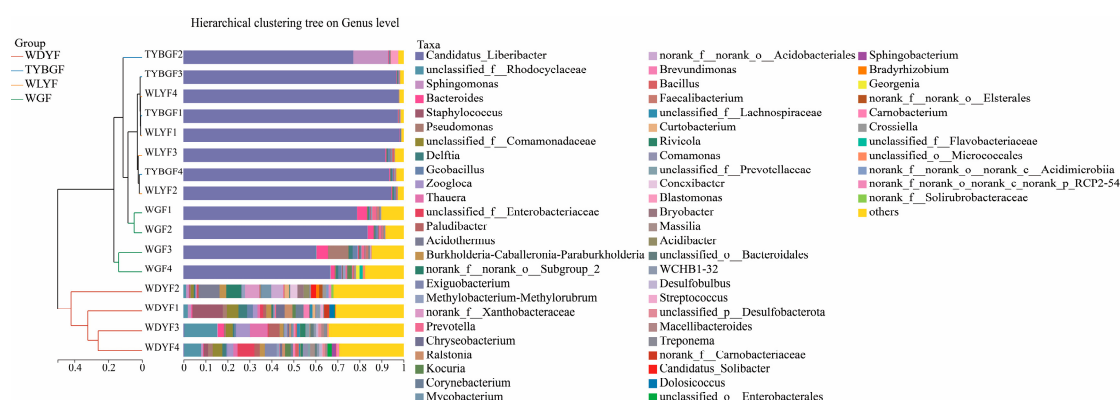


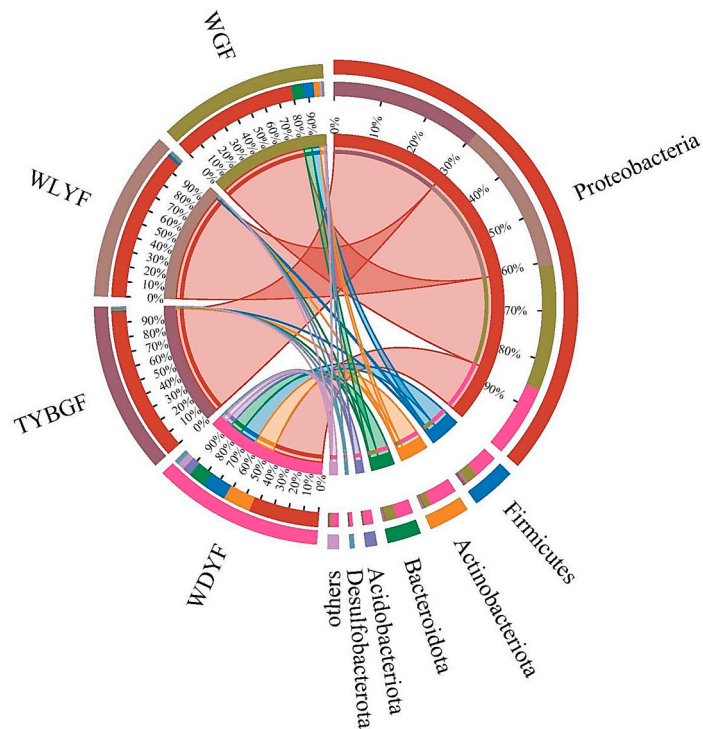
Supplementary Table S2. Statistical analysis of microbial Alfa-diversity conducted by Simpson Index and Shannon index

Treatment	Comparison	p-value
Simpson Index		
WDYF	WGF	0.0005001***
WDYF	TYBGF	0.00005997***
WDYF	WLYF	0.00000006676***
WLYF	WGF	0.003796**
WLYF	TYBGF	0.4283
TYBGF	WGF	0.03757*
Shannon index		
WDYF	WGF	0.0002765***
WDYF	TYBGF	0.000007224***
WDYF	WLYF	0.00001467***
WLYF	WGF	0.008492**
WLYF	TYBGF	0.5369
TYBGF	WGF	0.009984**

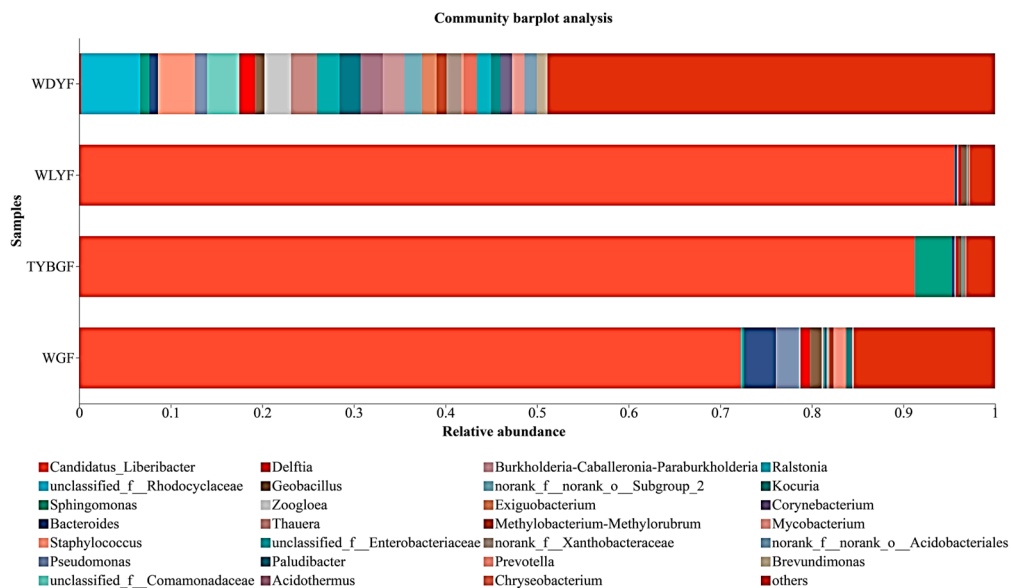
Note: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$



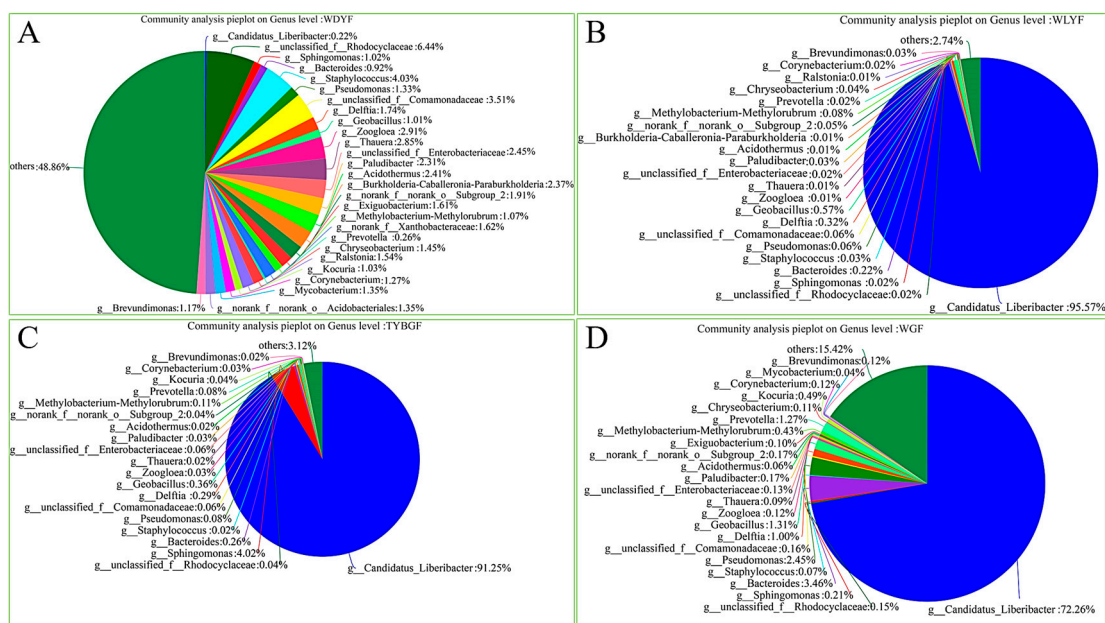
Supplementary Figure S1. Hierarchical clustering tree of bacterial in four types of pericarp samples



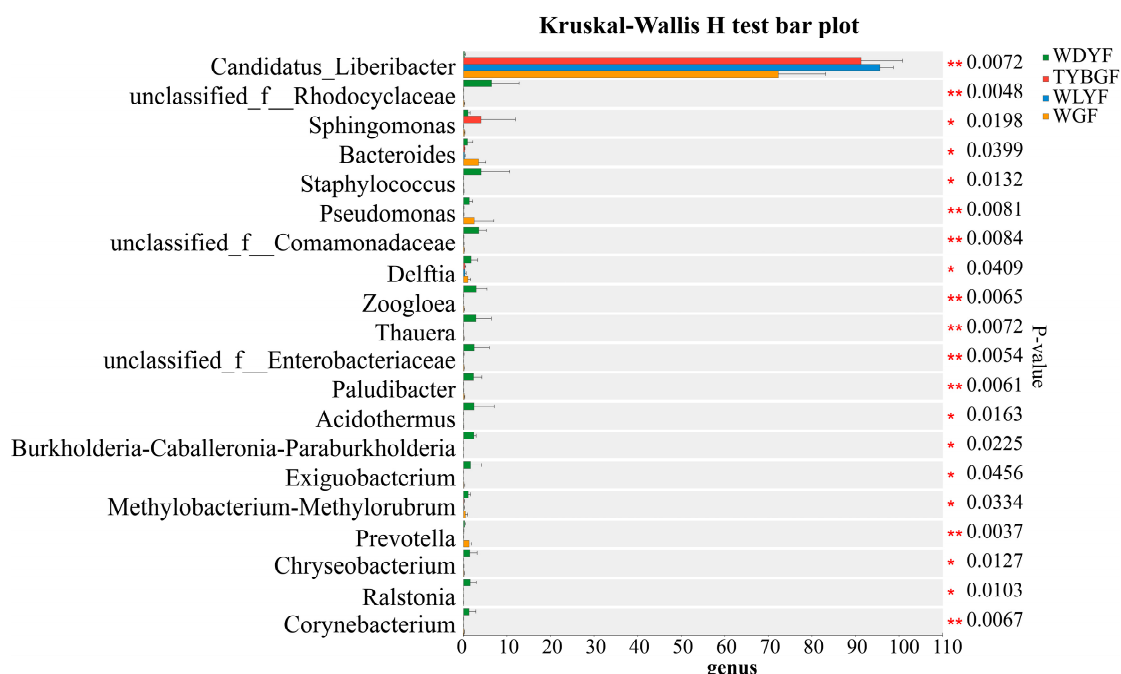
Supplementary Figure S2. Circos plot of bacterial composition in four types of pericarp samples



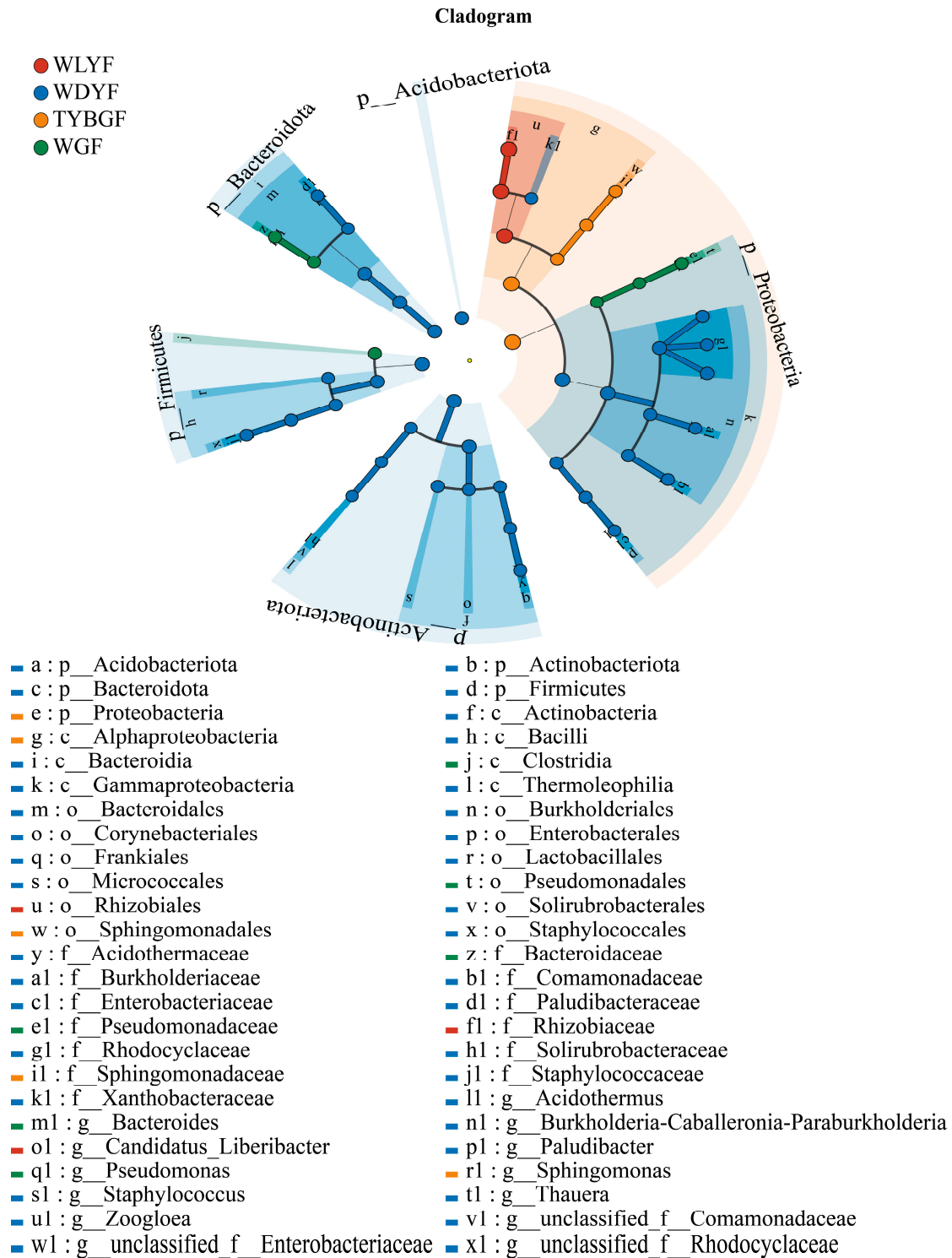
Supplementary Figure S3. The community bar plot analysis of bacterial composition in four types of pericarp samples



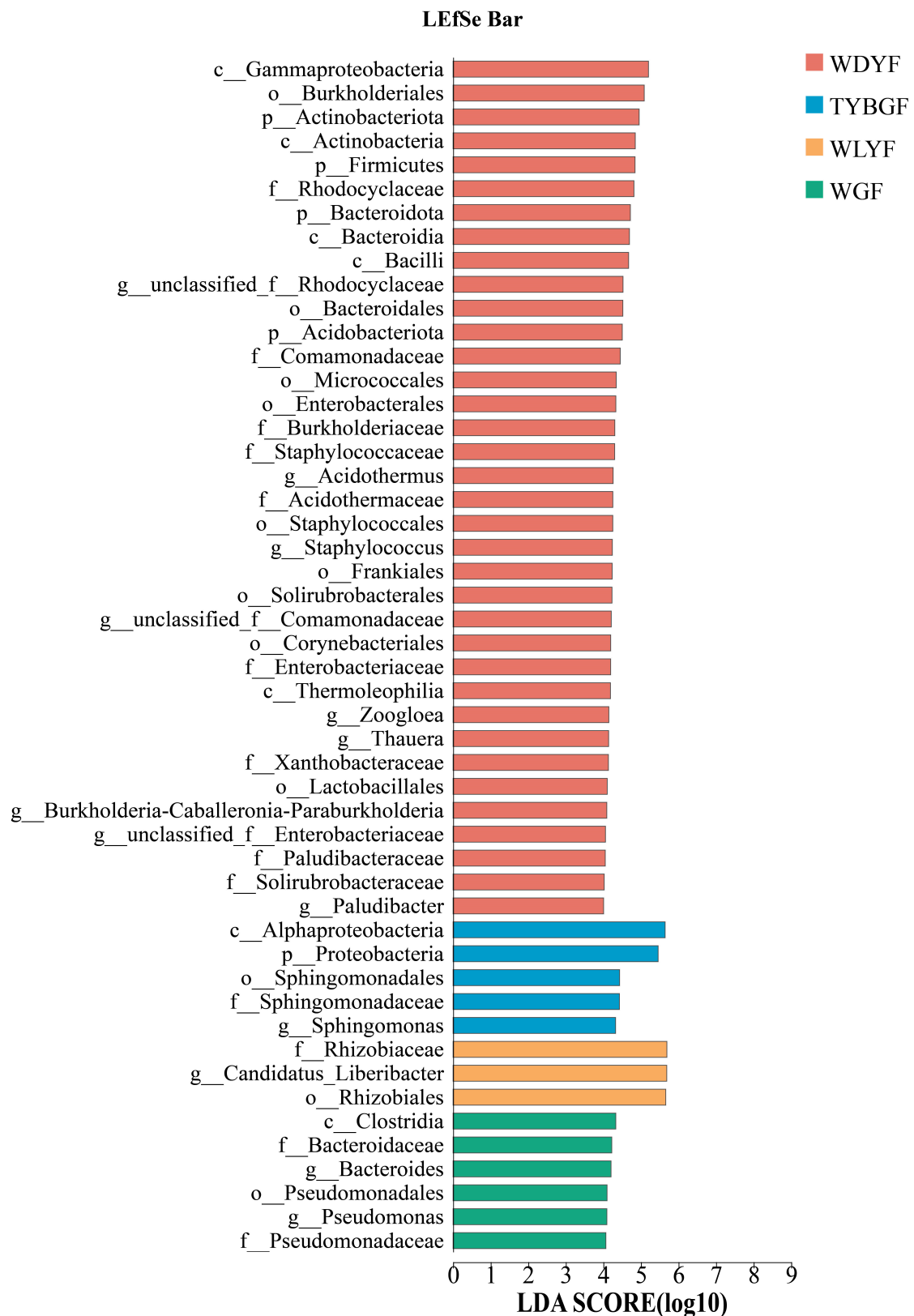
Supplementary Figure S4. Bacterial genera composition in the four types of pericarps. (A) Microbial community pie plot of bacteria in WDYF. (B) Microbial community pie plot of bacteria in WLYF. (C) Microbial community pie plot of bacteria in TYBGF. (D) Microbial community pie plot of bacteria in WGF.



Supplementary Figure S5. Kruskal-Wallis H test bar plot analysis of the relative proportions of major genera. p -values were calculated using the Kruskal-Wallis H test. *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$



Supplementary Figure S6. Taxonomic cladogram obtained from linear discriminant analysis effect size analysis of 16S sequences in four types of pericarp samples. The circles from inner to outer represent the taxonomic levels of phylum, class, order, family, genus, and species.



Supplementary Figure S7. Linear discriminative analysis (LDA) score of differentially enriched bacteria obtained from LEfSe analysis of microbiota from phylum to genus in four types of pericarp samples

Heatmap showing the relative abundance of 100 bacterial taxa across 100 chemical compounds. The color scale ranges from -1 (green) to 1 (red). The taxa are listed on the right, and the compounds are listed on the left. The heatmap shows a clear separation of taxa into two main groups based on their relative abundance across the compounds.

Chemical Compounds (Left):

- Daiphinidin O-malonyl-malonylhexoside
- Isosakuranetin (4'-Methylaringenin)
- N-Methyltryptamine
- Hordenine
- 1-O-Caffeoyl quinic acid
- Neochlorogenic acid (5-O-Caffeoyl quinic acid)
- Naringenin O-methylchalcone
- Peonidin 3-O-glucoside chloride
- Tricin O-glucuronide acid
- 5-Hydroxy-L-tryptophan
- N'-Formylkyurenine
- Peonidin O-hexoside
- 6-Methylcoumarin sakuranetin
- Cis-Aconitic acid
- 4-Methyl-5-thiazolethanol Crocin
- Forechlorofenuren
- Albricie
- Dihydroquinosylvin
- D-Pantothenic acid
- Decasaccharide
- Myricetin
- 3-Indolepropionic acid
- O-Caffeoyl maltotriose
- Tricin 4'-O-p-guaitacylglycerol
- N-hexacyl-p-coumaroyl serotonin
- trans-cinnamaldehyde
- p-Coumaraldehyde
- trans-cinnamaldehyde
- Chlorogenic acid (3-O-Caffeoyl quinic acid)
- Nicotinic Acid Methyl Ester (Methyl Nicotinate)
- L-Ascorbate
- L-Denichin
- Confertyl alcohol
- Tri-O-methylcinnamaldehyde
- 4-Hydroxy-3-methoxycinnamaldehyde
- "Genistein (4',5',7-Trihydroxyisoflavone)
- Nicotinic acid-hexoside
- 4-Aminocidine
- Gallie acid O-Feruloyl-O-hexoside
- Acetyl-erodictyol O-hexoside
- 3-O-p-Coumaroyl quinic acid
- Heliodiosin F

Bacterial Taxa (Right):

- Faecalibacterium
- Altiples
- Prevotella
- Bacteroides
- Blindobacterium
- Blasomones
- Candidatus_Liberibacter
- norank_f_Mitochondria
- Curtobacterium
- Staphylococcus
- Raquitella
- unclassified_f_Prevotellaceae
- norank_f_Carnobacteriaceae
- Doligracoccus
- Acidibacter
- Rupholderia-Caballeronia-Paraburkholderia
- Ralstonia
- Corynebacterium
- Escherichia-Shigella
- Comamonas
- Desulfobulbus
- Acidothermus
- unclassified_f_Rhodocyclaceae
- Zoogloea
- Racilius
- Chryseobacterium
- Brevundimonas
- Stenotrophomonas
- Delftia
- norank_f_norank_o_Subgroup_2
- haucra
- Palindbacter
- Bradyrhizobium
- Methylbacterium-Methylorubrum
- Rivicola
- Pelomonas
- Leptoternus
- Grobacillus
- norank_f_norank_o_Elsterales
- Mycobacterium
- norank_f_Xanthobacteraceae
- Conexibacter
- Pseudomonas
- unclassified_f_Lachnospiraceae
- Bryobacter
- Sirepincoccus
- norank_f_norank_o_Acidobacteriales
- Magellibacteroides
- Sphingomonas
- Candidatus_Solibacter

COG function classification

Samples

Relative Abundance

WLYF

TYBGF

WGF

WDYF

0 0.2 0.4 0.6 0.8 1

A : RNA processing and modification
 B : Chromatin structure and dynamics
 C : Energy production and conversion
 D : Cell cycle control, cell division, chromosome partitioning
 E : Amino acid transport and metabolism
 F : Nucleotide transport and metabolism
 G : Carbohydrate transport and metabolism
 H : Coenzyme transport and metabolism
 I : Lipid transport and metabolism
 J : Translation, ribosomal structure and biogenesis
 K : Transcription
 L : Replication, recombination and repair
 M : Cell wall/membrane/envelope biogenesis
 N : Cell motility
 O : Posttranslational modification, protein turnover, chaperones
 P : Inorganic ion transport and metabolism
 Q : Secondary metabolites biosynthesis, transport and catabolism
 S : Function unknown
 T : Signal transduction mechanisms
 U : Intracellular trafficking, secretion, and vesicular transport
 V : Defense mechanisms
 W : Extracellular structures
 Z : Cytoskeleton

Supplementary Figure S9. The COGs function predicted for 16S rRNA of the citrus pericarp by PICRUST

Figure 7. Significant difference in function predicted for KEGG pathway level_3, *, adjust *p*-value <0.05; **, adjust *p*-value <0.01; ***, adjust *p*-value <0.001. ko01100: Metabolic pathways; ko01110: Biosynthesis of secondary metabolites; ko01120: Microbial metabolism in diverse environments; ko01230: Biosynthesis of amino acids; ko02010: ABC transporters; ko03010: Ribosome.

Figure 8. Significant difference in function predicted for KO (A and B), and Enzyme (C and D). *, adjust *p*-value <0.05; **, adjust *p*-value <0.01; ***, adjust *p*-value <0.001. K03088: RNA polymerase sigma-70 factor, ECF subfamily; K01990: ABC-2 type transport system ATP-binding protein; K01992: ABC-2 type transport system permease protein; K06147: ATP-binding cassette, subfamily B, bacterial; K01952: phosphoribosylformylglycinamide synthase; K00058: D-3-phosphoglycerate dehydrogenase/2-oxoglutarate reductase; K07391: magnesium chelatase family protein; K00526: ribonucleoside-diphosphate reductase beta chain; K16079: outer membrane immunogenic protein; K02651: pilus assembly protein FliP/PilA; 2.7.7.7: DNA-directed DNA polymerase; 3.6.4.12: DNA helicase; 2.7.13.3: Histidine kinase; 1.6.5.3: NADH:ubiquinone reductase (H(+)-translocating); 5.2.1.8: Peptidylprolyl isomerase; 2.7.7.6: DNA-directed RNA polymerase; 6.3.5.7: Glutaminyl-tRNA synthase (glutamine-hydrolyzing); 6.3.5.6: Asparaginyl-tRNA synthase (glutamine-hydrolyzing); 6.4.1.2: Acetyl-CoA carboxylase; 3.6.3.14: H(+)-transporting two-sector ATPase; 1.17.4.1: Ribonucleoside-diphosphate reductase; 6.3.5.3: Phosphoribosylformylglycinamide synthase; 1.1.1.95: Phosphoglycerate dehydrogenase.