14_vs_TF_8).



Proteome

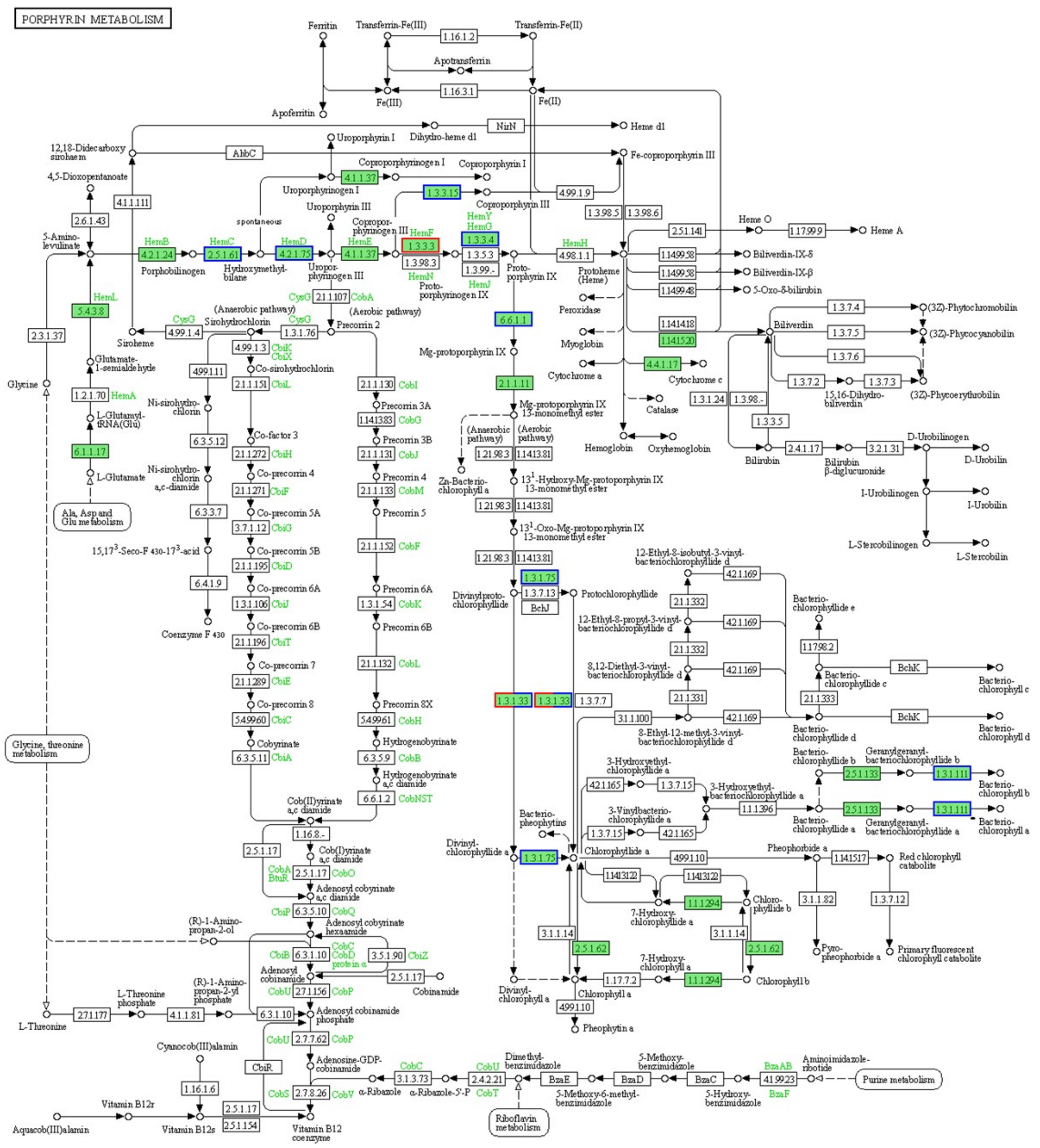
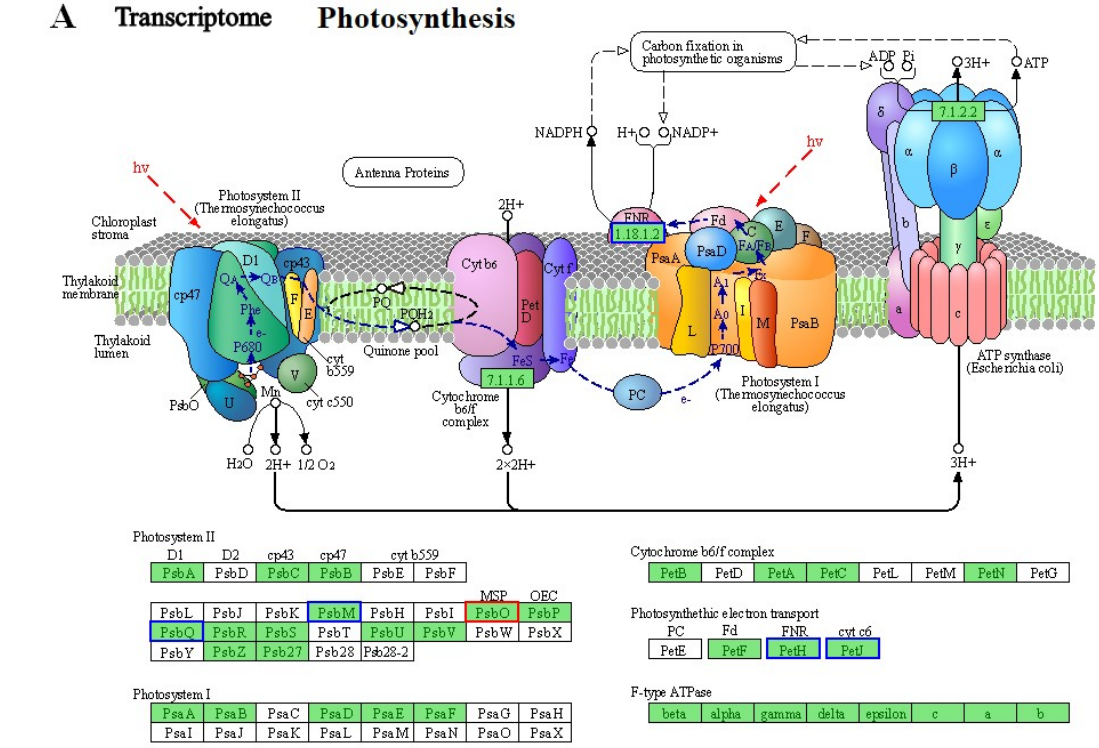

PORPHYRIN METABOLISM
Ferritin
Transferrin-Fe(III)
Transferrin-Fe(II)
Apotransferrin
Fe(III)
Fe(II)
Apoferritin
Heme d1
Dihydro-heme d1
12,18-Didecarboxy siroheam
Fe-coproporphyrin III
4,5-Dioxopentanoate
Uroporphyrin I
Coproporphyrinogen I
Coproporphyrin I
Uroporphyrinogen I
Coproporphyrin III
Uroporphyrin III
5-Amino-levulinate
Porphobilinogen
Hydroxymethyl-bilane
Uroporphyrinogen III
Coproporphyrinogen III
Protoporphyrinogen IX
Protoporphyrin IX
Protoheme (Heme)
Heme O
Heme A
Biliverdin-IX-δ
Biliverdin-IX-β
5-Oxo-δ-bilirubin
Biliverdin
(3Z)-Phytochromobilin
(3Z)-Phycocyanobilin
(3Z)-Phycoerythrobilin
15,16-Dihydro-biliverdin
Peroxidase
Myoglobin
Cytochrome a
Cytochrome c
Catalase
Hemoglobin
Oxyhemoglobin
Bilirubin
Bilirubin β-diglucuronide
D-Urobilinogen
D-Urobilin
I-Urobilinogen
I-Urobilin
L-Stercobilinogen
L-Stercobilin
Glycine
Glutamate-1-semialdehyde
L-Glutamyl-tRNA(Glu)
L-Glutamate
Ala, Asp and Glu metabolism
Siroheme
Sirohydrochlorin
Precorrin 2
Co-sirohydrochlorin
Ni-sirohydrochlorin
Co-factor 3
Co-precorrin 4
Co-precorrin 5A
Co-precorrin 5B
Co-precorrin 6A
Co-precorrin 6B
Co-precorrin 7
Co-precorrin 8
Cobyrinate
Precorrin 3A
Precorrin 3B
Precorrin 4
Precorrin 5
Precorrin 6A
Precorrin 6B
Precorrin 8X
Hydrogenobyrinate
Hydrogenobyrinate a,c diamide
Cob(II)yrinate a,c diamide
Cob(I)yrinate a,c diamide
Adenosyl cobyrinate a,c diamide
Adenosyl cobyrinate hexaamide
Adenosyl cobinamide
Adenosyl cobinamide phosphate
Adenosine-GDP-cobinamide
Vitamin B12 coenzyme
Cobinamide
Coenzyme F 430
Glycine, threonine metabolism
L-Threonine
L-Threonine phosphate
(R)-1-Amino-propan-2-ol
(R)-1-Amino-propan-2-yl phosphate
Cyanocob(III)alamin
Aquacob(III)alamin
Vitamin B12r
Vitamin B12s
α-Ribazole
α-Ribazole-5'-P
Dimethyl-benzimidazole
5-Methoxy-6-methyl-benzimidazole
5-Methoxy-benzimidazole
5-Hydroxy-benzimidazole
Aminoimidazole-ribotide
Purine metabolism
Riboflavin metabolism
Mg-protoporphyrin IX
Mg-protoporphyrin IX 13-monomethyl ester
Zn-Bacterio-chlorophyll a
Divinylproto-chlorophyllide
Protochlorophyllide
Divinyl-chlorophyllide a
Chlorophyllide a
Divinyl-chlorophyll a
Chlorophyll a
Chlorophyll b
Pheophytin a
Bacterio-pheophytins
Pheophorbide a
Red chlorophyll catabolite
Pyro-pheophorbide a
Primary fluorescent chlorophyll catabolite
7-Hydroxy-chlorophyllide a
7-Hydroxy-chlorophyll a
Chloro-phyllide b
Bacterio-chlorophyllide e
Bacterio-chlorophyllide c
Bacterio-chlorophyllide d
Bacterio-chlorophyllide b
Bacterio-chlorophyllide a
Bacterio-chlorophyll c
Bacterio-chlorophyll d
Bacterio-chlorophyll b
Bacterio-chlorophyll a
Geranylgeranyl-bacteriochlorophyllide b
Geranylgeranyl-bacteriochlorophyllide a
3-Hydroxyethyl-chlorophyllide a
3-Vinylbacterio-chlorophyllide a
3-Hydroxyethyl-bacteriochlorophyllide a
12-Ethyl-8-isobutyl-3-vinyl-bacteriochlorophyllide d
12-Ethyl-8-propyl-3-vinyl-bacteriochlorophyllide d
8,12-Diethyl-3-vinyl-bacteriochlorophyllide d
8-Ethyl-12-methyl-3-vinyl-bacteriochlorophyllide d

Fig. S11 KEGG pathways enrichment analysis in electron transport chain of photosynthesis of DEGs and DEPs in G3 (TF_14_vs_TF_8).



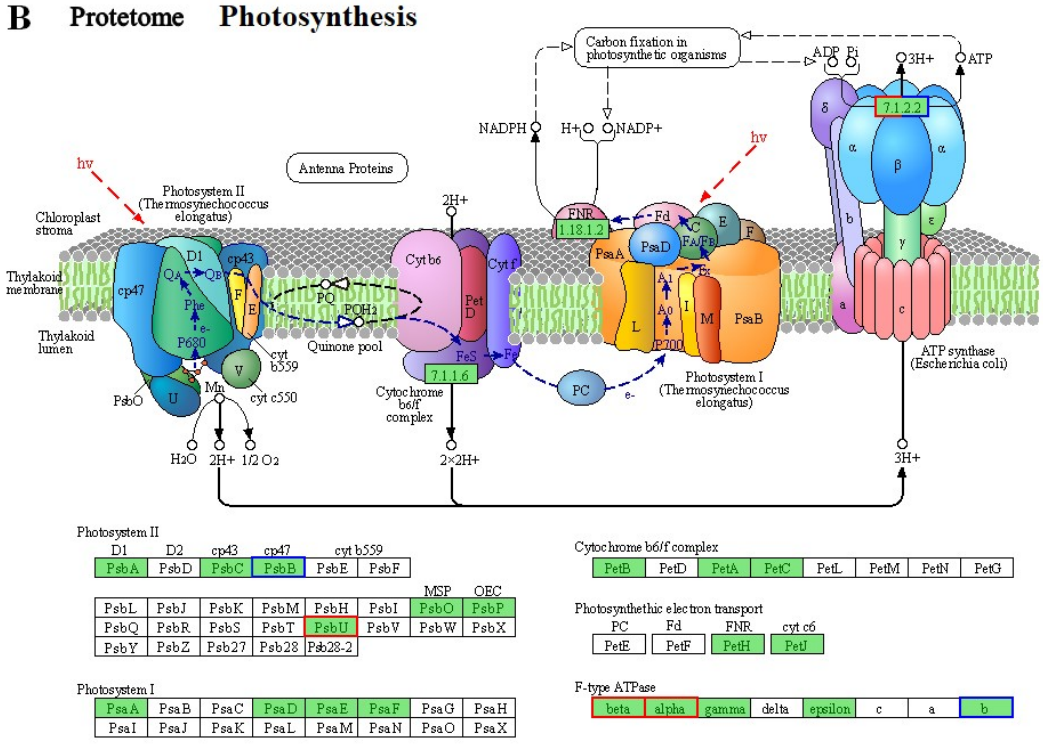
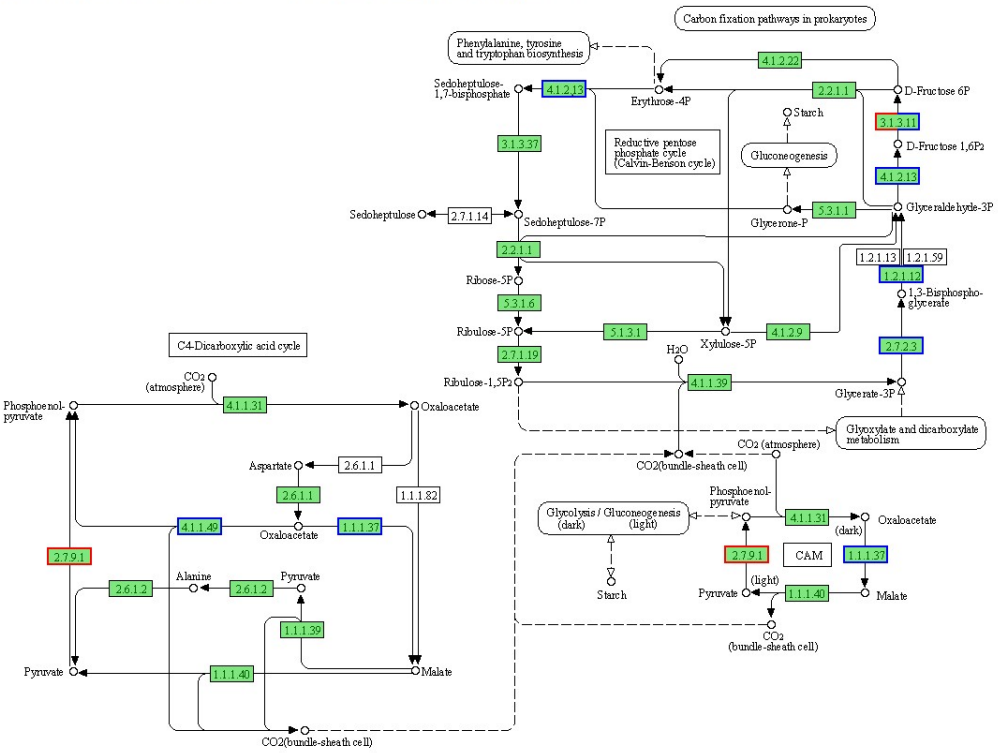


Fig. S12 KEGG pathways enrichment analysis in carbon fixation in photosynthetic organisms of DEGs and DEPs in G3 (TF_14_vs_TF_8).

A Transcriptome Carbon fixation in photosynthetic organism



B Proteome Carbon fixation in photosynthetic organism

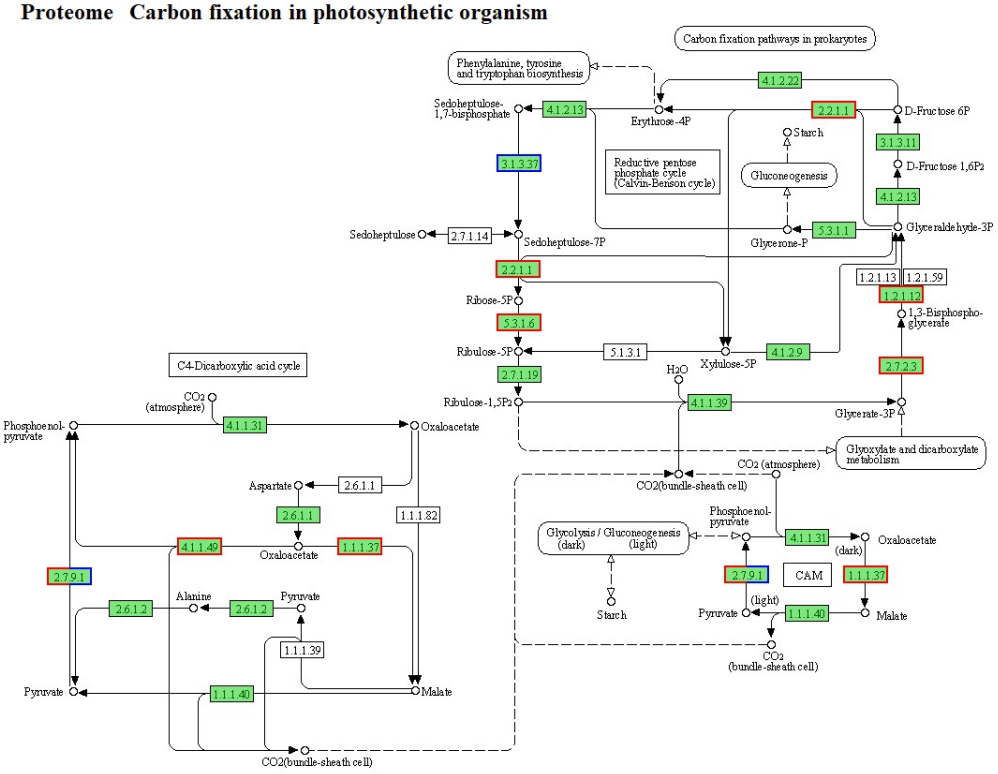
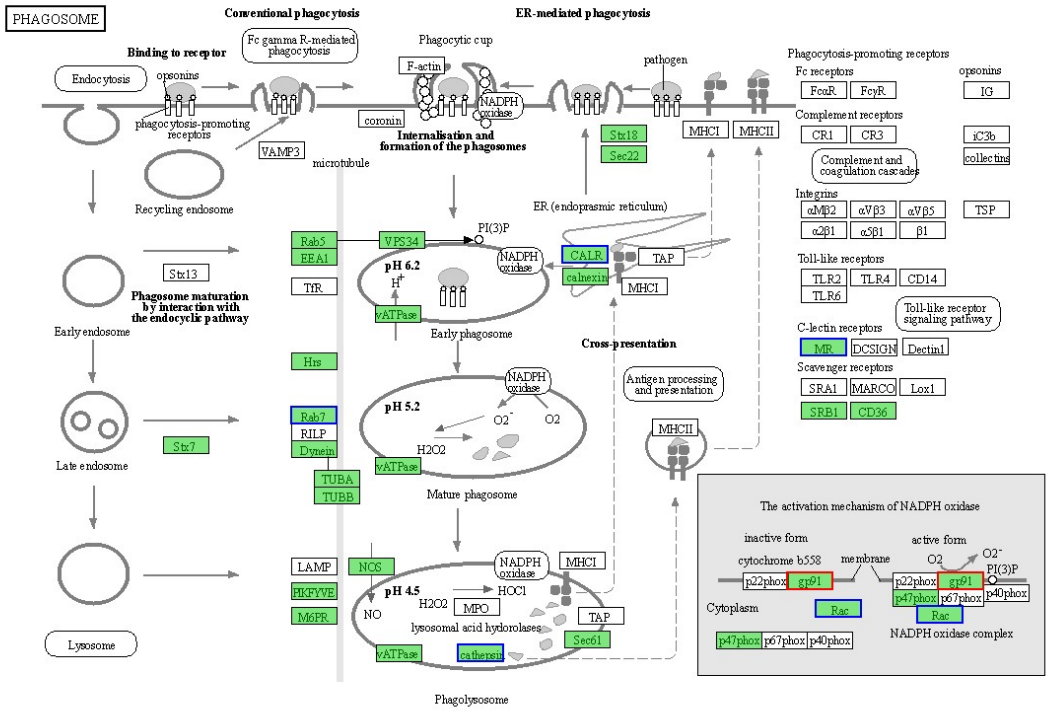


Fig. S13 KEGG pathways enrichment analysis in peroxisome and glutathione metabolism of DEGs and DEPs in G3 (TF_14_vs_TF_8).

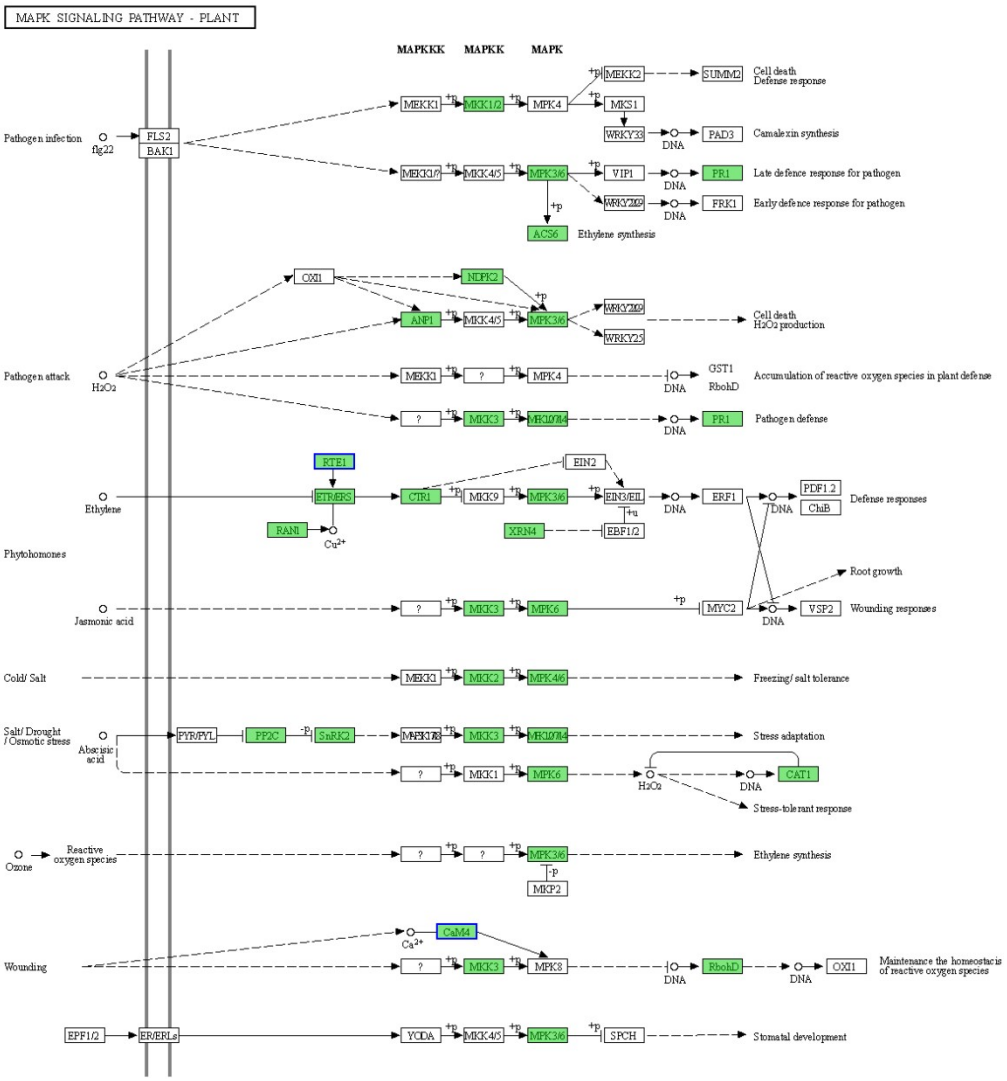
Phagosome

Transcriptome

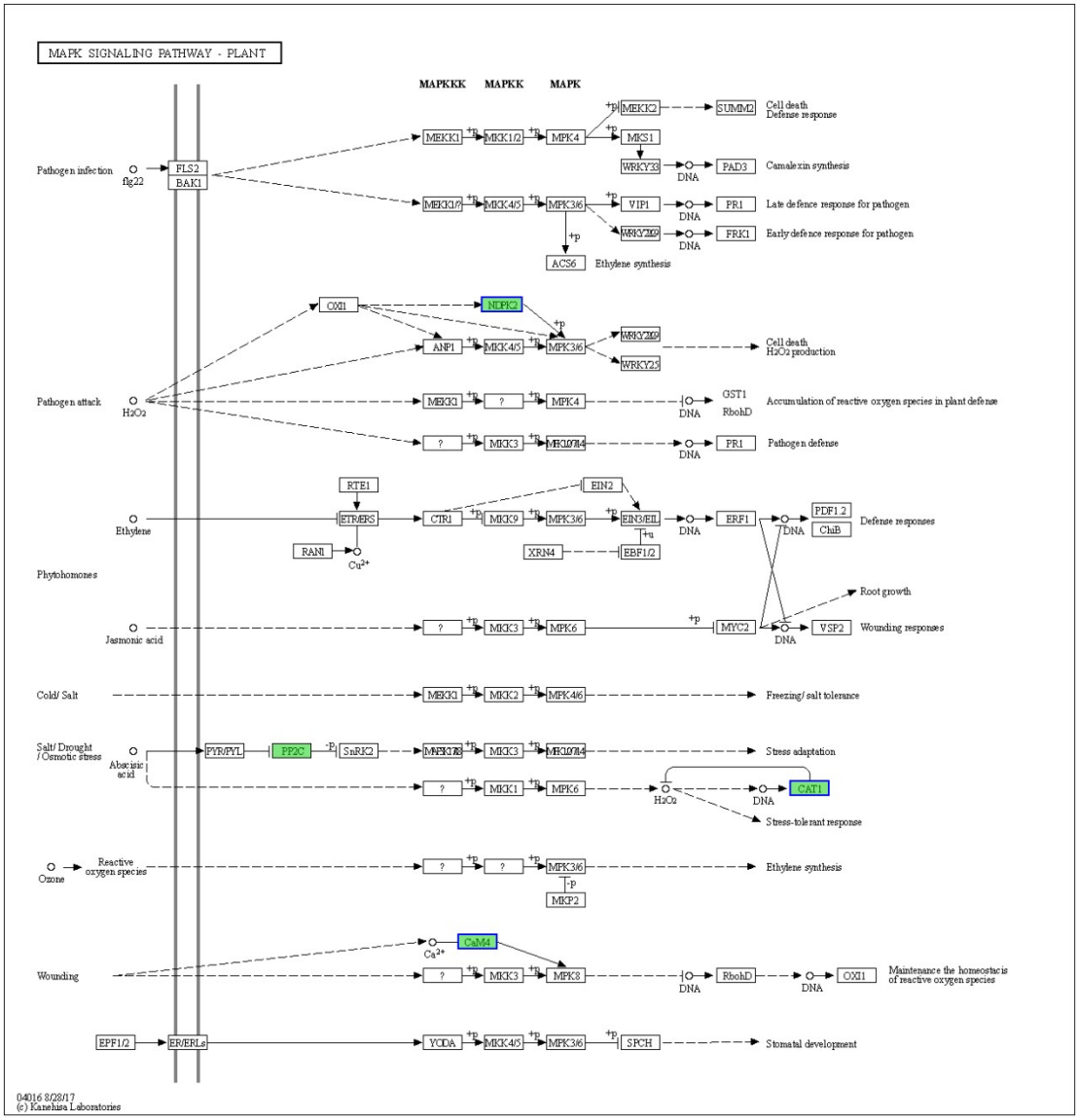


MAPK signaling pathway - plant

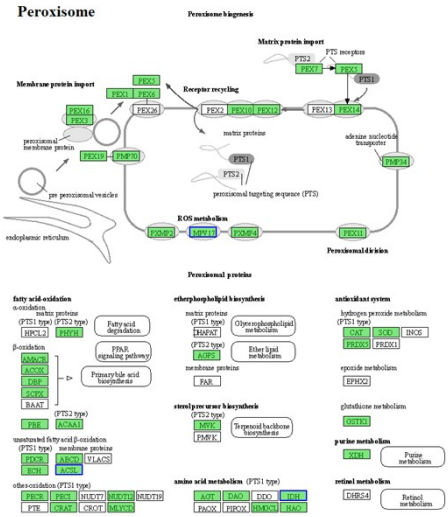
Transcriptome

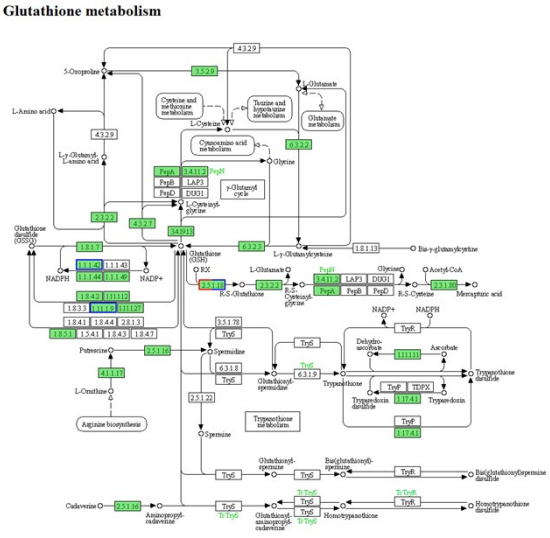

MAPK SIGNALING PATHWAY - PLANT
MAPKKK
MAPKK
MAPK
Pathogen infection
flg22
FLS2
BAK1
MEKK1
MKK1/2
MPK4
MEKK1
MKK4/5
MPK3/6
MEKK1/7
MEKK1/2
MKS1
WRKY33
PAD3
Camalexin synthesis
VIP1
PR1
Late defence response for pathogen
WRKY29
FRK1
Early defence response for pathogen
ACS6
Ethylene synthesis
SUMM2
Cell death
Defense response
DNA
Pathogen attack
H2O2
OXI1
NDPK2
ANP1
MKK4/5
MPK3/6
WRKY29
WRKY25
Cell death
H2O2 production
MEKK1
?
MPK4
GST1
RbohD
Accumulation of reactive oxygen species in plant defense
?
MKK3
MPK1/7/14
PR1
Pathogen defense
Ethylene
Phytohormones
ETR/ERS
CTR1
MKK9
MPK3/6
EIN2
EIN3/EIL
ERF1
PDF1.2
ChiB
Defense responses
RAN1
Cu2+
XRN4
EBF1/2
Root growth
Jasmonic acid
?
MKK3
MPK6
MYC2
VSP2
Wounding responses
Cold/ Salt
MEKK1
MKK2
MPK4/6
Freezing/ salt tolerance
Salt/ Drought
/ Osmotic stress
Abscisic acid
PYR/PYL
PP2C
SnRK2
MPK1/2/7/8
MKK3
MPK1/7/14
Stress adaptation
?
MKK1
MPK6
H2O2
CAT1
Stress-tolerant response
Ozone
Reactive
oxygen species
?
?
MPK3/6
MKP2
Ethylene synthesis
Wounding
Ca2+
CaM4
?
MKK3
MPK8
RbohD
OXI1
Maintenance the homeostacis
of reactive oxygen species
EPF1/2
ER/ERLs
YODA
MKK4/5
MPK3/6
SPCH
Stomatal development

Proteome


MAPK SIGNALING PATHWAY - PLANT
MAPKKK
MAPKK
MAPK
Pathogen infection
flg22
FLS2
BAK1
MEKK1
MKK1/2
MPK4
MEKK2
SUMM2
Cell death
Defense response
MKS1
WRKY33
DNA
PAD3
Camalexin synthesis
MEKK1/7
MKK4/5
MPK3/6
VIP1
PR1
Late defence response for pathogen
FRK1
Early defence response for pathogen
ACS6
Ethylene synthesis
OXI1
NDPK2
ANP1
Cell death
H2O2 production
Pathogen attack
H2O2
MEKK1
MPK4
GST1
RbohD
Accumulation of reactive oxygen species in plant defense
MKK3
PR1
Pathogen defense
RTE1
EIN2
Ethylene
ETR/ERS
CTR1
MKK9
EIN3/EIL
ERF1
PDF1.2
ChiB
Defense responses
RAN1
XRN4
EBF1/2
Phytohomones
Root growth
Jasmonic acid
MKK6
MYC2
VSP2
Wounding responses
Cold/ Salt
MKK2
MPK4/6
Freezing/ salt tolerance
Salt/ Drought
/ Osmotic stress
Abscisic acid
PYR/PYL
PP2C
SnRK2
Stress adaptation
CAT1
Stress-tolerant response
Reactive oxygen species
Ozone
MKP2
Ethylene synthesis
CaM4
Wounding
MPK8
RbohD
OXI1
Maintenance the homeostacis of reactive oxygen species
EPF1/2
ER/ERLs
YODA
SPCH
Stomatal development
04016 8/28/17
(c) Kanehisa Laboratories

Transcriptome





Proteome