

Table S1. Number of sequences, total OTUs in bacteria and fungi

		Lon (10 ³)	Zin (10 ³)	Cab (10 ³)	Cha (10 ³)	Syr (10 ³)	Mer (10 ³)	Gem (10 ³)	Rie (10 ³)	Pin (10 ³)
Bacteria	Sequence	--	52.27±20.87	52.98±20.45	59.34±15.85	77.50±38.31	47.19±9.34	44.10±21.70	47.50±8.75	64.99±11.06
	OTUs	--	3.89±0.95	3.97±0.74	4.19±0.59	4.45±0.71	3.72±0.36	3.48±0.82	3.84±0.39	4.49±0.43
Fungi	Sequence	75.62±27.91	97.78±118.78	53.56±26.06	96.38±25.58	100.07±25.74	71.88±27.44	77.82±31.79	68.73±48.55	79.70±24.48
	OTUs	0.89±0.22	1.09±0.20	1.00±0.26	1.31±0.13	1.29±0.12	1.08±0.27	1.24±0.25	1.07±0.37	1.17±0.18

Table S2. Indices of co-networks

	Nodes	Edges	Disgree distribution	Betweenness Centrality Distribution	Density	Modularity
Bacteria	1384	6973	10.077	4	0.007	0.073
Fungi	1020	4038	7.918	4	0.008	0.151

Table S3. Bacterial sequences aligned using BLAST from the NCBI nucleotide database.

OTU No.	References species	Accession.No	Similarity
OTU130	<i>Arthrobacter</i> sp.	MG860374.1	100
OTU375	Uncultured bacterium	MF113989.1	100
OTU646	<i>Bacillus</i> sp.	MK414968.1	100
OTU795	<i>Steroidobacter</i> sp.	JF515710.1	100
OTU1182	Uncultured bacterium	LC026882.1	100
OTU1203	<i>Kocuria</i>	MK696247.1	100
OTU1226	<i>Bradyrhizobium</i> sp.	FJ380996.1	100
OTU1496	<i>Romboutsia</i> sp.	LT996174.1	100
OTU2150	Uncultured bacterium	KM328768.1	100
OTU2257	<i>Blastococcus</i> sp.	MK696404.1	100
OTU2425	<i>Arthrobacter</i> sp.	MG860431.1	100
OTU2536	<i>Arthrobacter</i> sp.	MK696393.1	100
OTU3419	<i>Arthrobacter</i> sp.	KX171688.1	100
OTU3429	Uncultured bacterium	MH445072.1	100
OTU3574	<i>Arthrobacter</i> sp.	MK053924.1	100

OTU3775	Uncultured Actinobacterium	KJ081636.1	100
OTU3794	Nocardioides (family)	MK138625.1	100
OTU3854	Planomicrobium	MH550146.1	100

Table S4. Fungal sequences aligned using BLAST from the NCBI nucleotide database.

OTU No.	References species	Accession. No	Similarity(%)
OTU104	<i>Cladosporium</i> sp.	MG569541.1	100
OTU232	Nectriaceae	HG936943.1	100
OTU252	Uncultured fungi	KU931455.1	100
OTU445	Tremellomycetes	HG935384.1	100
OTU765	<i>Alternaria</i> sp.	MK461092.1	100
OTU858	Solicoccozyma	KY105435.1	100
OTU891	Uncultured fungi	MF148734.1	100
OTU896	<i>Alternaria</i> sp.	MK461092.1	100
OTU1019	<i>Alternaria</i> sp.	MK461092.1	100
OTU1146	Phoma	KT150684.1	99.61
OTU1289	Ascochyta	KF293988.1	100
OTU1514	Thyrostroma sp	MG020338.1	95.31
OTU1601	Uncultured fungi	JX390488.1	100
OTU1683	<i>Alternaria</i> sp.	MK461092.1	100
OTU1730	<i>Fusarium</i> sp.	MF509747.1	100

OTU1732	Tremellomycetes	HG935384.1	100
OTU1736	<i>Mortierella</i> sp.	MK281958.1	98.38
OTU1737	<i>Chaetomium</i> sp.	KY132110.1	100
OTU1740	Uncultured fungi	KU931358.1	100
OTU1781	Uncultured fungi	KU931455.1	100
OTU1795	Uncultured fungi	JX333053.1	100
OTU1800	Uncultured fungi	JX359333.1	100
OTU1819	<i>Fusarium</i> sp.	KJ690090.1	100
OTU1859	<i>Alternaria</i> sp.	MK461092.1	100
OTU1941	<i>Alternaria</i> sp.	MK461092.1	100
OTU1975	Uncultured fungi	KU534664.1	100
OTU1999	Uncultured fungi	GQ225148.1	100
OTU2024	Uncultured fungi	JX984789.1	98
OTU2025	Chaetomium	KY132110.1	100
OTU2094	Neonectria	MF782762.1	100
OTU2104	Uncultured fungi	JX333053.1	100
OTU2180	Tremellomycetes	HG935384.1	100

OTU2249	Tremellomycetes	HG935384.1	100
OTU2346	Uncultured fungi	JX352646.1	100
OTU2352	Uncultured fungi	GQ225160.1	100
OTU2365	Acremonium	KM816680.1	100

Table S5. Analysis of soil physical and chemical indexes of the rhizosphere soils

Name	pH	Salty	conductivity ($\mu\text{m}^{-1}\text{cm}$)
Cab	7.58	70.97	400.0
Mer	7.38	92.71	566.0
Pin	7.78	90.71	285.0
Gem	7.64	47.81	287.0
Zin	7.78	47.96	398.0
Syr	7.70	47.18	210.0
Lon	8.37	48.34	131.8
Rie	8.20	47.26	135.9
Cha	7.78	71.48	220.0

Table S6. Physico-chemical characteristics of the soil samples.

Item	Content (%)	Detection method
Organic matter	67.6	NY/T 1121.6-2006
Total nitrogen	2.35	NY/T 53-1987
Available phosphorus	1.26	GB/T 17141-1997
Available potassium	1.40	NY/T 889-2004

Table S7. Air condition in the sampling site

Tem (°C)	AQI	PM _{2.5} (μg. m ⁻³)	PM ₁₀ (μg. m ⁻³)	SO ₂ (μg. m ⁻³)	CO (mg. m ⁻³)	NO ₂ (μg. m ⁻³)	O ₃ _8 h (μg. m ⁻³)
16-29	63	12	40	10	0.4	13	116

Table S8. KEGG orthologs (KOs) identified the key genotypic features. Relative abundance pathways in KEGG level 2 in the grapevine rhizosphere.

Metabolism	Zin	Gem	Rie	Syr	Mer	Cha	Cab	Pin
Membrane Transport	12.21%	12.07%	12.48%	11.96%	12.08%	12.34%	12.29%	12.37%
Amino Acid Metabolism	11.41%	11.37%	11.32%	11.38%	11.46%	11.41%	11.47%	11.28%
Carbohydrate Metabolism	10.83%	10.84%	10.85%	10.80%	10.91%	10.88%	10.94%	10.74%
Replication and Repair	6.79%	6.76%	6.79%	6.85%	6.79%	6.75%	6.76%	6.80%
Energy Metabolism	5.48%	5.52%	5.41%	5.51%	5.50%	5.48%	5.45%	5.44%
Poorly Characterized	4.87%	4.91%	4.91%	4.91%	4.87%	4.85%	4.85%	4.93%
Xenobiotics Biodegradation and Metabolism	4.56%	4.52%	4.49%	4.47%	4.59%	4.58%	4.60%	4.43%
Lipid Metabolism	4.18%	4.20%	4.11%	4.13%	4.21%	4.17%	4.19%	4.10%
Metabolism of Cofactors and Vitamins	4.14%	4.14%	4.08%	4.17%	4.14%	4.12%	4.12%	4.11%
Translation	3.97%	3.96%	3.92%	4.02%	3.96%	3.94%	3.94%	3.96%
Nucleotide Metabolism	3.14%	3.13%	3.14%	3.17%	3.15%	3.13%	3.14%	3.14%
Cellular Processes and Signaling	3.11%	3.11%	3.15%	3.17%	3.07%	3.07%	3.05%	3.19%
Cell Motility	2.55%	2.61%	2.60%	2.64%	2.54%	2.56%	2.51%	2.66%

Metabolism	2.47%	2.47%	2.49%	2.51%	2.47%	2.48%	2.47%	2.48%
Metabolism of Terpenoids and Polyketides	2.48%	2.49%	2.44%	2.45%	2.50%	2.48%	2.49%	2.44%
Transcription	2.37%	2.38%	2.38%	2.37%	2.37%	2.37%	2.37%	2.37%
Folding, Sorting and Degradation	2.14%	2.15%	2.13%	2.16%	2.14%	2.13%	2.13%	2.14%
Genetic Information Processing	2.07%	2.07%	2.12%	2.12%	2.06%	2.06%	2.04%	2.15%
Metabolism of Other Amino Acids	2.07%	2.06%	2.05%	2.05%	2.06%	2.07%	2.07%	2.05%
Signal Transduction	2.00%	2.03%	2.03%	1.98%	1.98%	2.00%	1.98%	2.04%
Enzyme Families	1.85%	1.86%	1.85%	1.86%	1.85%	1.84%	1.85%	1.84%
Glycan Biosynthesis and Metabolism	1.49%	1.53%	1.48%	1.51%	1.47%	1.46%	1.46%	1.52%
Biosynthesis of Other Secondary Metabolites	1.04%	1.04%	1.02%	1.03%	1.04%	1.04%	1.04%	1.01%
others	2.81%	2.79%	2.79%	2.80%	2.79%	2.80%	2.80%	2.81%

Table S9. KEGG orthologs (KOs) identified the key genotypic features. Relative abundance pathways in KEGG level 3 in the grapevine rhizosphere.

Metabolism	Zin	Gem	Rie	Syr	Mer	Cha	Cab	Pin
Transporters	6.26%	6.15%	6.38%	6.06%	6.19%	6.34%	6.32%	6.28%
ABC transporters	3.84%	3.80%	3.90%	3.72%	3.79%	3.90%	3.87%	3.86%
General function prediction only	3.42%	3.46%	3.43%	3.44%	3.43%	3.41%	3.41%	3.43%
DNA repair and recombination proteins	2.31%	2.30%	2.32%	2.33%	2.32%	2.30%	2.31%	2.31%
Two-component system	1.87%	1.91%	1.91%	1.86%	1.86%	1.88%	1.86%	1.92%
Purine metabolism	1.89%	1.88%	1.88%	1.89%	1.89%	1.88%	1.88%	1.89%
Ribosome	1.61%	1.61%	1.59%	1.63%	1.61%	1.60%	1.60%	1.60%
Function unknown	1.45%	1.45%	1.49%	1.47%	1.44%	1.44%	1.44%	1.50%
Peptidases	1.43%	1.43%	1.42%	1.45%	1.43%	1.42%	1.43%	1.42%
Transcription factors	1.40%	1.39%	1.44%	1.39%	1.39%	1.40%	1.40%	1.43%
Secretion system	1.38%	1.40%	1.42%	1.43%	1.38%	1.38%	1.37%	1.44%
Bacterial motility proteins	1.31%	1.35%	1.33%	1.36%	1.31%	1.31%	1.29%	1.36%
Butanoate metabolism	1.33%	1.34%	1.32%	1.31%	1.35%	1.34%	1.35%	1.30%

Oxidative phosphorylation	1.31%	1.32%	1.27%	1.32%	1.31%	1.30%	1.29%	1.29%
Arginine and proline metabolism	1.27%	1.27%	1.27%	1.27%	1.27%	1.28%	1.28%	1.27%
Pyrimidine metabolism	1.26%	1.26%	1.25%	1.27%	1.26%	1.25%	1.26%	1.26%
Valine, leucine and isoleucine degradation	1.21%	1.22%	1.20%	1.19%	1.23%	1.22%	1.23%	1.19%
Propanoate metabolism	1.19%	1.20%	1.18%	1.17%	1.21%	1.20%	1.21%	1.17%
Pyruvate metabolism	1.17%	1.18%	1.18%	1.18%	1.18%	1.18%	1.18%	1.17%
Amino acid related enzymes	1.16%	1.16%	1.15%	1.17%	1.16%	1.16%	1.15%	1.16%
Glycolysis / Gluconeogenesis	1.12%	1.12%	1.13%	1.12%	1.13%	1.13%	1.13%	1.11%
Carbon fixation pathways in prokaryotes	1.09%	1.10%	1.07%	1.10%	1.10%	1.09%	1.09%	1.08%
Methane metabolism	1.08%	1.09%	1.07%	1.08%	1.10%	1.09%	1.08%	1.06%
Chromosome	1.08%	1.08%	1.08%	1.10%	1.07%	1.07%	1.06%	1.09%
Fatty acid metabolism	1.03%	1.04%	1.02%	1.01%	1.05%	1.04%	1.05%	1.01%
Ribosome Biogenesis	0.99%	0.99%	0.99%	1.00%	0.99%	0.98%	0.98%	1.00%
Others	0.96%	0.96%	0.97%	1.01%	0.97%	0.97%	0.97%	0.98%
Glycine, serine and threonine metabolism	0.97%	0.96%	0.97%	0.97%	0.98%	0.97%	0.97%	0.97%
Amino sugar and nucleotide sugar metabolism	0.96%	0.96%	0.96%	0.96%	0.96%	0.96%	0.96%	0.95%
Other ion-coupled transporters	0.95%	0.93%	0.99%	0.97%	0.95%	0.94%	0.94%	0.98%

Alanine, aspartate and glutamate metabolism	0.94%	0.93%	0.93%	0.93%	0.94%	0.94%	0.94%	0.93%
Aminoacyl-tRNA biosynthesis	0.91%	0.90%	0.89%	0.91%	0.90%	0.90%	0.90%	0.89%
Citrate cycle (TCA cycle)	0.89%	0.90%	0.88%	0.89%	0.90%	0.89%	0.90%	0.88%
Lipid biosynthesis proteins	0.89%	0.89%	0.86%	0.88%	0.89%	0.88%	0.88%	0.87%
Porphyrin and chlorophyll metabolism	0.87%	0.88%	0.85%	0.87%	0.87%	0.88%	0.87%	0.87%
Tryptophan metabolism	0.85%	0.85%	0.84%	0.83%	0.86%	0.86%	0.86%	0.83%
Glyoxylate and dicarboxylate metabolism	0.84%	0.84%	0.84%	0.82%	0.84%	0.84%	0.84%	0.84%
Transcription machinery	0.84%	0.86%	0.81%	0.84%	0.85%	0.84%	0.84%	0.82%
Energy metabolism	0.81%	0.81%	0.81%	0.80%	0.80%	0.81%	0.80%	0.81%
Benzoate degradation	0.79%	0.79%	0.79%	0.77%	0.81%	0.80%	0.81%	0.77%
Chaperones and folding catalysts	0.77%	0.78%	0.77%	0.78%	0.76%	0.76%	0.76%	0.78%
Cysteine and methionine metabolism	0.77%	0.76%	0.76%	0.77%	0.76%	0.76%	0.76%	0.76%
Valine, leucine and isoleucine biosynthesis	0.75%	0.76%	0.74%	0.76%	0.76%	0.75%	0.76%	0.75%
DNA replication proteins	0.75%	0.75%	0.76%	0.76%	0.75%	0.75%	0.75%	0.76%
Nitrogen metabolism	0.75%	0.75%	0.75%	0.74%	0.75%	0.75%	0.74%	0.75%
Protein folding and associated processing	0.70%	0.70%	0.70%	0.70%	0.69%	0.70%	0.69%	0.70%
Lysine degradation	0.69%	0.69%	0.68%	0.67%	0.69%	0.69%	0.69%	0.67%

Pentose phosphate pathway	0.66%	0.66%	0.67%	0.66%	0.66%	0.66%	0.66%	0.67%
Phenylalanine, tyrosine and tryptophan biosynthesis	0.64%	0.64%	0.63%	0.65%	0.64%	0.64%	0.64%	0.64%
beta-Alanine metabolism	0.64%	0.64%	0.63%	0.62%	0.65%	0.64%	0.65%	0.63%
Homologous recombination	0.64%	0.63%	0.63%	0.65%	0.64%	0.63%	0.63%	0.64%
Aminobenzoate degradation	0.64%	0.64%	0.62%	0.62%	0.64%	0.64%	0.64%	0.61%
Bacterial secretion system	0.62%	0.62%	0.65%	0.64%	0.61%	0.62%	0.62%	0.66%
others	34.08%	34.08%	33.94%	34.19%	34.04%	33.98%	33.99%	34.04%

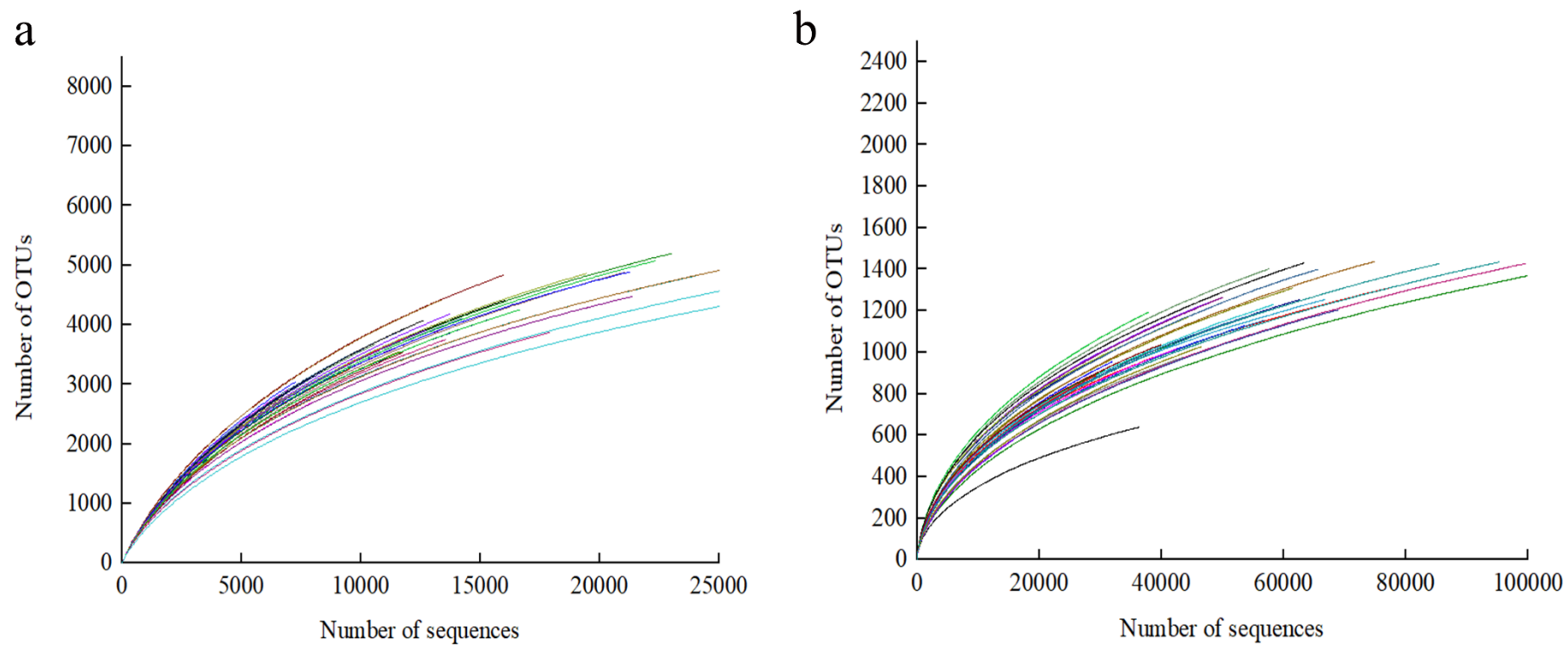


Figure S1. The rarefaction curves of bacteria (a) and fungi (b).

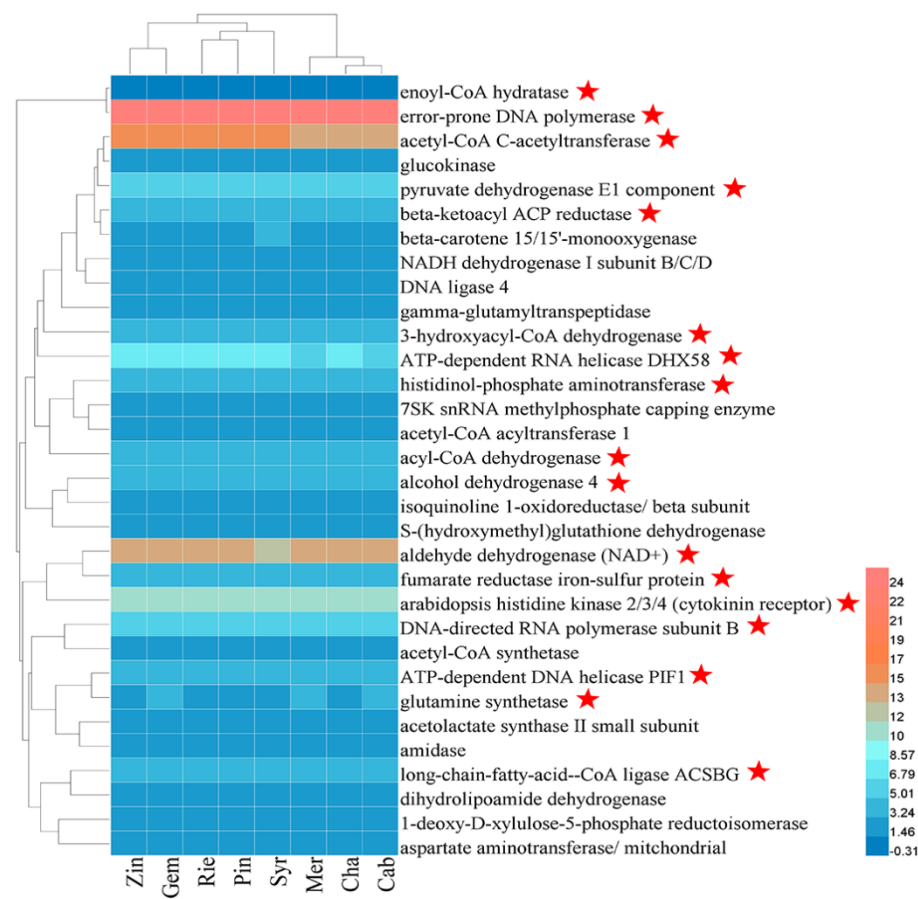


Figure S2. KEGG orthologs (KOs) identified the key genotypic features. The 32 most prevalent ECs, standardized by Z-score across all data sets, and the stars represents the relatives of enzyme larger than 3.0%.