

Supplemental Figure Legends

Supplementary Figure S1. eggNOG function classification on blue module genes.

Supplementary Figure S2. KEGG analysis on blue module genes. Column length indicates the number of genes under this category.

Supplemental Figure S3. Real-time quantitative PCR validation of RNA-Seq data in three persimmon fruit. Each dot represents the \log_2FC (CK vs CO₂) of each gene. Person correlation shows the relationship between RNA-seq and relative expression data.

Supplemental Table Legends

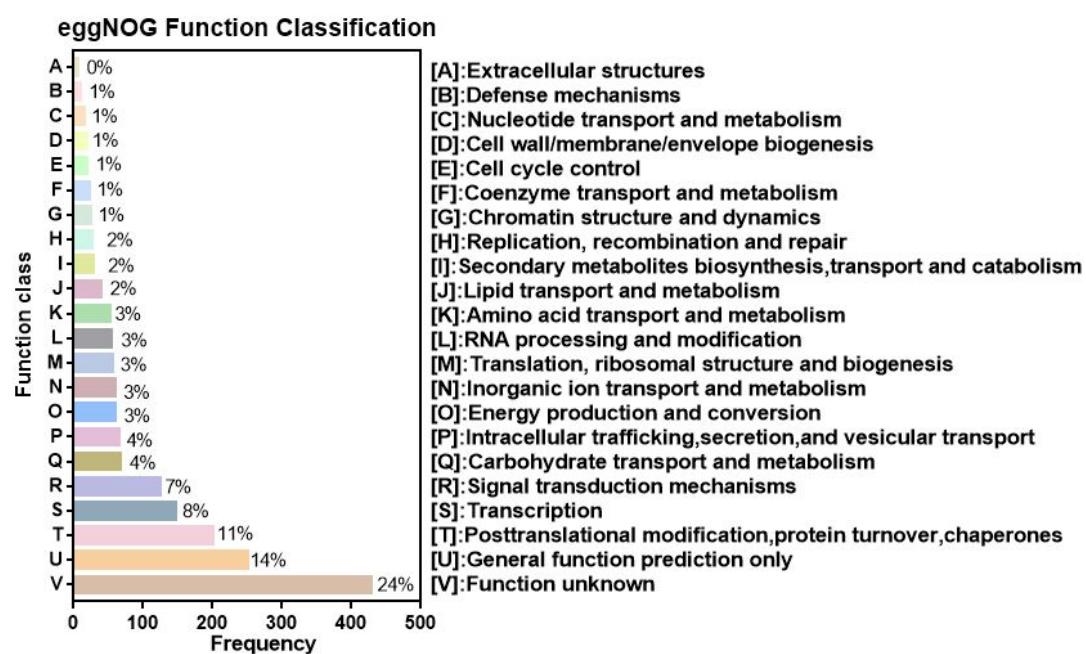
Supplemental Table S1. Cultivar full name of tested persimmon

Supplemental Table S2. Primers for real-time quantitative PCR.

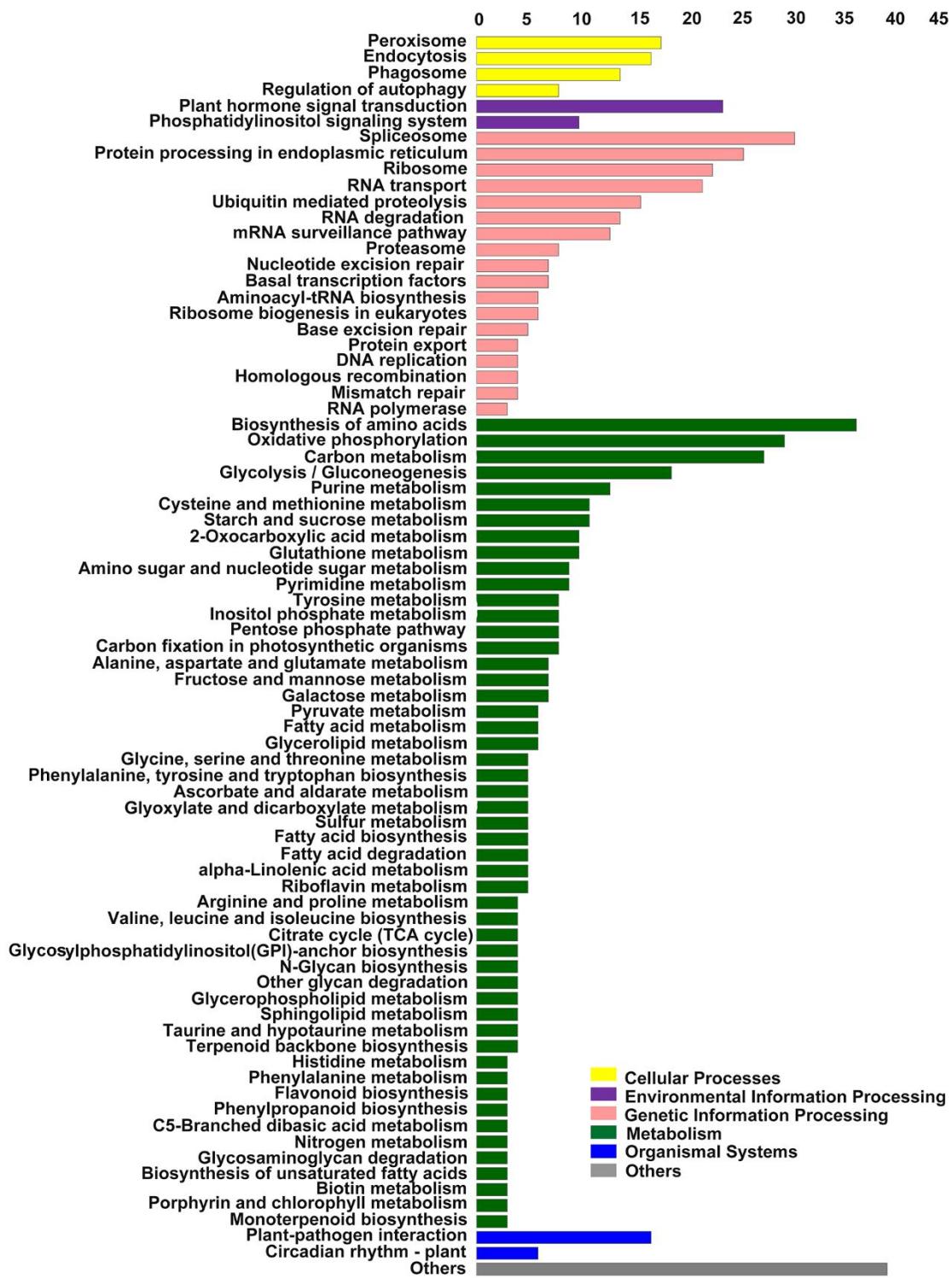
Supplemental Table S3. DEGs number of three persimmon cultivars under CO₂ treatment

Supplemental Table S4. Details of genes involved in the paper

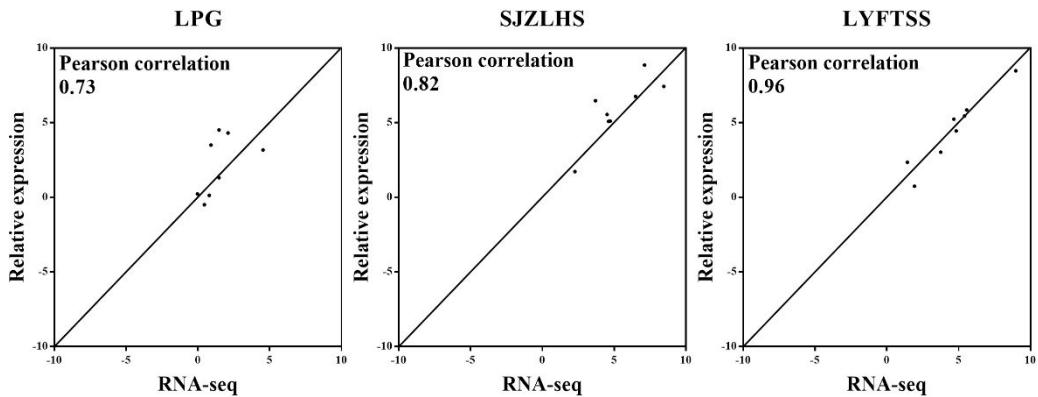
Supplementary Figure S1.



Supplementary Figure S2.



Supplemental Figure S3.



Supplemental Table S1. Cultivar full name of tested persimmon

Abbreviation	Cultivar full name
LPG	'Laopige'
MXHQMNT	'Meixianhengqumanaitou'
TTTS	'Xingtaitaishi'
LCMS	'Lichengmianshi'
MRS	'Mianrangshi'
YYWGS	'Yunyangwaguanshi'
SGS	'Shigoushi'
GYS	'Guyishi'
SJZLHS	'Shijiangzhuanglianhuashi'
HXHGS	'Huxianhuoguanshi'
JS	'Jishi'
SYSS	'Sanyuanshaoshi'
LYFTSS	'Luoyangfangtianshengshi'
XHeS	'Xiaoheshi'
JSHX	'Jishanhanxin'
ENZ	'Ernizi'
LTBS	'Lintongbanshi'

Supplemental Table S2. Primers for real-time quantitative PCR.

geneID	Sense primer	Antisense primer
EVM0028205	TGAGTCAACAGTCGGA GGTG	CTCAATCTGGCTGCCCTCA
EVM0007568	AGGCTTCCTGAGGAGTG TGA	GTTTCCTTGAGCCTCCA
EVM0023054	TGGTTGGCTACACTGCT ACT	ACCGATTGTCACCAGAAC C
EVM0018130	TTTCGACGAATCATCAG GCG	ACGACACGACCTCTGAGATC
EVM0025771	CGCTTGGATCTCTGGA GCT	TCCAAATTACAGACTGCCA AAC
EVM0002315	ACTTACATGATCCGGGC TGT	TGGCCCACATTCTATCGGTT
EVM0027273	GGTATGCACAGAGGAA CAGC	AAACCTGGTGTGGGAGAACT
EVM0008535	GAGTCGGTTCTGAAGGT TGC	TGGCGCAATAATGGCTGAAA
EVM0030653	CATGCTTGCTGATCCTC GTC	AAAAGTGGCCCCAACAAA G
EVM0005033	GAGAGACGGGATCAAC AGCT	TCATTGGCCGTCCTCTCTTT
EVM0023314	GGCAGCCTACCAGGAA ACAC	CTTCACCTCCCTCCATAGC
EVM0022732	TGAAGCAATTGACACG GCAA	TAATCCACCCAAGAGCTGCA
EVM0007501	ATTCTCGGAGATCAACA AGGCC	CTTATTCACTCAGTTACAGA CGATGC
EVM0027066	ATTCTCGGAGATCAACA AGGCC	TCATTAGTTATTGATCAGTT TGCAGA

Supplemental Table S3. DEGs number of three persimmon cultivars under CO₂

treatment

Number	LPG	SJZLHS	LYFTSS
Total	23520	23520	23520
Up	2649	3851	3796
Down	1836	2931	3655
Normal	19035	16738	16069
DEGs	4485	6782	7451
DEG percentage	19.07%	28.84%	31.68%

Supplemental Table S4. Details of genes involved in the paper

geneID	NR_annotation
EVM0023314	PREDICTED: phosphoenolpyruvate carboxykinase [ATP]-like [Sesamum indicum]
EVM0014273	probable starch synthase 4, chloroplastic/amyoplastic [Vitis vinifera]
EVM0000358	phosphoenolpyruvate carboxylase [Manihot esculenta subsp. flabellifolia]
EVM0030229	PREDICTED: bifunctional enolase 2/transcriptional activator-like [Tarenaya hassleriana]
EVM0023033	PREDICTED: isocitrate dehydrogenase [NADP] isoform X2 [Nelumbo nucifera]
EVM0008535	unnamed protein product [Coffea canephora]
EVM0007501	alcohol dehydrogenase 1 [Diospyros kaki]
EVM0008986	PREDICTED: starch synthase 3, chloroplastic/amyoplastic [Vitis vinifera]
EVM0005033	phosphoenolpyruvate carboxylase kinase [Solanum lycopersicum]
EVM0014076	PREDICTED: glucose-6-phosphate isomerase, cytosolic [Sesamum indicum]
EVM0022732	pyruvate decarboxylase 2 [Diospyros kaki]
EVM0020781	sucrose synthase 2 [Camellia sinensis]
EVM0007329	pyruvate decarboxylase 3, partial [Diospyros kaki]
EVM0017156	ADP-glucose pyrophosphorylase family protein isoform 1 [Theobroma cacao]
EVM0030425	PREDICTED: granule-bound starch synthase 1, chloroplastic/amyoplastic [Nelumbo nucifera]
EVM0001415	beta-amylase 2 [Camellia sinensis]
EVM0006659	PREDICTED: ATP-dependent 6-phosphofructokinase 3-like [Vitis vinifera]
EVM0018405	PREDICTED: granule-bound starch synthase 2, chloroplastic/amyoplastic isoform X2 [Vitis vinifera]
EVM0012438	hypothetical protein JCGZ_10511 [Jatropha curcas]
EVM0017809	PREDICTED: phosphoglycerate mutase [Sesamum indicum]
EVM0012828	alcohol dehydrogenase family protein [Populus trichocarpa]
EVM0026661	UGP-glucose pyrophosphorylase [Actinidia eriantha]
EVM0030653	hypothetical protein JCGZ_16628 [Jatropha curcas]
EVM0027273	hypothetical protein CISIN_1g007800mg [Citrus sinensis]
EVM0028451	hypothetical protein CICLE_v10011317mg [Citrus clementina]
EVM0006954	PREDICTED: beta-amylase 1, chloroplastic [Sesamum indicum]
EVM0010186	hypothetical protein PRUPE_ppa003994mg [Prunus persica]
EVM0013703	PREDICTED: enolase [Vitis vinifera]
EVM0031484	unnamed protein product [Vitis vinifera]
EVM0015294	PREDICTED: NAD-dependent malic enzyme 59 kDa isoform, mitochondrial [Sesamum indicum]
EVM0002315	phosphofructokinase [Hevea brasiliensis]
EVM0003043	hypothetical protein JCGZ_08022 [Jatropha curcas]
EVM0030132	unnamed protein product [Coffea canephora]
EVM0027066	alcohol dehydrogenase 1 [Diospyros kaki]