Electronic Supplementary Material

Interfacing biosynthetic CdS with engineered *Rhodopseudomonas palustris* for efficient visible light-driven CO_2–CH_4 conversion

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SI brief description

Number of Tables: 4, Number of Figures: 4

Table S1. Catalysis performance of various biohybrid

Organism	Photocatalytic material	Synthesis method	CH_4 production rate	Quantum Efficiency (QE)	Reference
M.barkeri	CdS	biosynthesize	0.19 μmol/h	0.34%	[1]
M.barkeri	NCS	chemical synthesis	1.42 nmol/h	0.08%	[2]
R. palustris	CdS	biosynthesize	--	--	[3]
R.palustris (N₂ase)*	CdS	chemical synthesis	3.56 nmol/h/mg total protein	--	[4]
R.palustris (N₂ase)*	CdS	biosynthesize	19.05 nmol/h	0.12%	This paper

Table S2. Expressions of gene-encoded PioABC

Gene ID	Gene Name	Gene Description	RP (TPM)	RP-CdS(TPM)
HZF03_RS03780	-	MtrB/PioB family decaheme-associated outer membrane protein	1.94	1.85
HZF03_RS03785	-	DmsE family decaheme c-Type cytochrome PioA	7.44	5.16
HZF03_RS03775	-	hypothetical protein PioC	7.11	4.99

Table S3. Expressions of gene-encoded the Calvin cycle

Gene ID	Gene Name	Gene Descripition	RP (TPM)	RP-CdS (TPM)
HZF03_RS01340	-	ribulose 1%2C5-bisphosphate carboxylase	9.54	9.19
HZF03_RS07640	-	form I ribulose bisphosphate carboxylase large subunit	8.36	10.72
HZF03_RS07645	-	ribulose bisphosphate carboxylase small subunit	9.98	17.04
HZF03_RS10835	-	ribulose 1%2C5-bisphosphate carboxylase	12.38	10.75
HZF03_RS19300	-	ribulose-phosphate 3-epimerase	41.78	49.77
HZF03_RS23335	-	ribulose-bisphosphate carboxylase	140.22	209.47
HZF03_RS04750	-	fructose-bisphosphate aldolase class I	103.32	139.56
HZF03_RS12205	glpX	class II fructose-bisphosphatase	34.5	34.91
HZF03_RS23340	fba	fructose-bisphosphate aldolase class II	96.87	118.43
HZF03_RS23355	-	class 1 fructose-bisphosphatase	98.57	73.5

Table S4. Expressions of gene-related to chemotaxis

Gene ID	Gene Name	Gene Description	RP (TPM)	RP-CdS (TPM)
HZF03_RS07975	-	chemotaxis protein CheW	36.68	142.44
HZF03_RS08250	-	chemotaxis protein CheW	11.27	64.1
HZF03_RS07990	-	chemotaxis response regulator protein-glutamate methylesterase	12.99	40.38
HZF03_RS07995	-	protein-glutamate O-methyltransferase CheR	14.95	40.06
HZF03_RS09970	-	MotA/TolQ/ExbB proton channel family protein	21.26	48.69
HZF03_RS02190	-	PAS domain-containing methyl-accepting chemotaxis protein	21.49	68.73
HZF03_RS21520	-	methyl-accepting chemotaxis protein	9.21	19.39
HZF03_RS21540	-	cache domain-containing protein	5.86	23.99
HZF03_RS07980	-	chemotaxis protein CheW	20.29	91.8
HZF03_RS07985	-	response regulator	18.76	84.84
HZF03_RS08245	-	chemotaxis protein CheW	13.74	34.73
HZF03_RS23320	-	MCP four helix bundle domain-containing protein	22.21	52.63

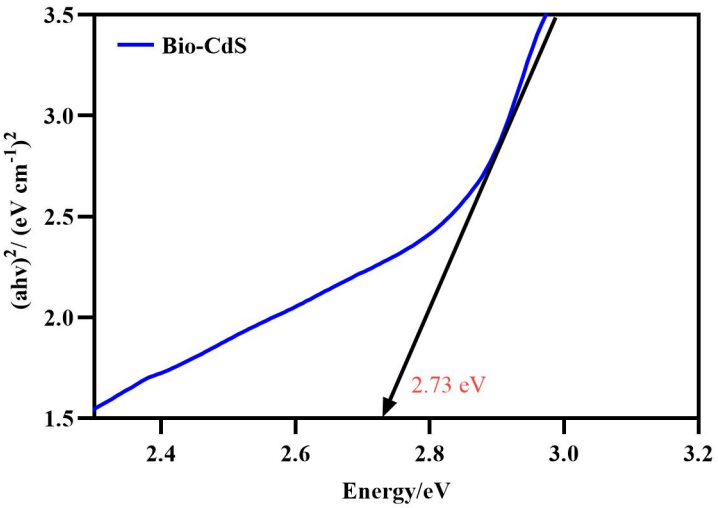

Fig. S1. The band gap of CdS NPs.

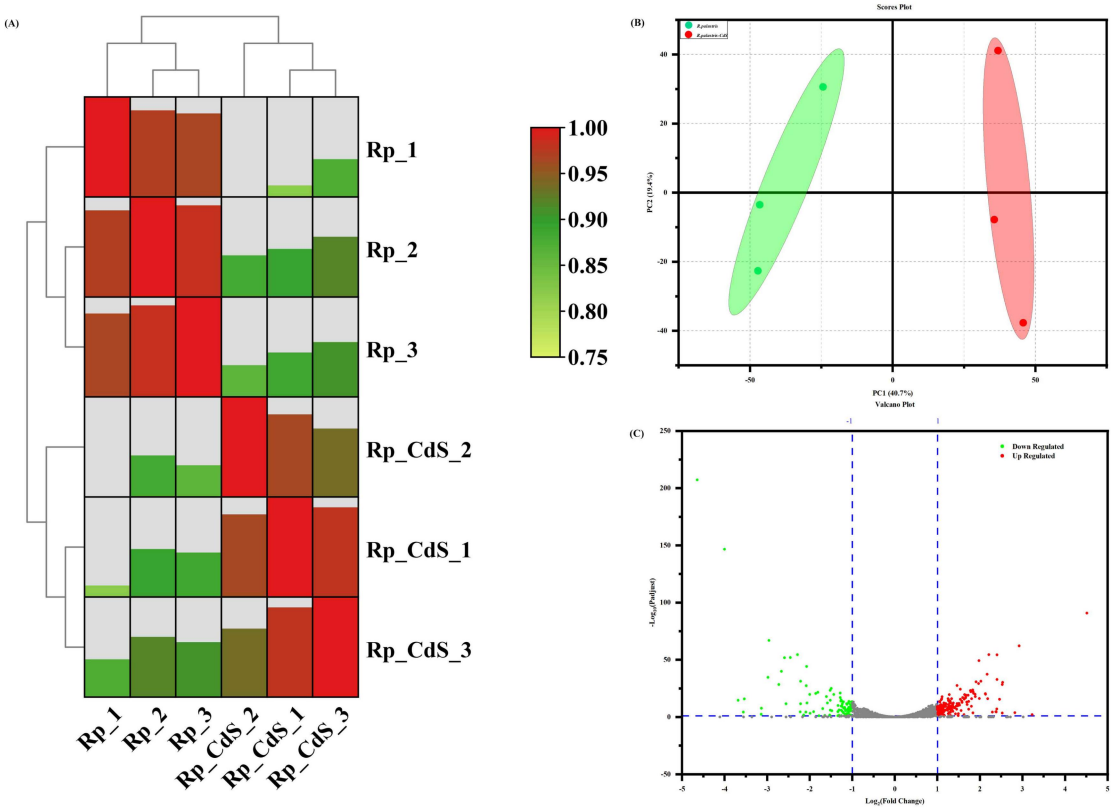

Fig. S2. Assessment of physiological perturbation of *R. palustris* based on various samples' transcriptome data. (A) Hierarchical clustering analysis for calculating the distance between the *R. palustris* (N_2ase*) and *R. palustris* (N_2ase*)-CdS biohybrid; (B) Principal component analysis (PCA) of transcriptome data; (C) Volcano plots of the

transcriptome of *R. palustris* (N_2ase*)-CdS compared to *R. palustris* (N_2ase*) only.

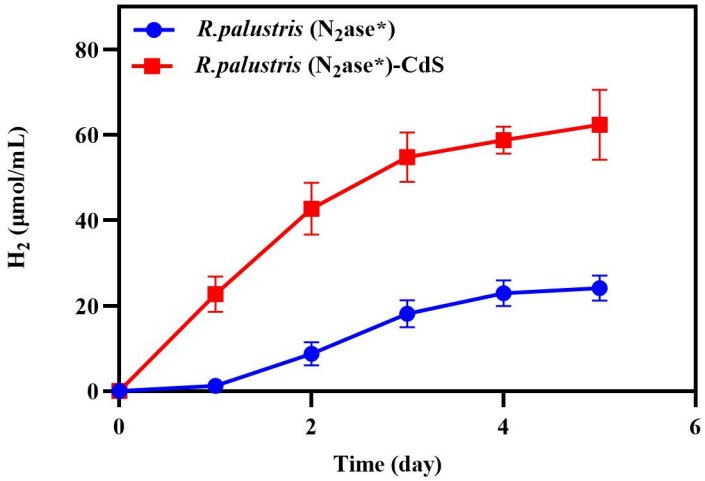

Fig. S3. H_2 production in *R. palustris* (N_2ase*)-CdS biohybrid.

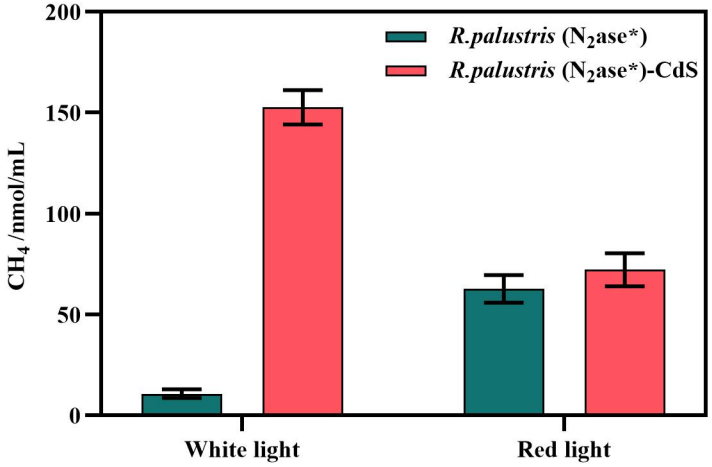

Fig. S4. CO_2-CH_4 photosynthesis of *R. palustris* (N_2ase*)-CdS biohybrid under varied light sources.

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