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Supplementary Material

Comparative genomic insights into habitat adaptation of coral-associated *Prosthecochloris*

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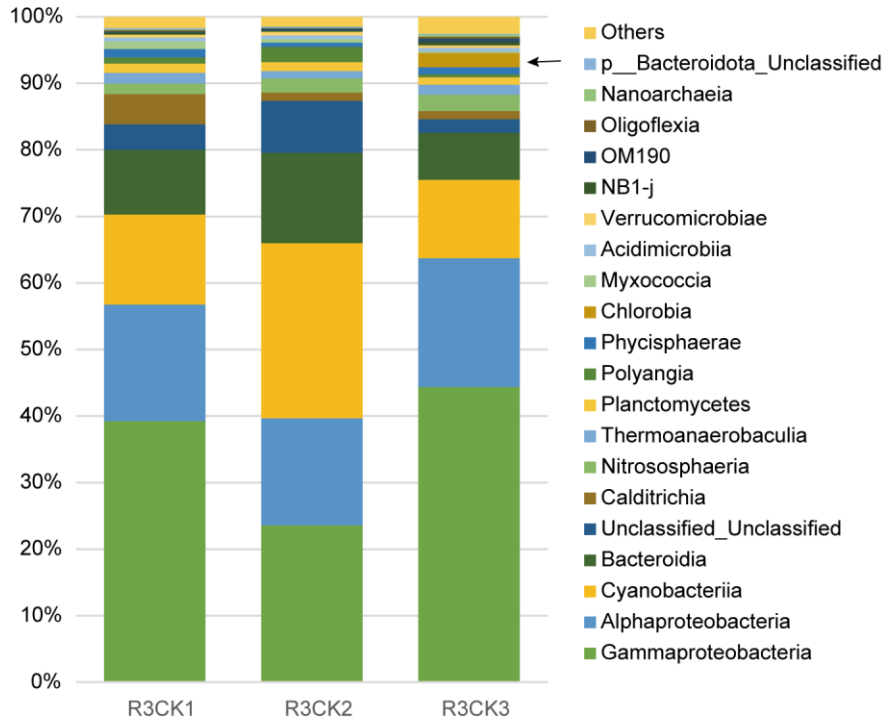

Figure S1. Green sulfur bacteria were detected in the stony coral *Galaxea fascicularis*. The amplicon sequencing data of 16S rRNA gene V4 region of three polype samples (R1CK1, R3CK2 and R3CK3) from our previous study (Wang et al., 2022) was reanalyzed. *Prosthecochloris* is the only genus in the phylum Chlorobi in these data.

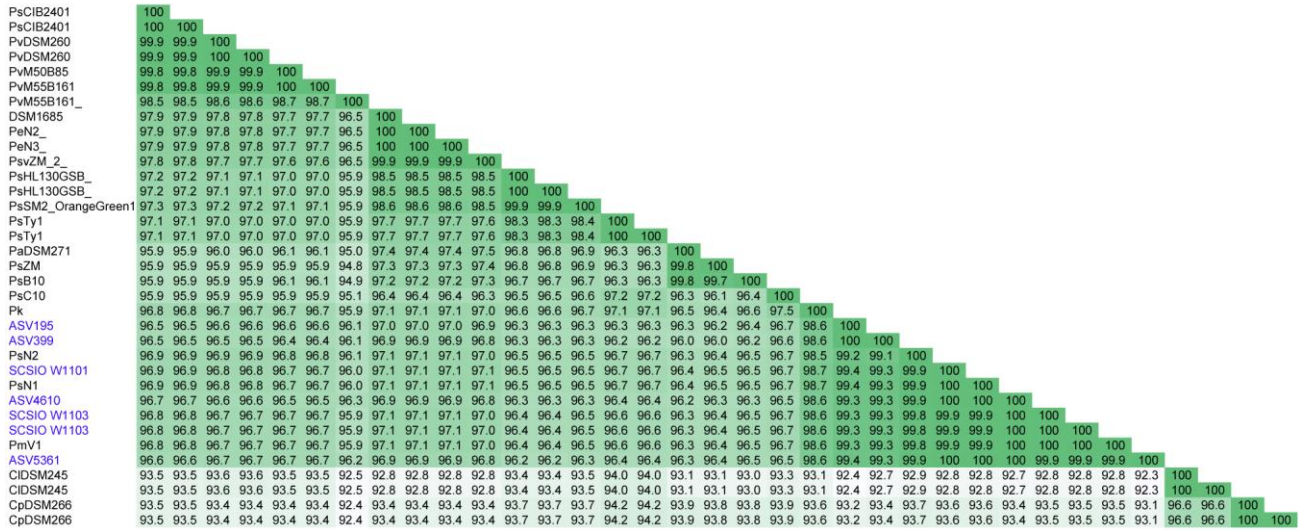

Figure S2. Matrix of 16S rRNA genes sequence identity. Sequence names in blue color are derived from this study.

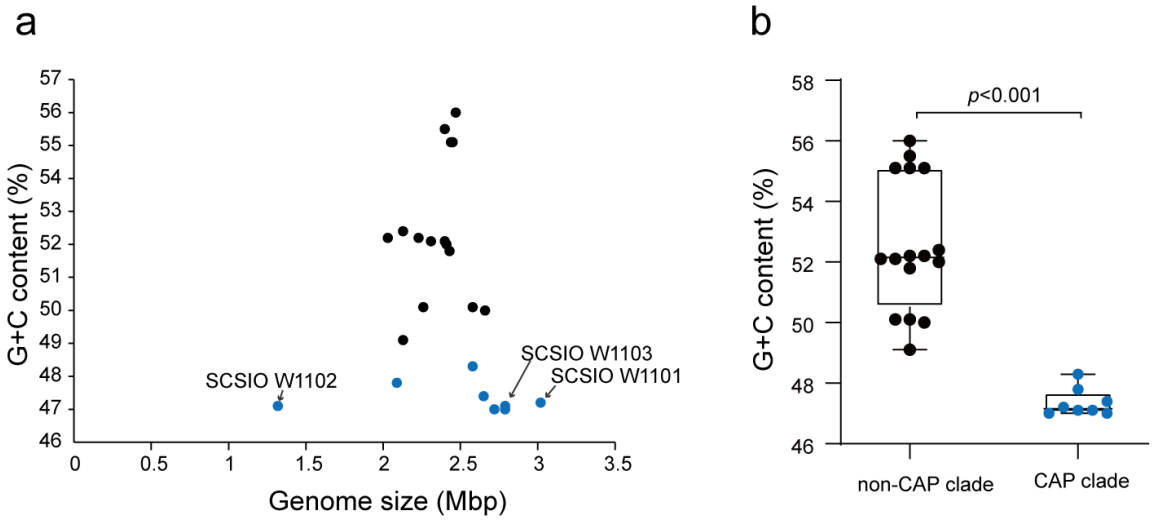

Figure S3. The CAP clade genomes have a significant lower G+C content. a, Scatter diagram of genome sizes and G+C contents of *Prosthecochloris* genomes. **b**, Comparison of G+C content between coral-associated *Prosthecochloris* (CAP) genomes and non-CAP genomes. Blue dots indicate the CAP genomes.

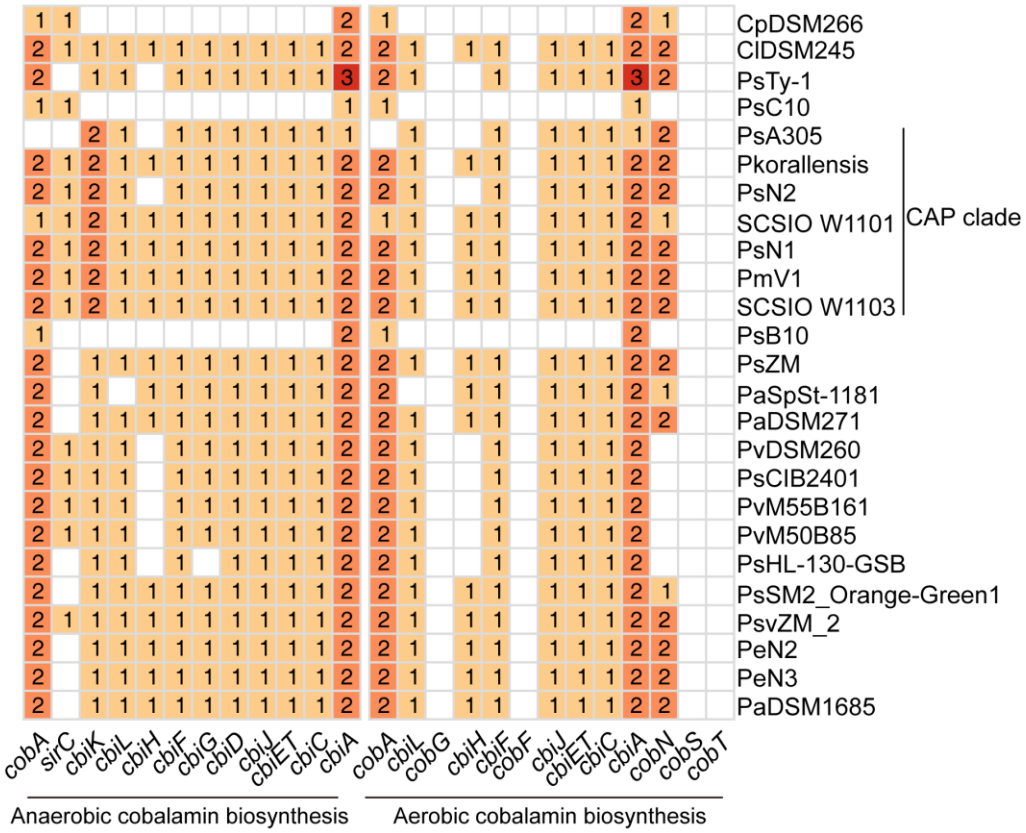

Figure S4. Presence and absence of genes involved in anaerobic and aerobic cobalamin biosynthesis pathways. Analysis was based on the KEGG orthology. Numbers in the cells indicate the numbers of genes predicted.

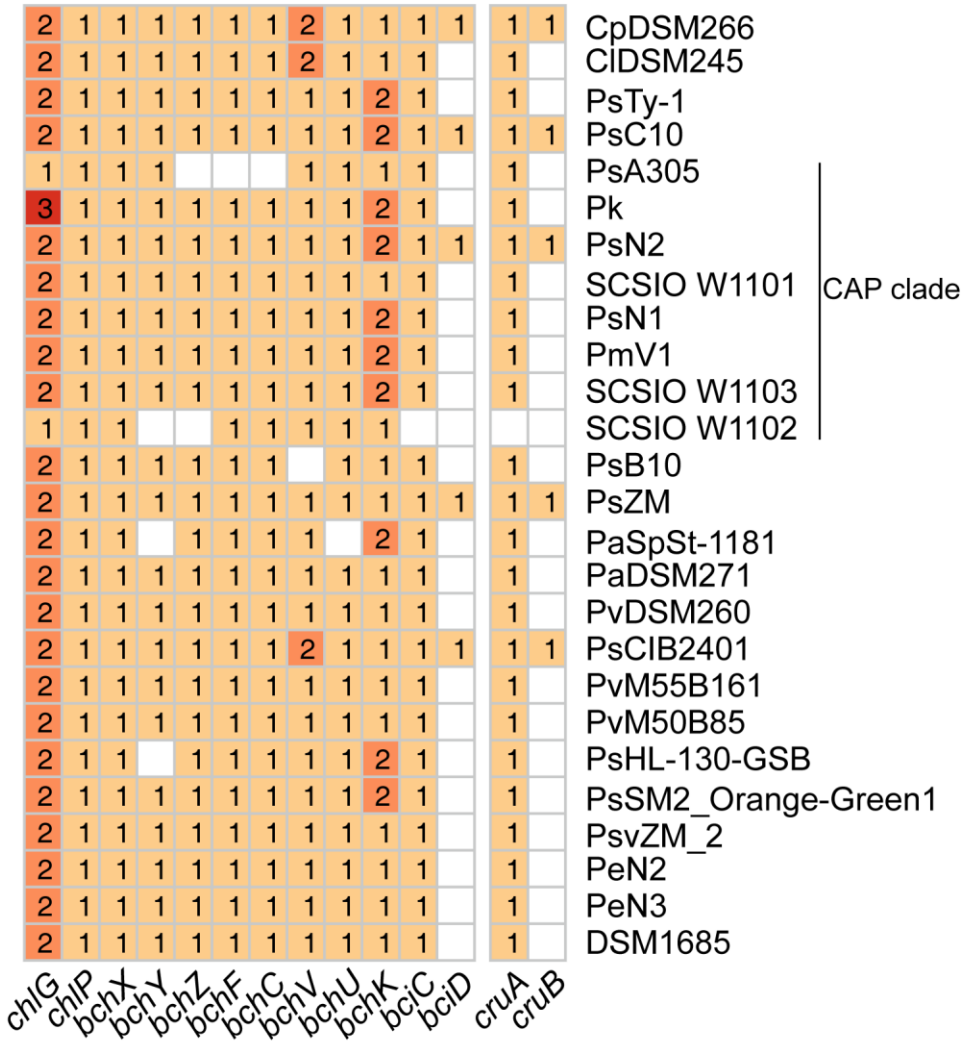

Figure S5. Presence and absence of genes involved in bacteriochlorophyll and carotenoid synthesis pathways. Analysis was based on the KEGG orthology. Numbers in the cells indicate the numbers of genes predicted.

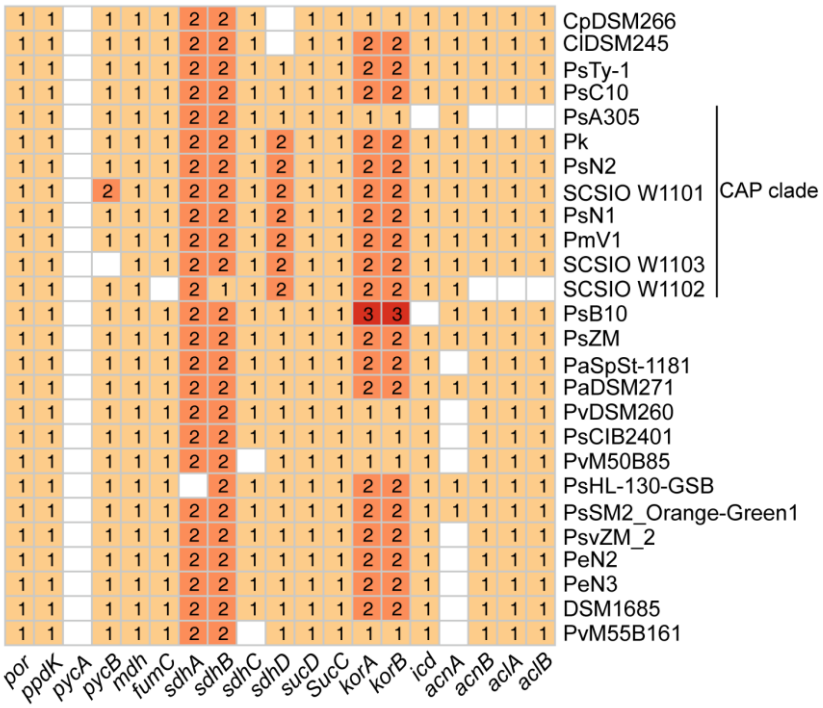

Figure S6. Presence and absence of genes involved in reductive citrate cycle. Analysis was based on the KEGG orthology. Numbers in the cells indicate the numbers of genes predicted.

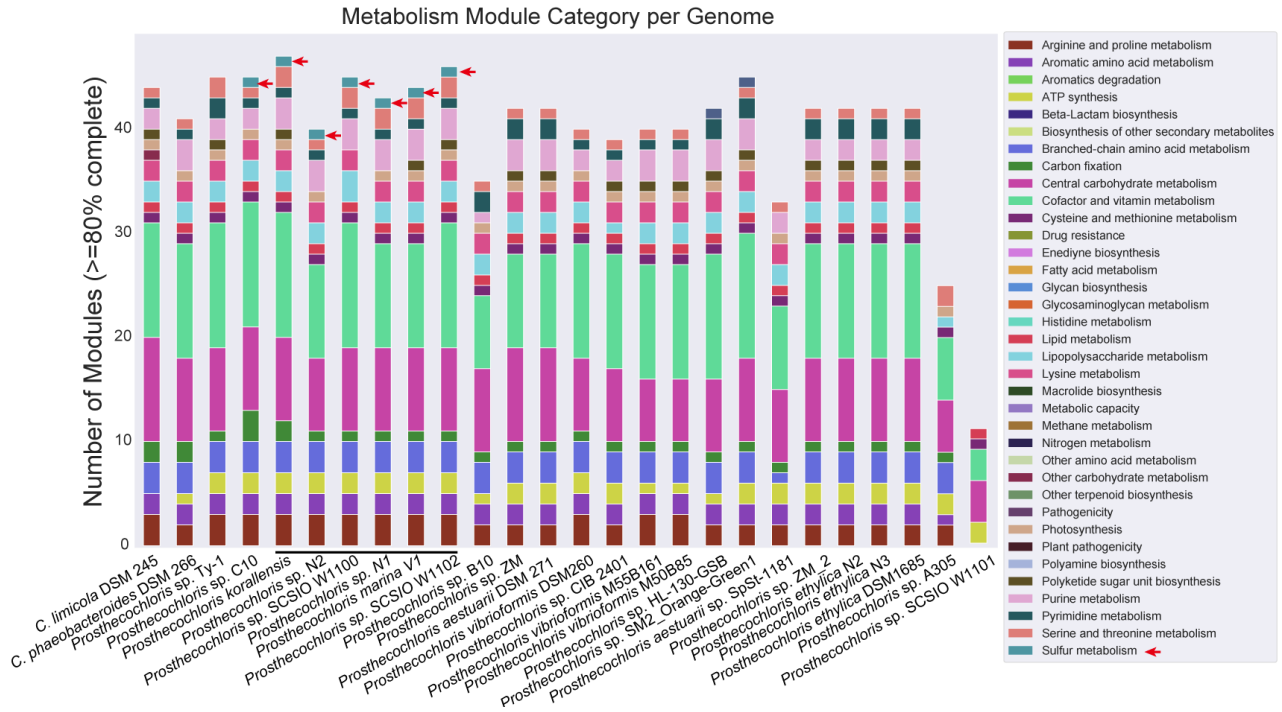

Fig S7. Metabolic summary based on KEGG pathways. Analysis was based on gene annotation by KofamKOALA using KEMET. The red arrow indicates the sulfur metabolism pathway.

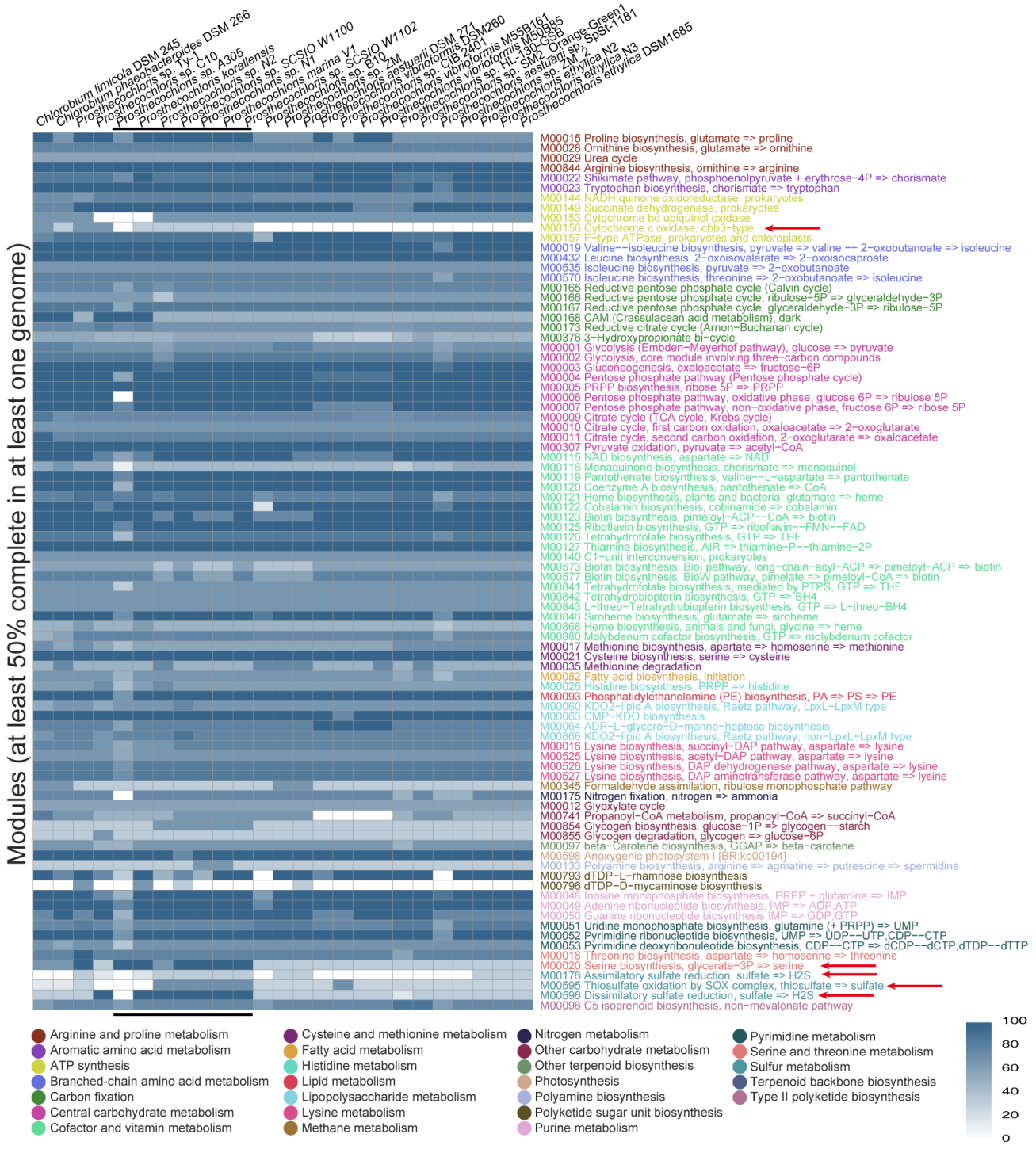

Figure S8. Comparison of metabolism modules of KEGG pathways. Analysis was based on gene annotation by KofamKOALA using KEMET. The red arrows indicate that completenesses of these modules are different between CAP and non-CAP genomes.

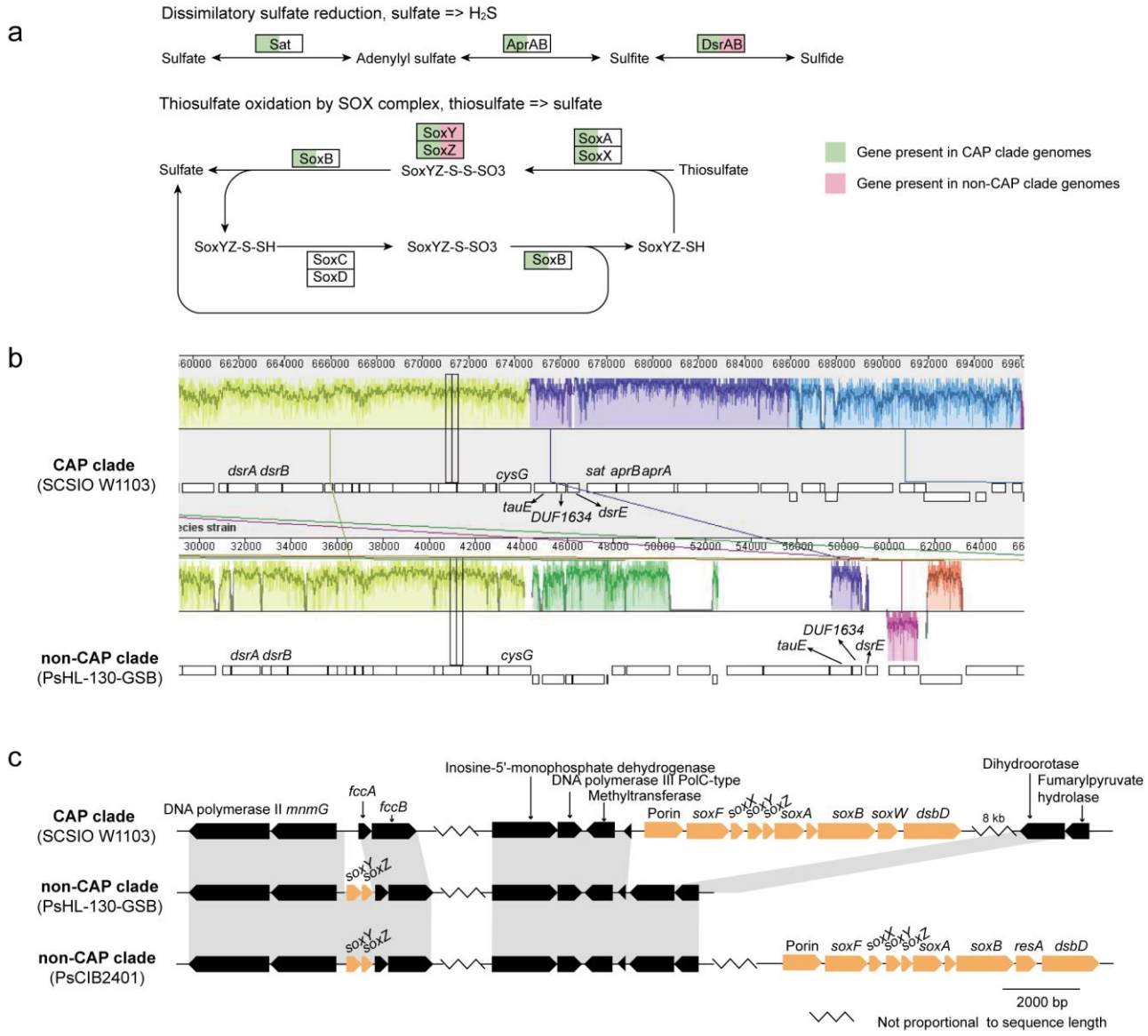

Figure S9. Presence and absence of genes involved in sulfur cycle. a, Presence and absence of genes involved in dissimilatory sulfate reduction and thiosulfate oxidation by SOX complex. **b,** Genetic maps of genes involved in dissimilatory sulfate reduction in coral-associated *Prosthecochloris* (CAP) genomes and non-CAP genomes. Genome sequences were aligned by Mauve. **c**, Location of two different SOX complex related gene cluster in CAP and non-CAP genomes. Gray shading indicates aligned genomic regions.

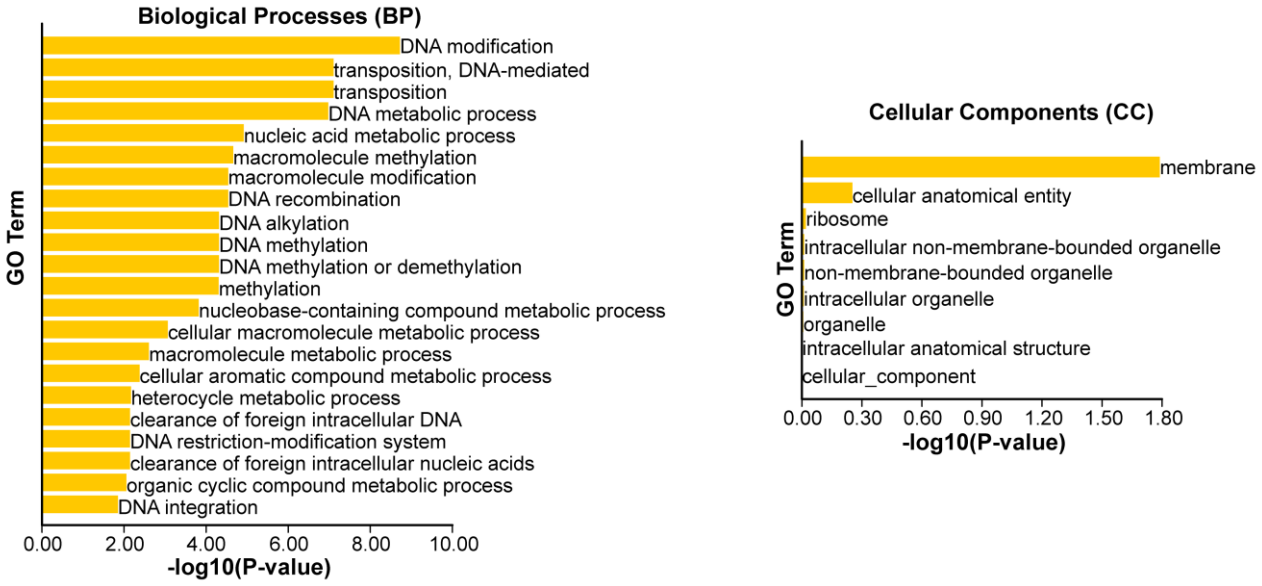

Figure S10. Enrichment of *Candidatus* Prosthecochloris sp. SCSIO W1101 specific genes based on GO annotation of biological processes (BP) and cellular components (CC).

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Table S1. Assessment and classification of bins in enrichment culture metagenomes.

Bin Id	Assessment of quality and profile of bins by CheckM							Classification by GTDB-tk		
	Bin size (Mbp)	mapped reads	% mapped reads	% binned populations	% community	Completeness	Contamination	Classification	fastani_reference	fastani_ani
E1-1	3.67	296419	6.49	5.25	4.98	97.36	0.61	*Marinobacter hydrocarbonoclasticus*	GCF_000284615.1	98.47
E1-2	3.73	252523	5.53	4.4	4.17	98.71	0.57	*Halomonas piezotolerans*	GCF_012427705.1	98.59
E1-3	4.13	164192	3.59	2.58	2.45	87.07	1.77	f__Geopsychrobacteraceae; g__BM522	NA	NA
E1-4	3.37	1916569	41.94	36.98	35.05	92.73	16.48	*Prosthecochloris marina*	GCF_003182595.1	97.54
E1-5	2.16	1622896	35.51	48.87	46.32	81.19	4.95	*Prosthecochloris marina*	GCF_003182595.1	98.66
E1-6	2.69	79223	1.73	1.92	1.82	84.21	4.15	*Halodesulfovibrio* sp015482765	GCA_015482765.1	98.63
unbinned	2.28	238154	5.21	NA	5.21	NA	NA	NA	NA	NA
E2-1	5.26	1178217	15.03	9.77	8.94	99.86	0.11	*Vibrio alginolyticus*	GCF_000354175.2	98.41
E2-2	2.75	4011173	51.16	63.65	58.24	93.74	1.39	*Prosthecochloris marina*	GCF_003182595.1	98.96
E2-3	3.24	1487806	18.98	20.02	18.32	89.86	4.46	*Marinobacter hydrocarbonoclasticus*	GCF_000284615.1	98.33
E2-4	4.32	142665	1.82	1.44	1.32	99.43	1.37	*Halodesulfovibrio* sp.	NA	NA
E2-5	3.19	261218	3.33	3.58	3.27	89.86	4.46	*Halomonas piezotolerans*	GCF_012427705.1	99.15
E2-6	2.65	93633	1.19	1.54	1.41	32.56	5.77	*Halodesulfovibrio* sp.	NA	NA
unbinned	6.74	665876	8.49	NA	8.49	NA	NA	NA	NA	NA

NA: not available

Reference

Wang, W., Tang, K., Wang, P., Zeng, Z., Xu, T., Zhan, W., Liu, T., Wang, Y., and Wang, X. (2022). The coral pathogen *Vibrio coralliilyticus* kills non-pathogenic holobiont competitors by triggering prophage induction. *Nat Ecol Evol* 6, 1132-1144.