Unique genes carried by abundant species enhance CH_4 emissions during the growing season at the Tibetan Plateau

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Table S1. The summary of unique genes carried by abundant species.

KO	KEGG Name	KO Description	Enzyme ID	Module ID
K10978	AksF	methanogen homoisocitrate dehydrogenase	1.1.1.87;1.1.1.	M00608
K00192	CdhA	anaerobic carbon-monoxide dehydrogenase, CODH/ACS complex subunit alpha	1.2.7.4	M00422
K00195	CdhB	anaerobic carbon-monoxide dehydrogenase, CODH/ACS complex subunit epsilon	-	M00422
K00193	CdhC	acetyl-CoA decarbonylase/synthase, CODH/ACS complex subunit beta	2.3.1.169	M00422; M00357
K11780	CofG	7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase	4.3.1.32	M00378
K11781	CofH	5-amino-6-(Dribitylamino) uracil---L-tyrosine 4-hydroxyphenyl transferase	2.5.1.147	M00378
K13812	fae-hps	bifunctional enzyme Fae/Hps	4.1.2.43;4.2.1.147	M00345; M00580
K00672	Ftr	formylmethanofuran--tetrahydromethanopterin N-formyltransferase	2.3.1.101	M00567
K00203	fwdD, fmdD	formylmethanofuran dehydrogenase subunit D	1.2.7.12	M00567
K11260	FwdG	4Fe-4S ferredoxin	-	M00567
K13831	hps-phi	3-hexulose-6-phosphate synthase / 6-phospho-3-hexuloisomerase	4.1.2.43;5.3.1.27	M00345; M00580
K18933	mfnA, adc	tyrosine decarboxylase / aspartate 1-decarboxylase	4.1.1.11;4.1.1.25	-
K09733	MfnB	(5-formylfuran-3-yl) methyl phosphate synthase	4.2.3.153	-
K06914	MfnD	tyramine---L-glutamate ligase	6.3.4.24	-
K07144	MfnE	5-(aminomethyl)3furanmethanol phosphate kinase	2.7.4.31	-
K07072	MfnF	(4-(4- [2-(gamma-L glutamylamino) ethyl] phenoxymethyl) furan-2-yl) methanamine synthase	2.5.1.131	-
K16158	MmoY	methane monooxygenase component A beta chain	1.14.13.25	M00174

K14081	MtaC	methanol corrinoid protein	-	M00356
K14082	MtbA	[methyl-Co (III) methylamine-specific corrinoid protein]: coenzyme M methyltransferase	2.1.1.247	M00563
K16178	MtbB	dimethylamine---corrinoid protein Co-methyltransferase	2.1.1.249	M00563
K16179	MtbC	dimethylamine corrinoid protein	-	M00563
K10944	pmoA-amoA	methane/ammonia monooxygenase subunit A	1.14.18.3;1.14.99.39	M00174; M00528; M00804

Table S2. The relationship between environment variables and CH_4 emission rates, abundant species, and unique genes during the growing season.

	CH_4 emission rates	Abundant species	Unique genes
MMT	**0.314***	-0.033	0.208
MMP	**0.321***	0.024	-0.023
pH	-0.020	**-0.400***	0.020
SWC	-0.085	-0.019	0.237
SOC	-0.175	0.291	0.158
SON	-0.315	0.028	**-0.478****
TP	0.690	0.197	0.178
TN	0.141	0.361	-0.189
NO_3^-	-0.242	0.278	-0.201
NH_4^+	0.132	0.122	-0.216
CH_4 emission rates	1.000***	-0.032	**0.423***
Abundant species	-0.032	1.000***	**0.543***
Unique genes	**0.423***	**0.543***	1.000***

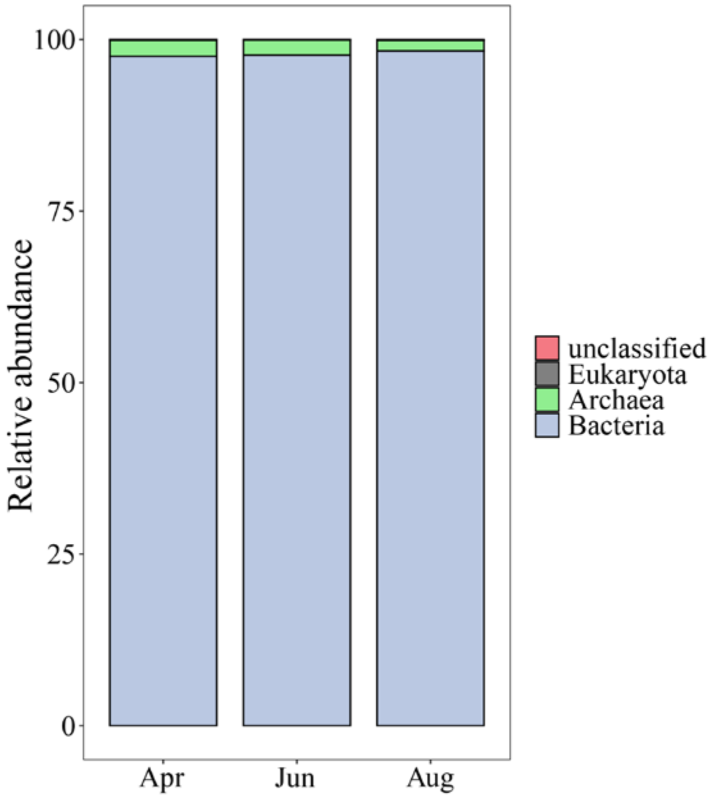

Figure S1. The classification of species related to methane metabolism at the domain level.

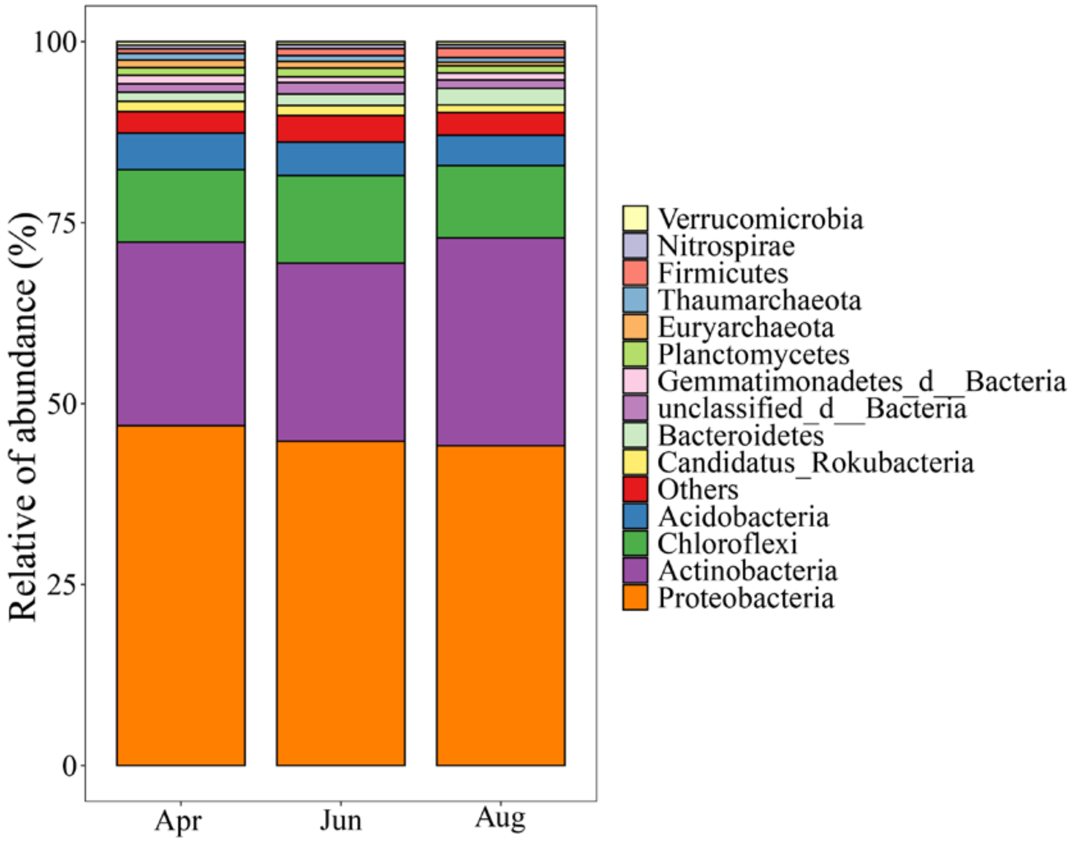

Figure S2. The composition of microbial community at phylum level during the growing season.

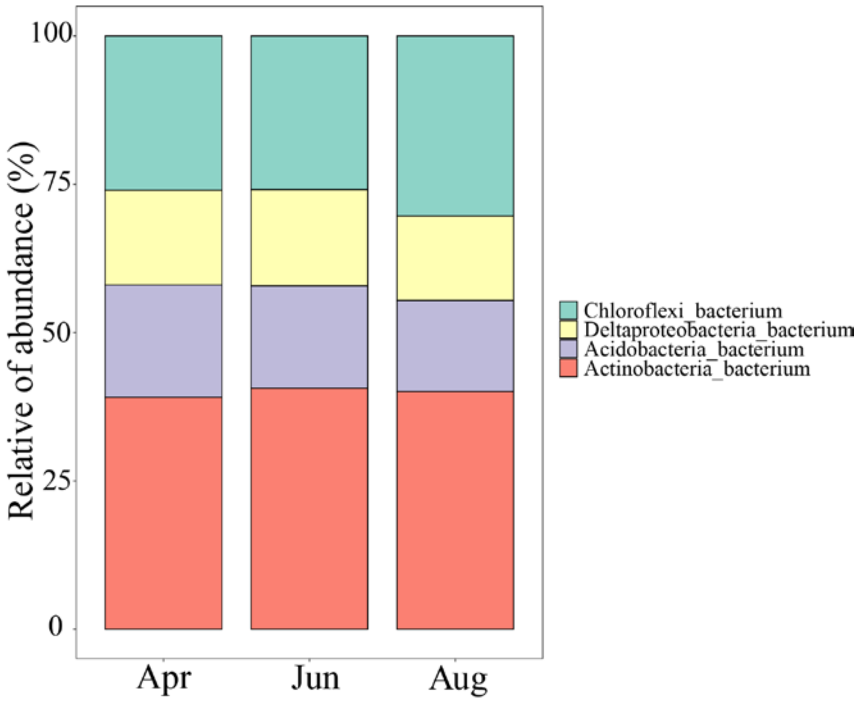

Figure S3. The relative abundance of abundant species at species level during the growing season.

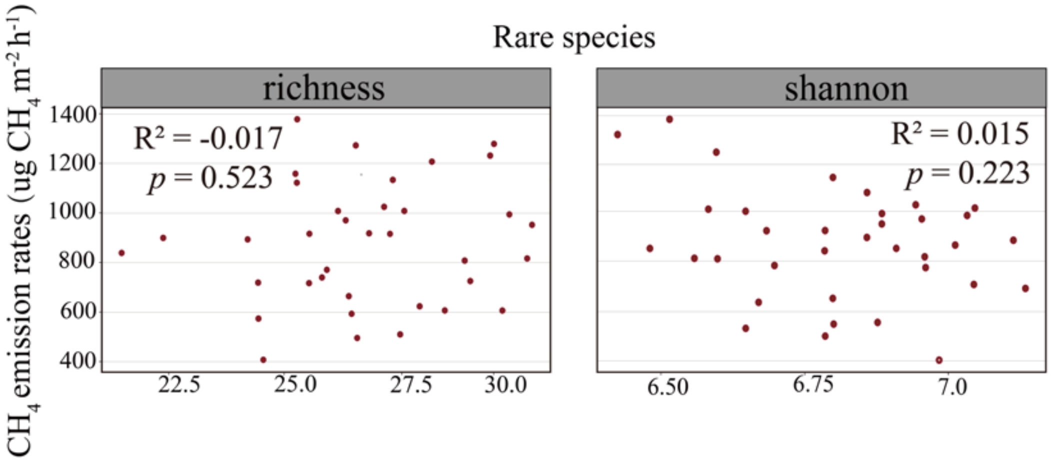

Figure S4. The relationship between the richness and shannon indexes of rare species and CH_4 emission rates.

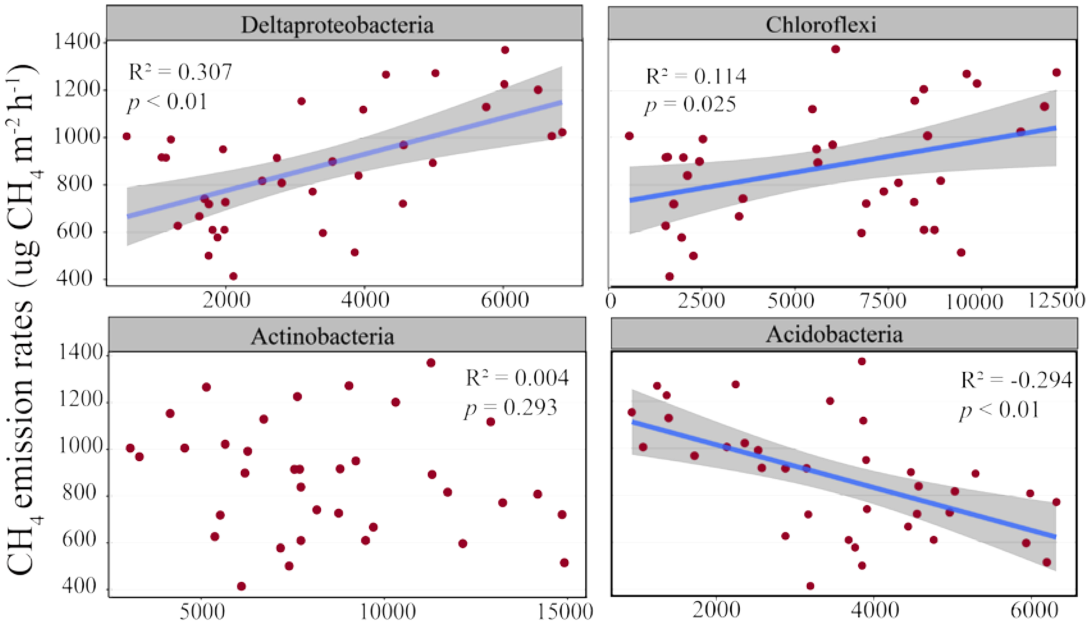

Figure S5. The relationship between the relative abundant of abundant species and CH$_4$ emission rates; a) *Deltaproteobacteria*; b) *Chloroflexi*; c) *Actinobacteria* and d) *Acidobacteria*.

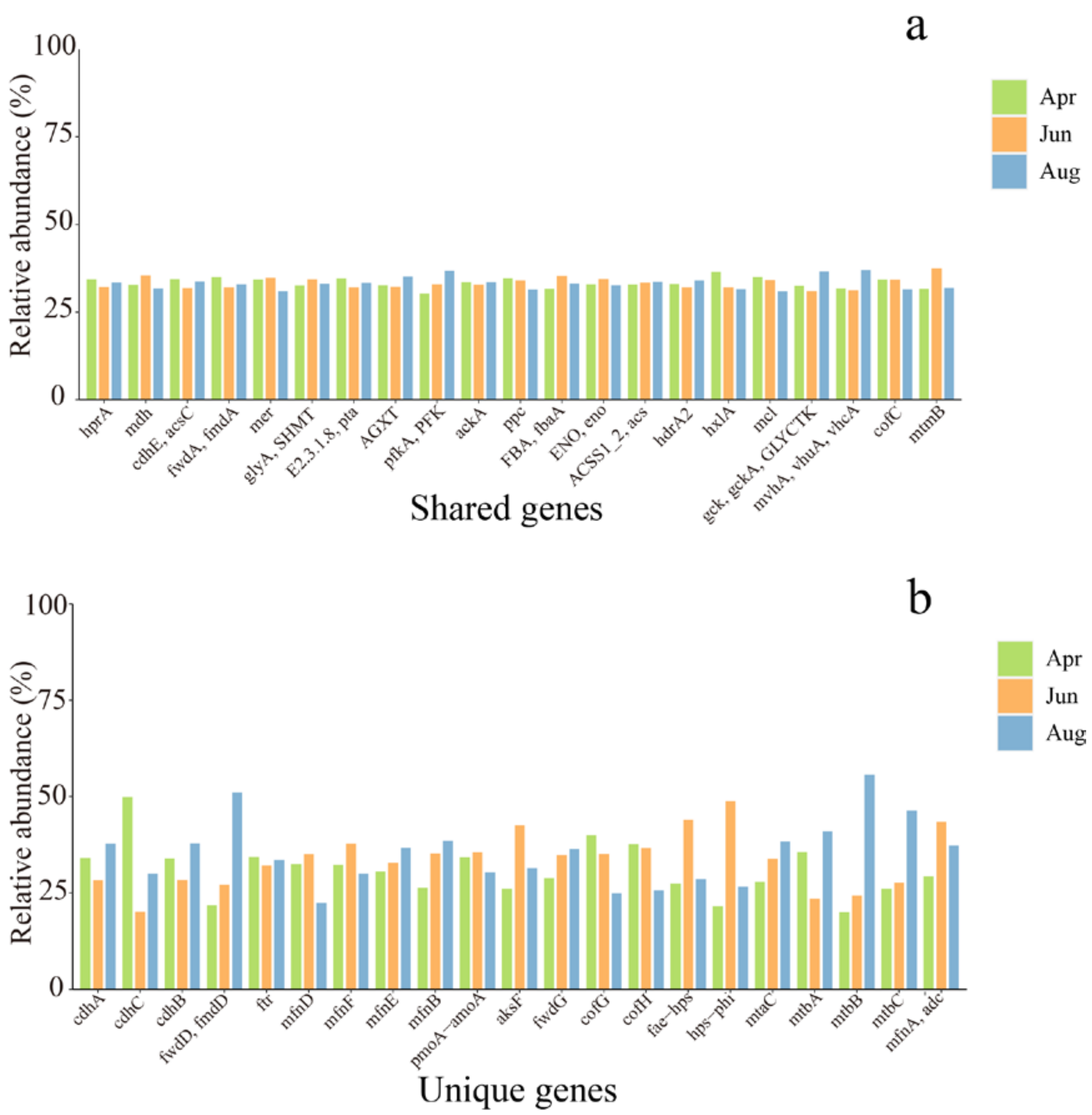

Figure S6. The relative abundance of shared and unique genes carried by species during the growing season. a) shared genes carried by species; b) unique genes carried by specie.

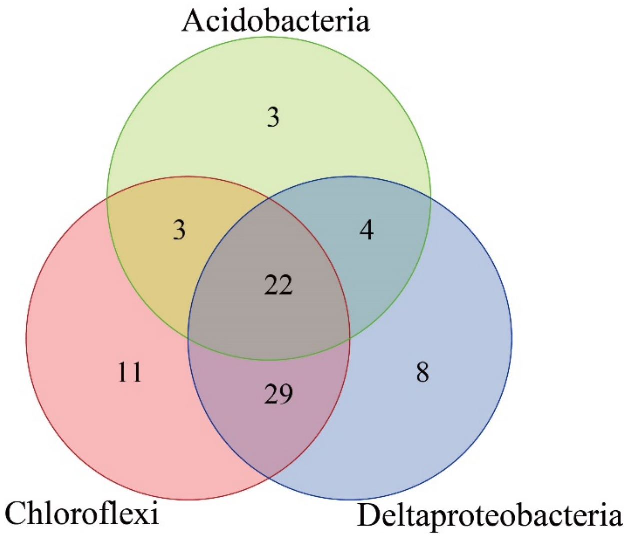

Figure S7. The proportion of unique genes carried by abundant species in abundant microorganisms.

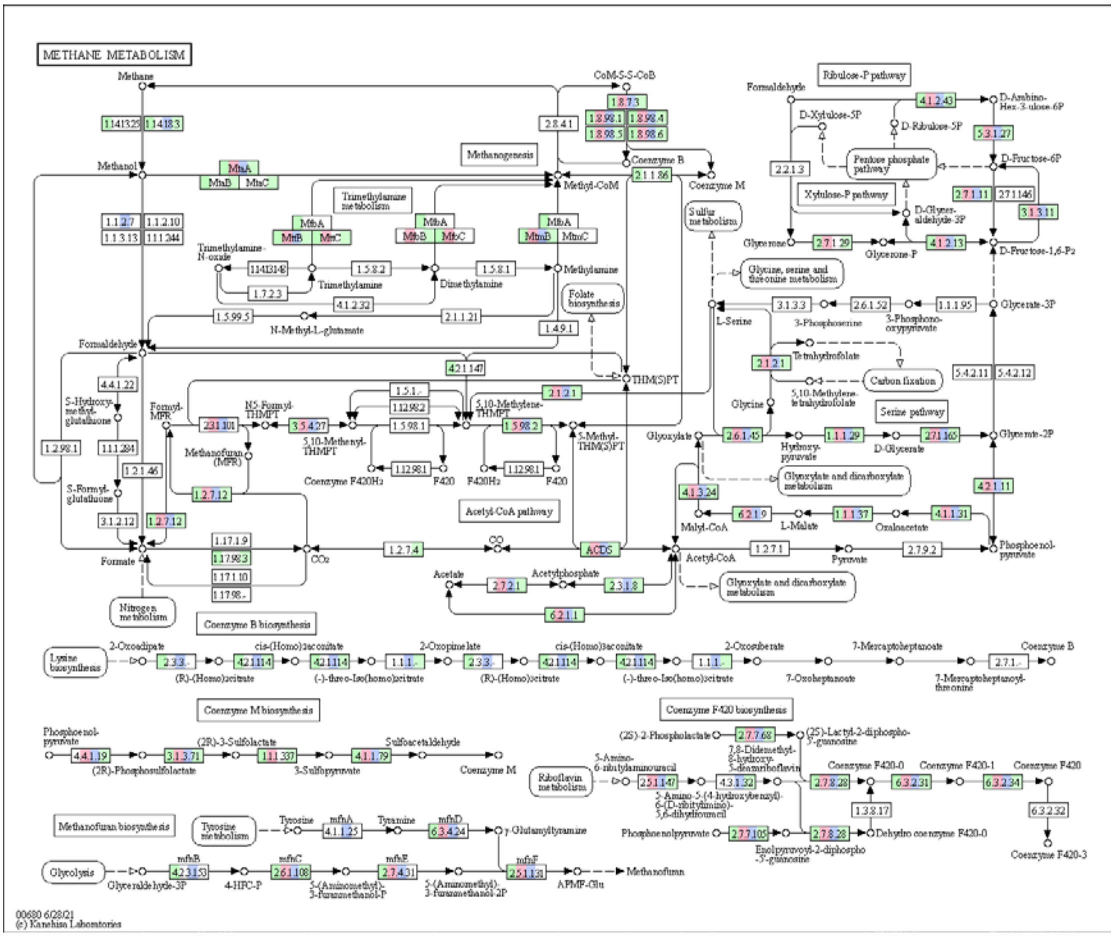

Figure S8. The unique genes carried by abundant species involved in methane metabolism. The different colors on each unique genes carried by abundant species indicated different microorganisms.