Supplementary Figures for

Substrate-dependent competition and cooperation relationships between *Geobacter* and *Dehalococcoides* for their organohalide respiration

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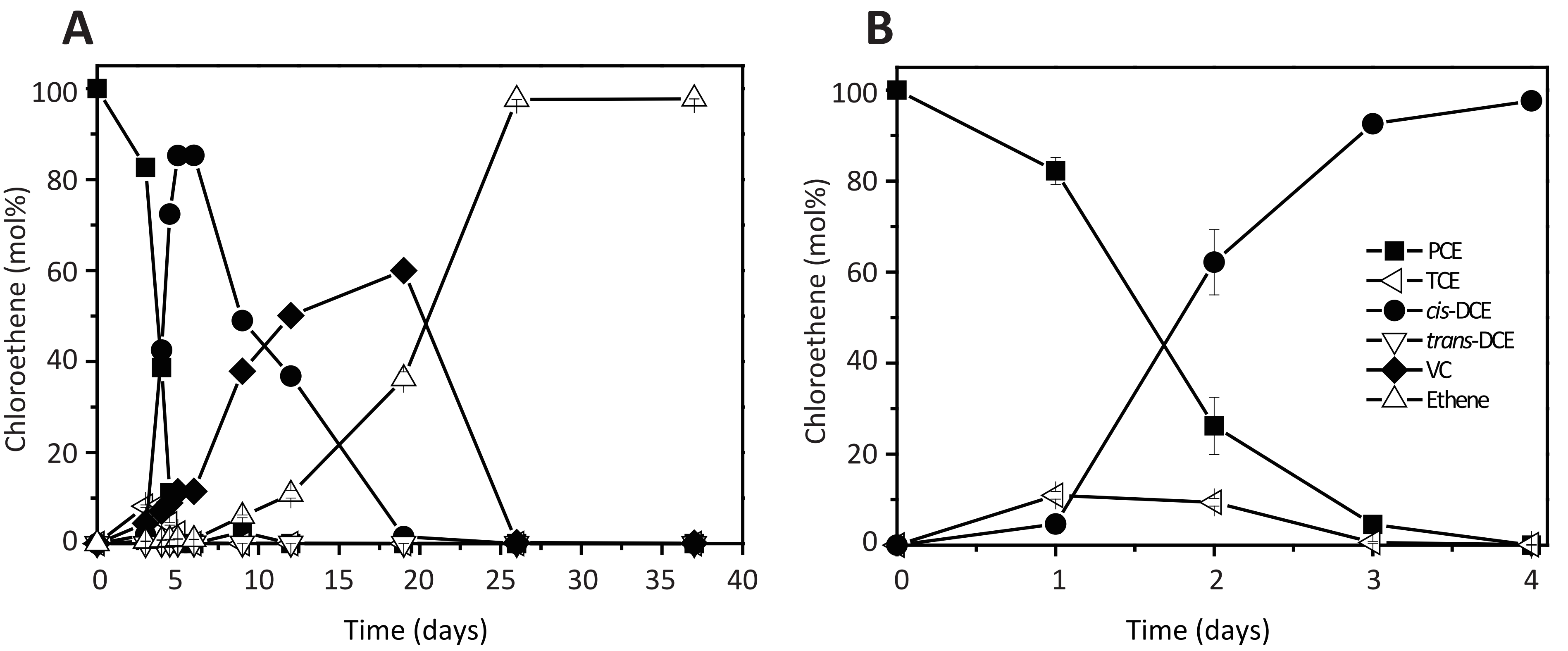
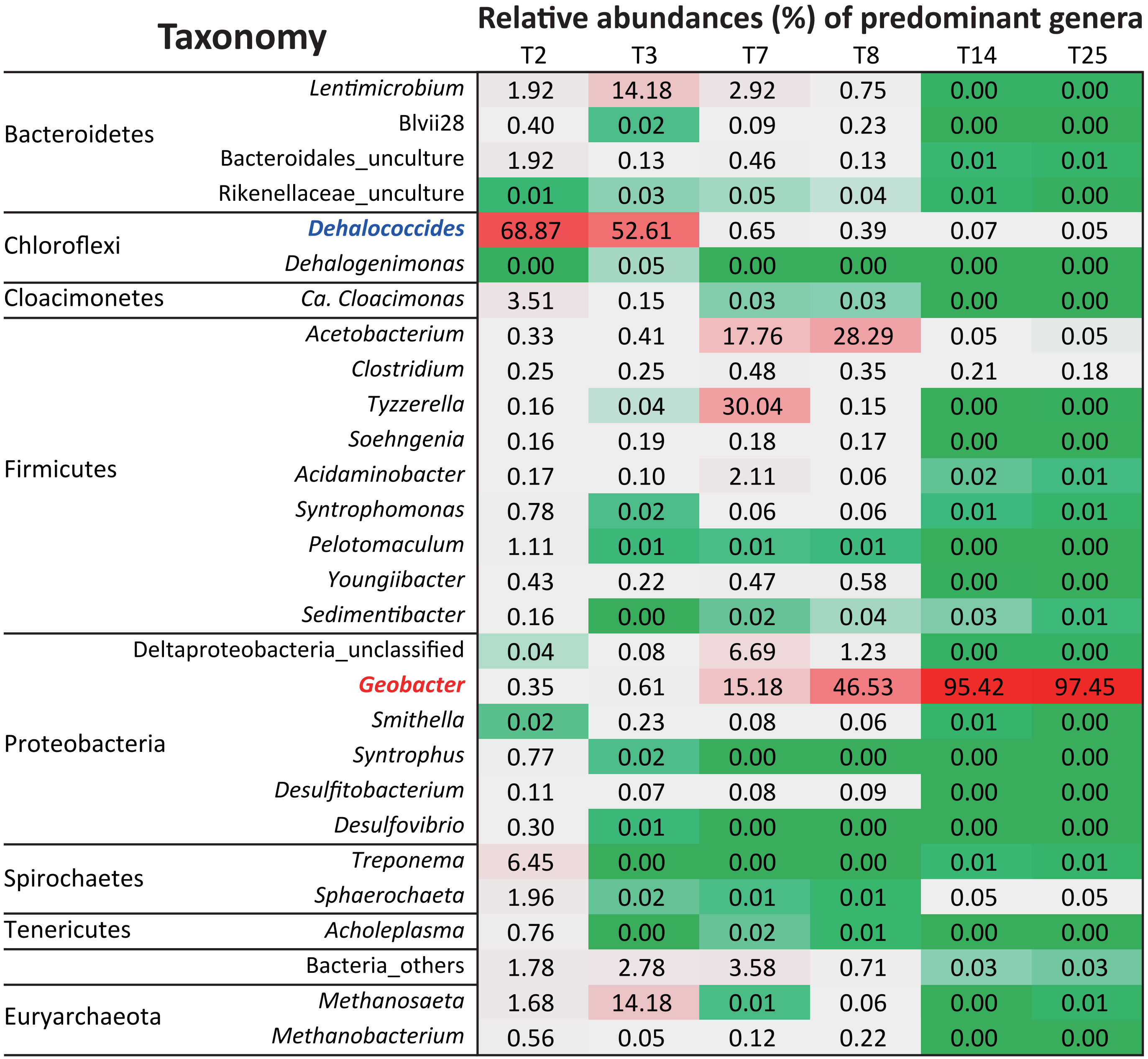


Fig. S1. Reductive dechlorination of PCE. (A) PCE dechlorination in microcosm LY (T1). **(B)** PCE dechlorination in *Geobacter lovleyi* LYY pure culture. Error bars represent SDs of triplicate cultures.



Taxonomy		Relative abundances (%) of predominant genera					
		T2	T3	T7	T8	T14	T25
Bacteroidetes	*Lentimicrobium*	1.92	14.18	2.92	0.75	0.00	0.00
	Blvii28	0.40	0.02	0.09	0.23	0.00	0.00
	Bacteroidales_unculture	1.92	0.13	0.46	0.13	0.01	0.01
	Rikenellaceae_unculture	0.01	0.03	0.05	0.04	0.01	0.00
Chloroflexi	***Dehalococcides***	68.87	52.61	0.65	0.39	0.07	0.05
	Dehalogenimonas	0.00	0.05	0.00	0.00	0.00	0.00
Cloacimonetes	*Ca. Cloacimonas*	3.51	0.15	0.03	0.03	0.00	0.00
Firmicutes	*Acetobacterium*	0.33	0.41	17.76	28.29	0.05	0.05
	Clostridium	0.25	0.25	0.48	0.35	0.21	0.18
	Tyzzerella	0.16	0.04	30.04	0.15	0.00	0.00
	Soehngenia	0.16	0.19	0.18	0.17	0.00	0.00
	Acidaminobacter	0.17	0.10	2.11	0.06	0.02	0.01
	Syntrophomonas	0.78	0.02	0.06	0.06	0.01	0.01
	Pelotomaculum	1.11	0.01	0.01	0.01	0.00	0.00
	Youngiibacter	0.43	0.22	0.47	0.58	0.00	0.00
	Sedimentibacter	0.16	0.00	0.02	0.04	0.03	0.01
Proteobacteria	Deltaproteobacteria_unclassified	0.04	0.08	6.69	1.23	0.00	0.00
	Geobacter	0.35	0.61	15.18	46.53	95.42	97.45
	Smithella	0.02	0.23	0.08	0.06	0.01	0.00
	Syntrophus	0.77	0.02	0.00	0.00	0.00	0.00
	Desulfitobacterium	0.11	0.07	0.08	0.09	0.00	0.00
	Desulfovibrio	0.30	0.01	0.00	0.00	0.00	0.00
Spirochaetes	*Treponema*	6.45	0.00	0.00	0.00	0.01	0.01
	Sphaerochaeta	1.96	0.02	0.01	0.01	0.05	0.05
Tenericutes	*Acholeplasma*	0.76	0.00	0.02	0.01	0.00	0.00
	Bacteria_others	1.78	2.78	3.58	0.71	0.03	0.03
Euryarchaeota	*Methanosaeta*	1.68	14.18	0.01	0.06	0.00	0.01
	Methanobacterium	0.56	0.05	0.12	0.22	0.00	0.00

Fig. S2. The microbial community composition of PCE-dechlorinating microcosms in different transfers. Only genera with relative abundances higher than 0.05% in one or more of the microcosms are shown.

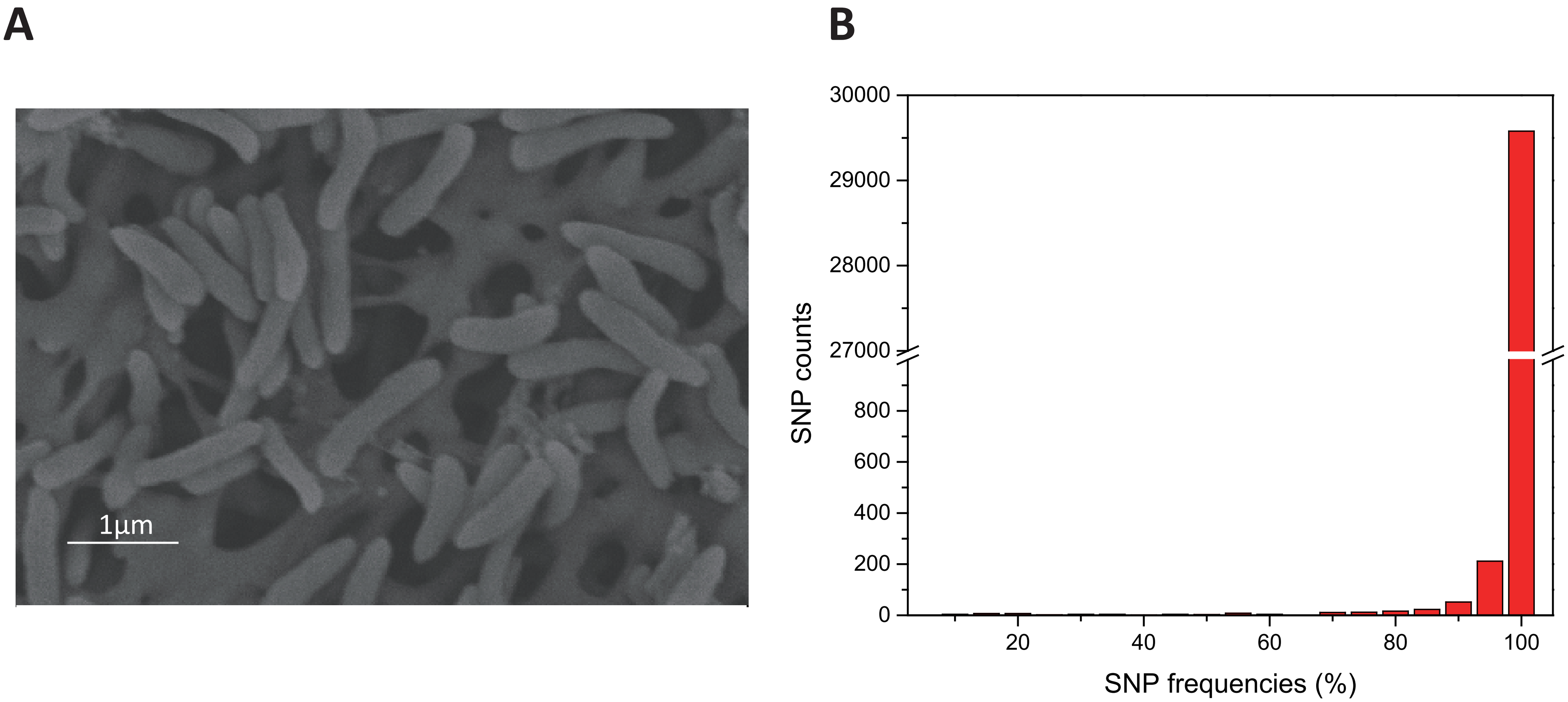


Fig. S3. Conformation of culture purity with SEM and SNP profiling analyses. (A) SEM image of pure culture LYY; **(B)** SNP profile of strain LYY. SNPs were called against the reference strain SZ. The sole peaks at 100% frequency of culture LYY suggest a single *Geobacter* strain.

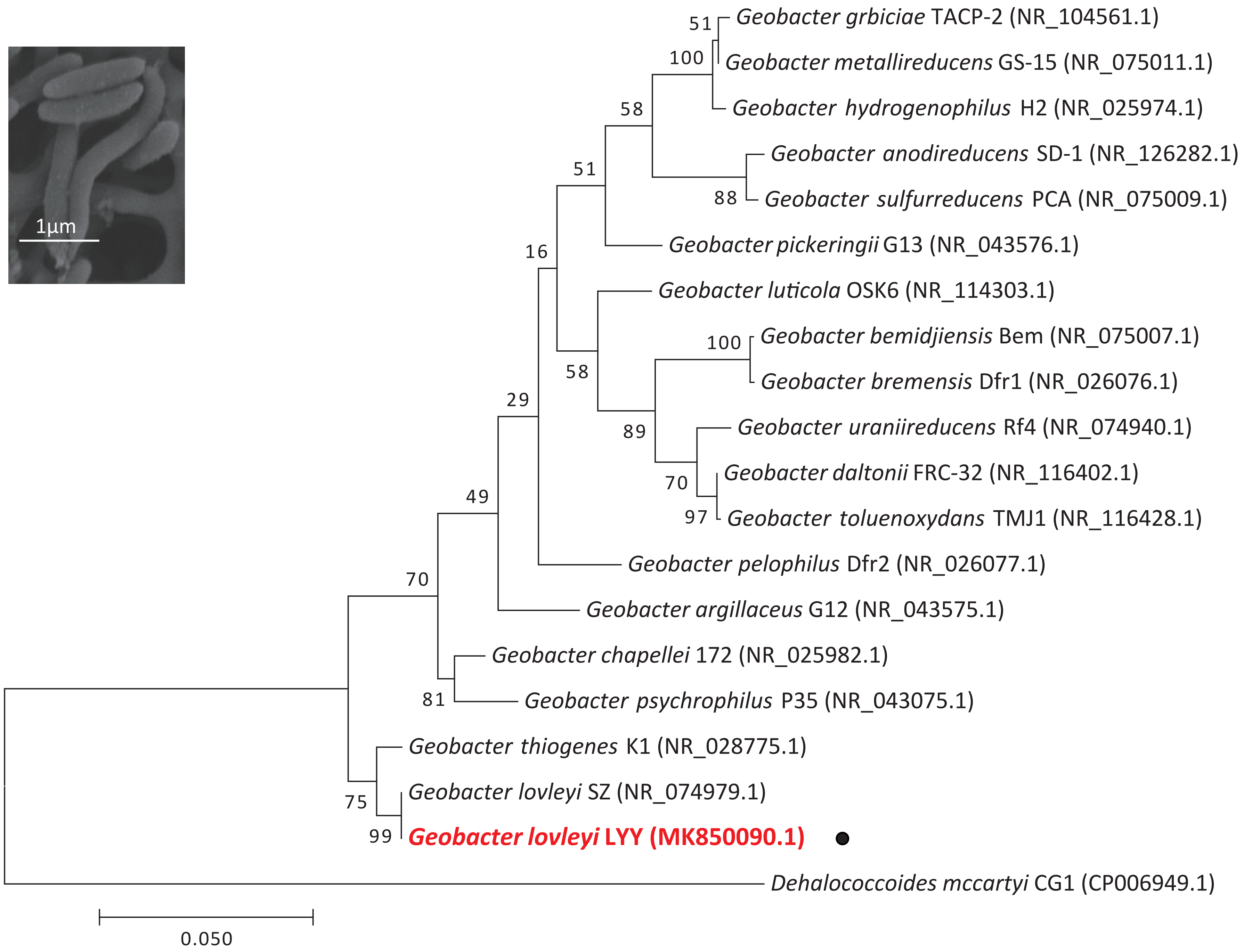


Fig. S4. Phylogeny of *Geobacter lovleyi* LYY. The phylogenetic tree of strain LYY and related strains has been constructed with neighbor-joining method (MEGA 7) based on their full-length 16S rRNA gene sequences. The bootstrap values at nodes are based on 1,000 replicates. The scale bar represents a 5-bp substitution per 100 nucleotides. A SEM image inside figure shows the cell morphology of *G. lovleyi* LYY.

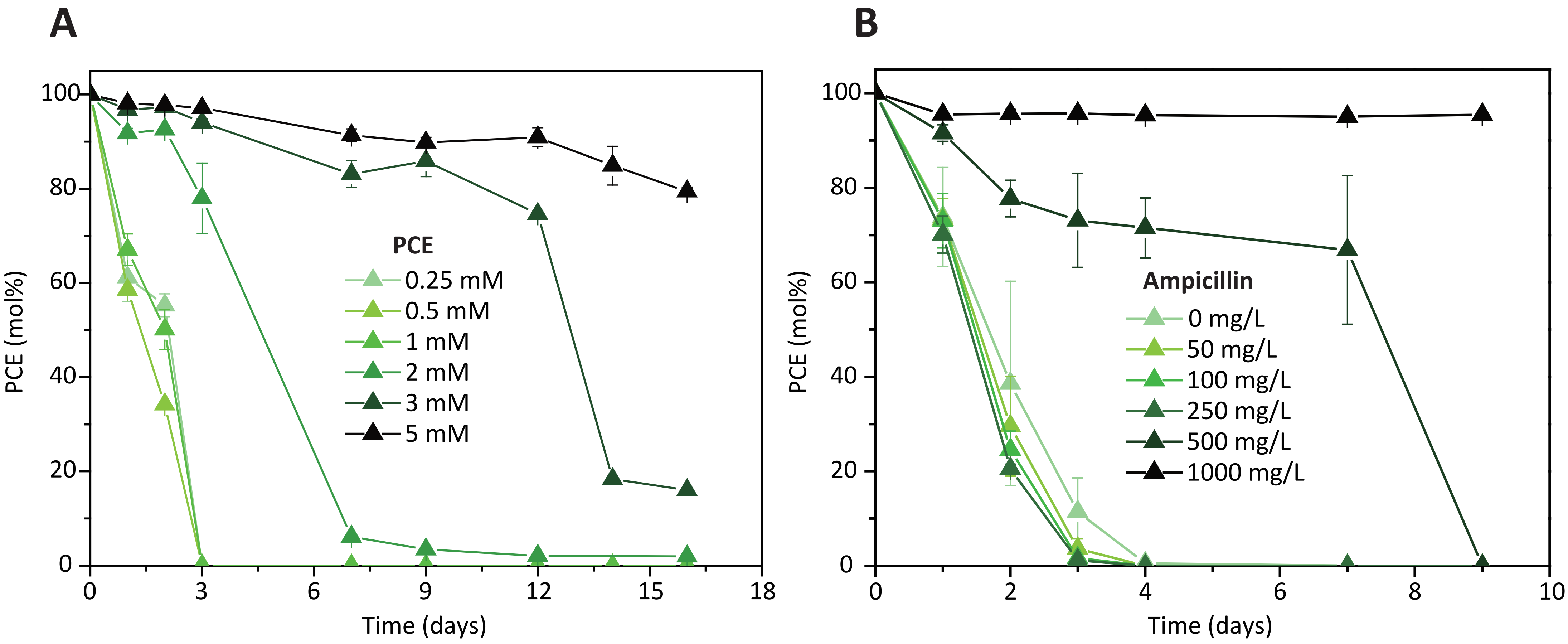
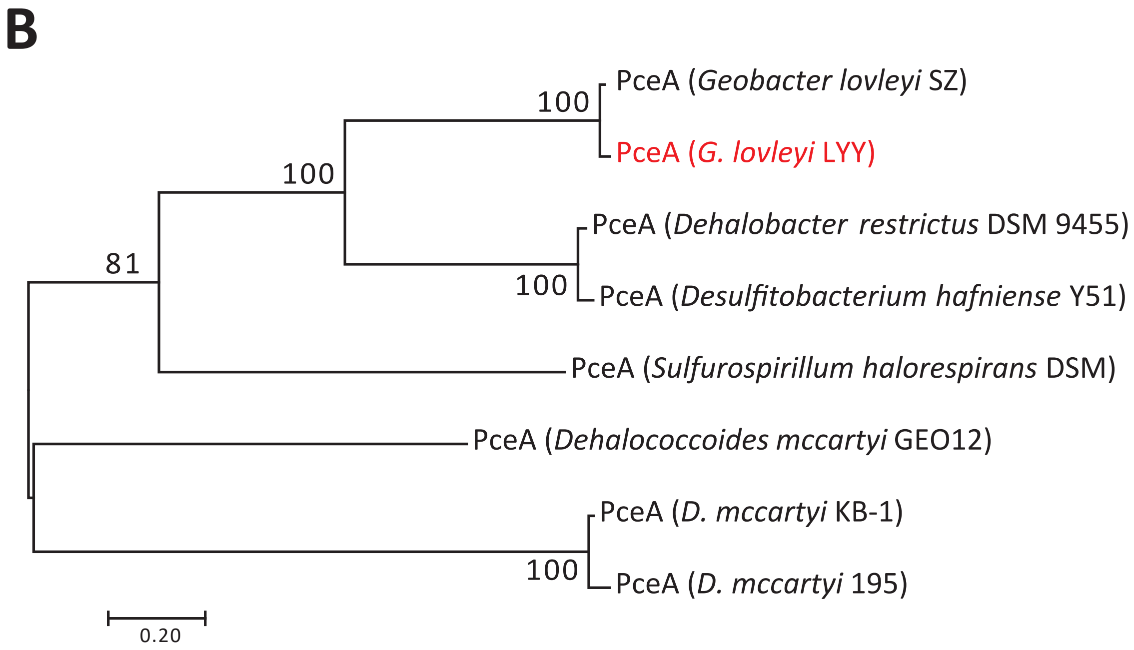


Fig. S5 PCE dechlorination in *Geobacter lovleyi* LYY pure cultures. (A) PCE-dechlorinating pure cultures fed with 0.25-5 mM PCE. **(B)** PCE-dechlorinating pure cultures amended with 0-1000 mg/L ampicillin and 1 mM PCE. Error bars represent SDs of triplicate cultures.

A

	G. lovleyi		*G. thiogenes*	*G. sulfurreducens*
	LYY	SZ	K1	PCA
Size (Mb)	3.7	3.9	3.6	3.8
G+C Contant (%)	54.9	54.8	55.1	60.9
Genes (total)	3572	3726	3369	3490
CDSs (total)	3521	3672	3308	3432
tRNA	42	44	48	48
rRNA (5S, 16S, 23S)	2	2	3	2
rdhA genes	1	2	N.I.	0
Plasmid (Size, bp)	1 (81261)	1 (77113)	0	0

N.I.: Not identified



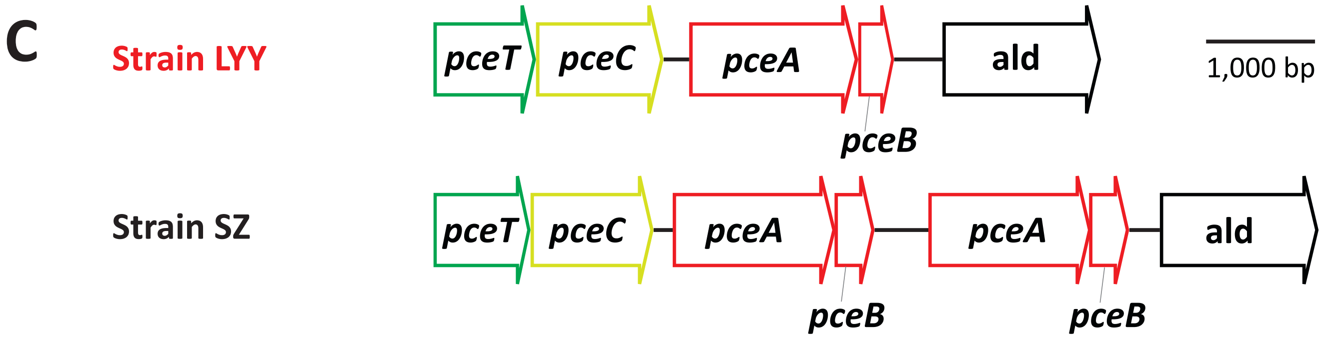


Fig. S6. Genomic characterization of *Geobacter lovleyi* LYY. (A) Overview of genomes of strain LYY and previously sequenced isolates (i.e., SZ, K1 and PCA) belonging to the Geobacter genus. **(B)** Phylogeny of PCE reductive dehalogenases (PceA) in OHRB of different lineages (*Geobacter lovleyi* SZ, WP_012470907.1; *Dehalobacter restrictus* DSM 9455, CAD28792.1; *Desulfitobacterium hafniense* Y51, BAC00915.1; *Sulfurospirillum halorespirans* DSM, AHJ12791.1.; *Dehalococcoides mccartyi* GEO12, POZ59159.1; *D. mccartyi* KB-1, AQX75192.1; *D. mccartyi* 195, WP_010936099.1). The tree has been generated for 550-aa aligned positions using Clustal W (MEGA 7), and bootstrap values at nodes are based on 1,000 replicates. The scale bar represents changes per amino acid position. **(C)** PCE reductive dehalogenase-encoding genomic loci on the chromosomes of *G. lovleyi* LYY and SZ.

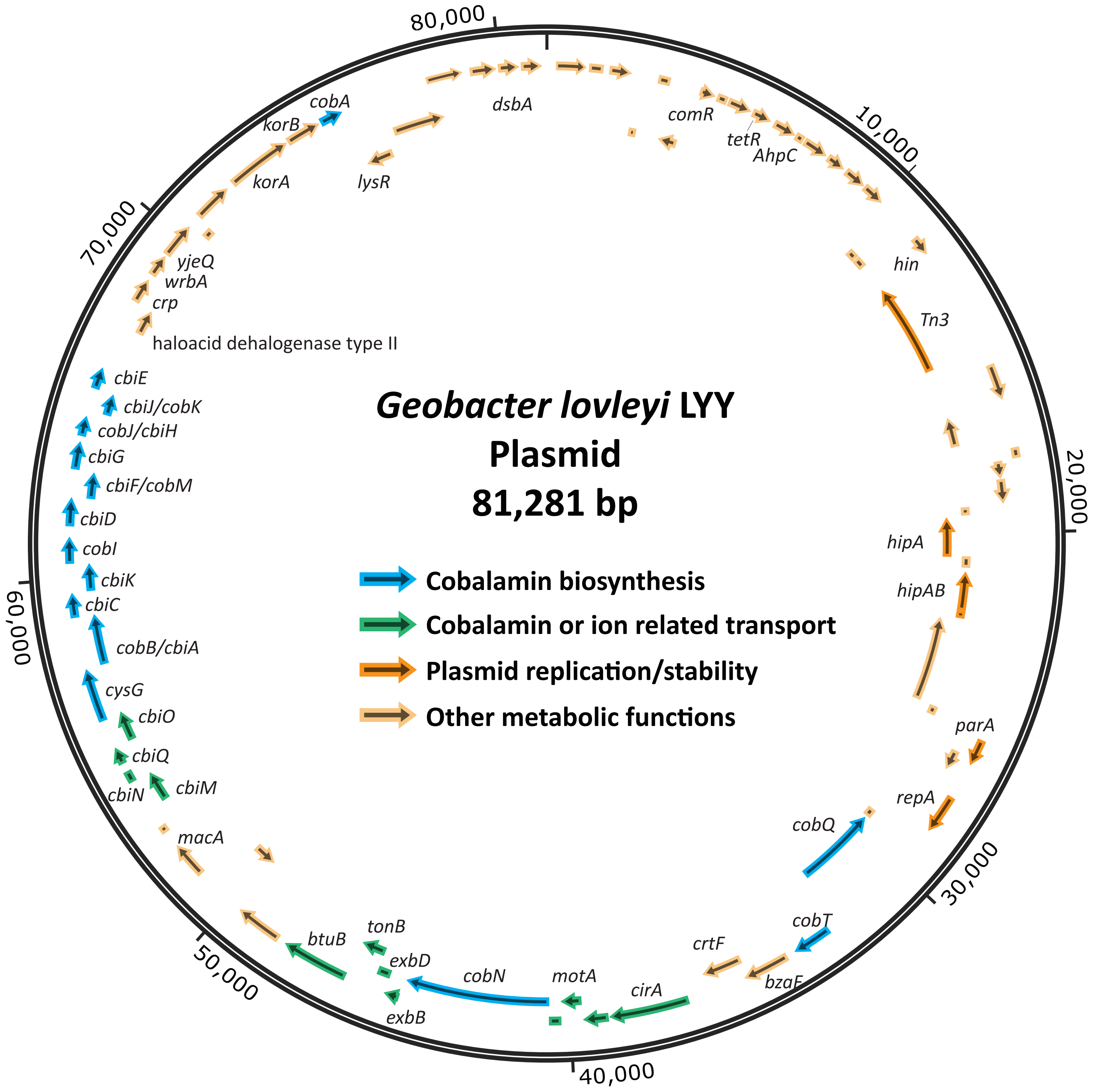


Fig. S7. A plasmid map of *Geobacter lovleyi* LYY. Genes for cobalamin synthesis and transport are shown in blue and green colors, respectively.

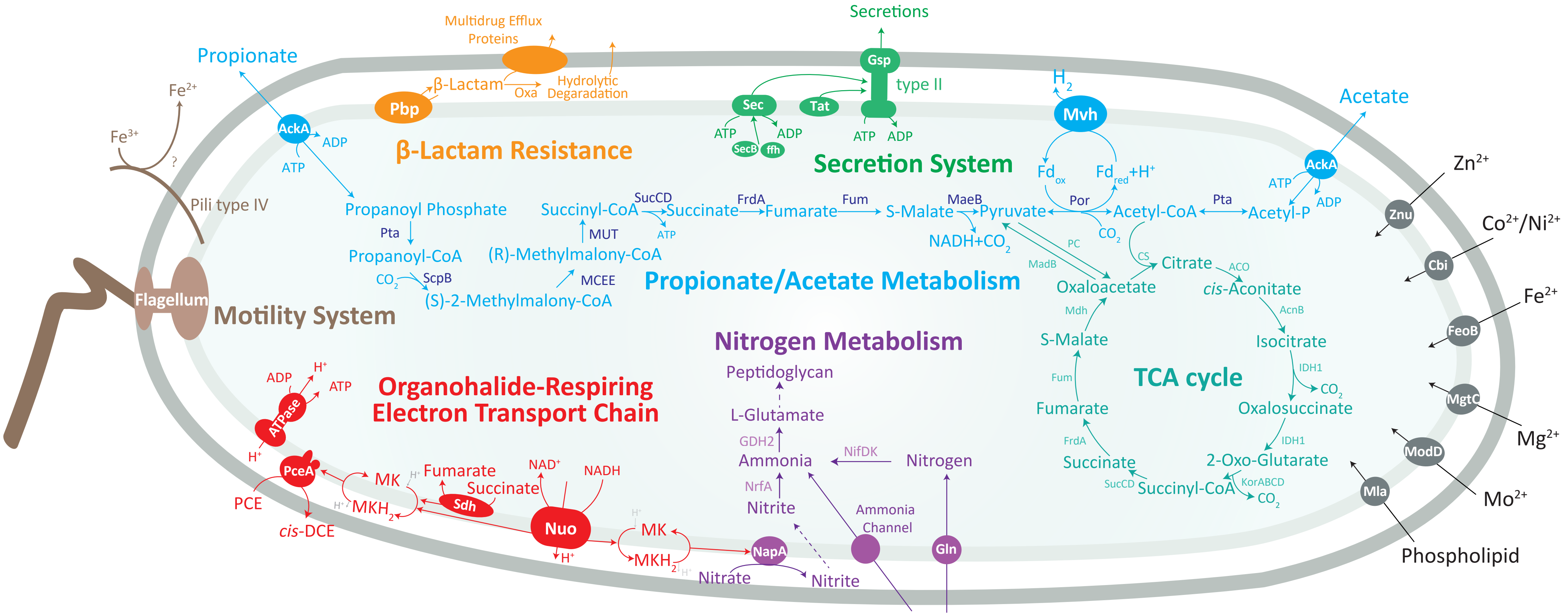


Fig. S8. Predicted metabolic capabilities of *Geobacter lovleyi* LYY. Metabolic pathways include organohalide-respiration (red) , propionate-to-acetate/hydrogen metabolism (blue), TCA cycle (cyan) and nitrogen metabolism (purple), as well as type II secretion systems (orange) and β-lactam resistance (blue). See **Table S3** for detailed information on genes assigned to specific metabolic pathways.

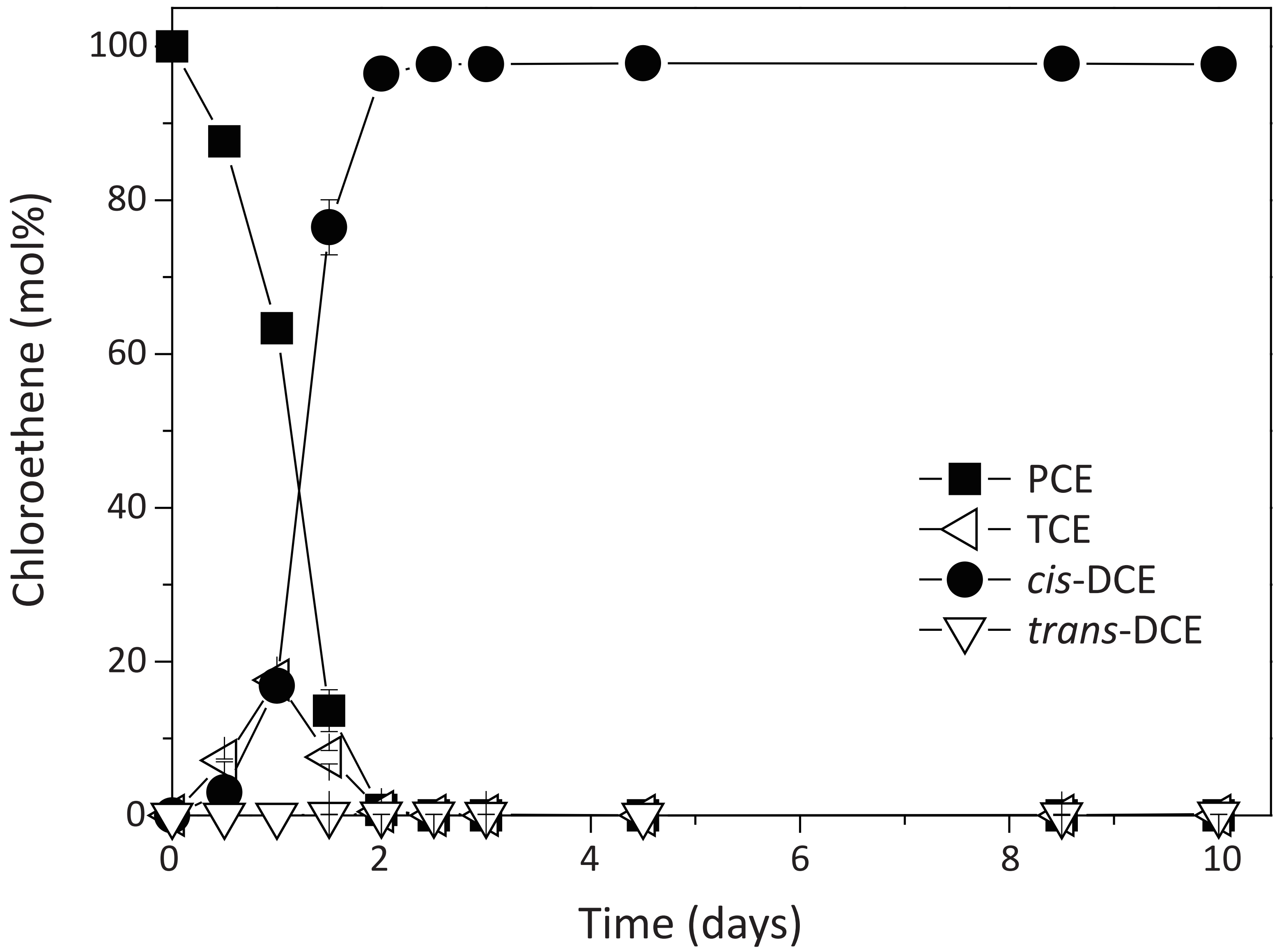


Fig. S9. PCE dechlorination in a *Geobacter-Dehalococcoides* co-culture. The coculture was prepared with *Geobacter lovleyi* LYY and *Dehalococcoides mccartyi* CG1.