

Supplementary information for

Resilience of *Dehalococcoides* enables complete reductive dechlorination of trichloroethene to ethene under high PFOS stress

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This file includes: Figures S1–S7, Tables S1-S6.

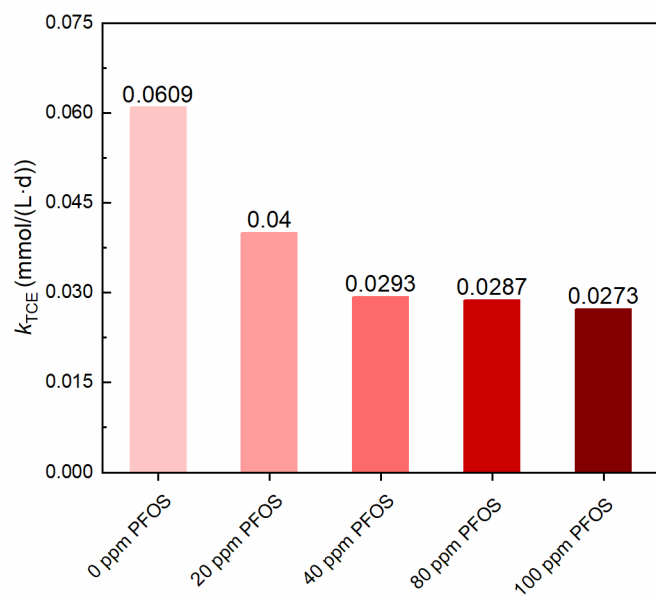


Fig. S1 The kinetics of TCE dechlorination under varying concentrations of PFOS were evaluated.

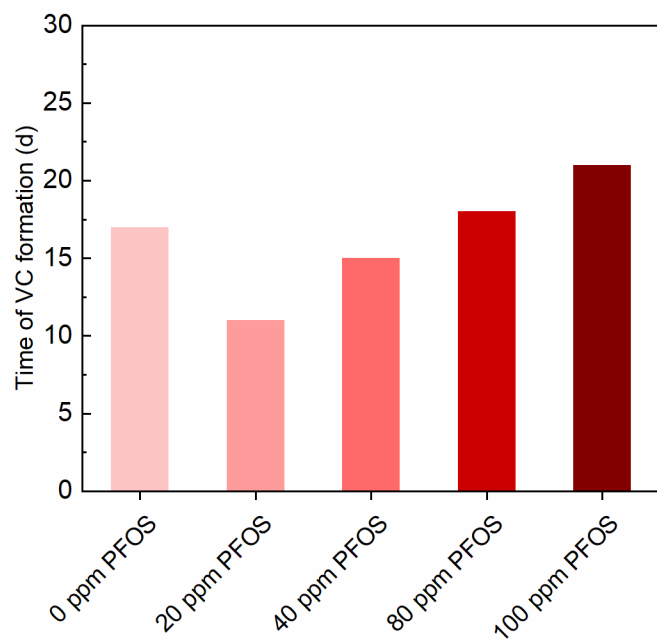


Fig. S2 The time to convert VC into ethene in the presence of various PFOS concentrations.

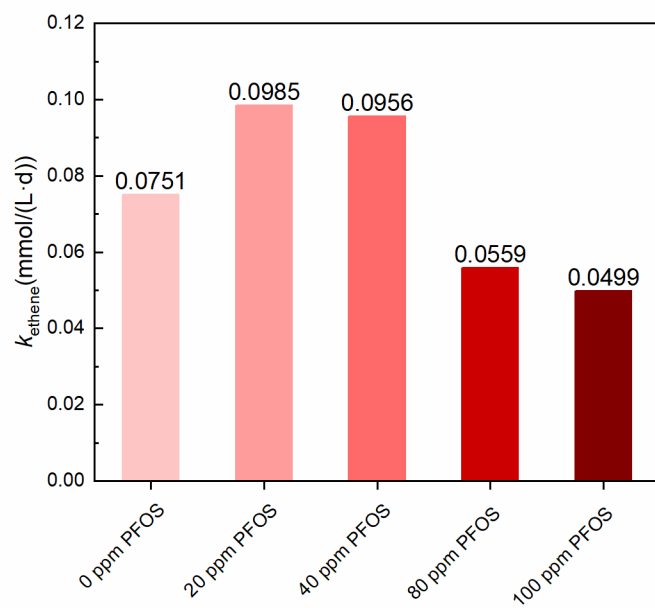


Fig. S3 The kinetics of ethene formation under varying concentrations of PFOS were evaluated.

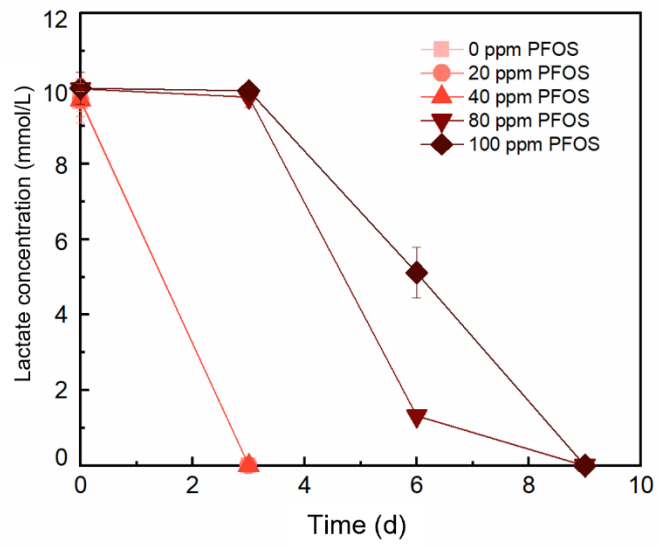


Fig. S4 Variations of lactate with time in the presence of various PFOS concentrations.

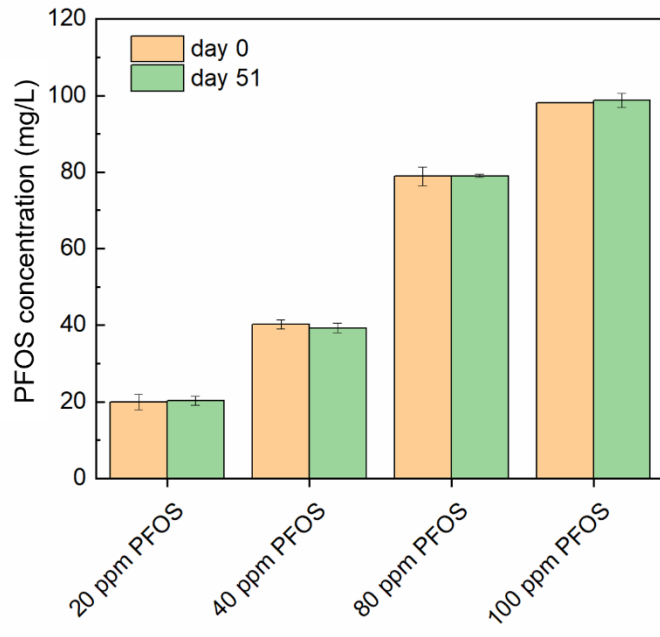


Fig. S5 Comparison of PFOS concentrations on day 1 and on day 51.

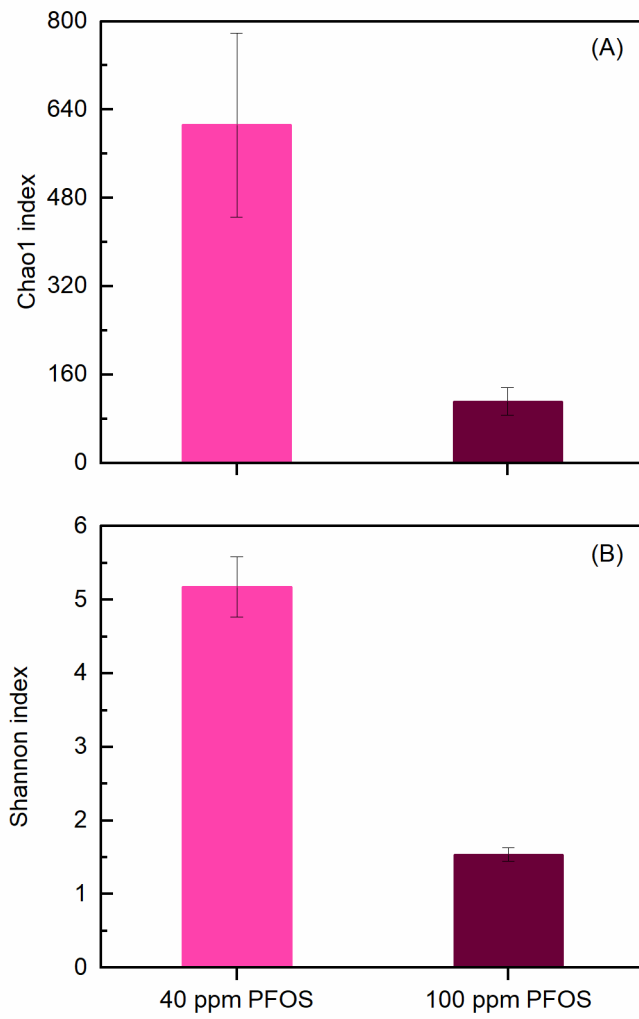


Fig. S6 the Chao 1 (A) and Shannon (B) index of alpha biodiversity in the presence of 40 and 100 mg/L PFOS. Errors bars show the standard deviation.

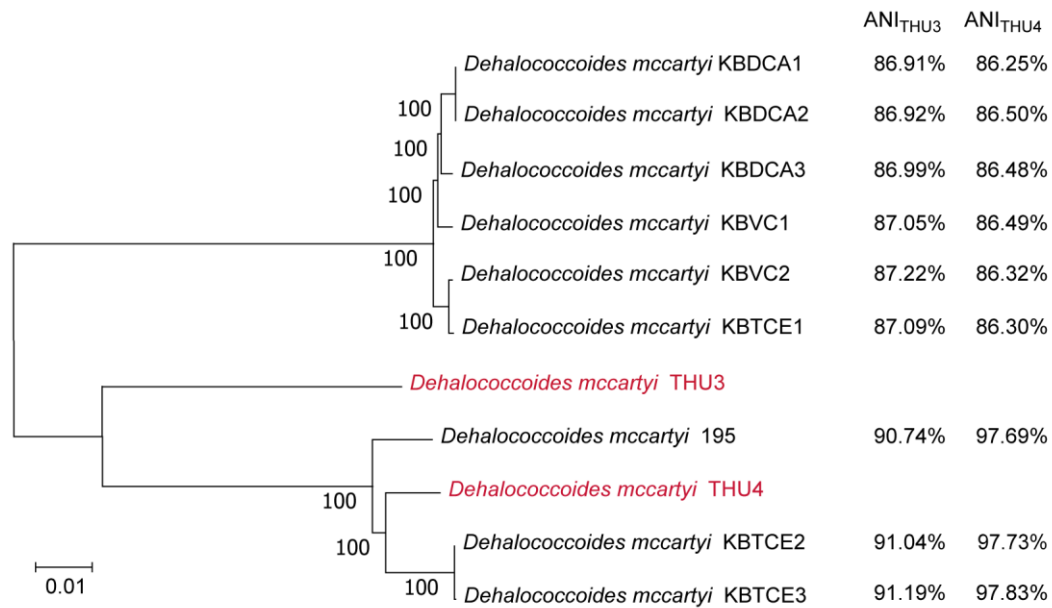


Fig. S7 Maximum likelihood tree of draft genomes of *Dhc* strains. The tree with the highest log likelihood is shown and drawn to scale with branch lengths measured in the number of substitutions per site. The average nucleotide identity (ANI) values indicate similarity to strain THU3 and THU4 genome. Bootstrap values expressed as a percentage of 1000 resamplings are shown at the branching points. The scale bar indicates nucleotide substitutions per site.

Table S1 The information of data fitting for TCE dechlorination under varying concentrations of PFOS.

PFOS	Fitting equation	R^2	$k_{\text{TCE}}(\text{mmol}/(\text{L}\cdot\text{d}))$
0 ppm	$y = 0.0609x + 0.0193$	0.9986	0.0609
20 ppm	$y = 0.04x - 0.0962$	0.9522	0.0400
40 ppm	$y = 0.0293x - 0.1273$	0.9237	0.0293
80 ppm	$y = 0.0287x - 0.0826$	0.9478	0.0287
100 ppm	$y = 0.0273x - 0.0581$	0.9373	0.0273

Table S2 The information of data fitting for ethene formation under varying concentrations of PFOS.

PFOS	Fitting equation	R^2	K_{ethene} (mmol/(L·d))
0 ppm	$y = 0.0751x - 1.1764$	0.9772	0.0751
20 ppm	$y = 0.0985x - 2.2879$	0.9574	0.0985
40 ppm	$y = 0.0956x - 3.2301$	0.9999	0.0956
80 ppm	$y = 0.0559x - 1.632$	0.9874	0.0559
100 ppm	$y = 0.0499x - 1.49$	0.9732	0.0499

Table S3 The information of genomes for strains THU2, THU3, and THU4.

Strains	Completeness (%)	Contamination (%)	GC (%)	Genome size (Mb)	Scaffolds
<i>Dhg</i> THU2	96.69966997	0	55.24	1.72	19
<i>Dhc</i> THU3	99.00990099	0	47.14	1.48	16
<i>Dhc</i> THU4	99.00990099	0	48.63	1.42	1

Table S4 The raw read counts for the key ASVs classified as *Dhc* and *Dhg*.

Time (Day)	40 mg/L PFOS		100 mg/L PFOS	
	<i>Dhc</i>	<i>Dhg</i>	<i>Dhc</i>	<i>Dhg</i>
0	549	7927	549	7927
9	41	7	80	4
13	646	4	674	0
18	1392	14	805	0
23	2601	92	852	1
30	2646	2450	3283	10
40	9312	1993	6493	2
51	10947	1367	7387	3

Table S5 The relative abundances of key genera in our inoculum at different stages.

Genus	Generation 0 (%)	Generation 8 (%)	0 mg/L PFOS (%)
<i>Dehalococcoides</i>	6.13	1.45	5.89
<i>Dehalogenimonas</i>	0.10	10.95	5.44
<i>Clostridium_sensu_stricto_7</i>	3.54	1.26	0.15
<i>Acetobacterium</i>	0.11	0.22	0.06
<i>Desulfovibrio</i>	0.01	0.19	0.07
<i>Petrimonas</i>	0.005	0.42	0.33
<i>Bacteroides</i>	0.05	3.70	0.27
<i>Sedimentibacter</i>	0.40	1.22	0.66
<i>Sphaerochaeta</i>	0.01	9.74	26.8
<i>Lentimicrobium</i>	0.02	30.5	32.38
<i>Macellibacteroides</i>	0.06	0.04	0.02
<i>Christensenellaceae_R-7_group</i>	0.39	1.24	0.55

Note: Generation 0 (initial enrichment from sediment), Generation 8 (stable culture used for PFOS exposure experiments), and the 0 mg/L PFOS control at the endpoint of the batch experiment.

Table S6 Identifiable *rdhA* genes in the *Dhc* strains.

Species	Identifiable <i>rdhA</i> gene	NCBI accession number
Strain THU3	<i>pceA, vcrA</i>	JBDLLV000000000
Strain THU4	<i>pceA, tceA</i>	CP171266
Strain 195	<i>pceA, tceA</i>	NC002936
KBVC1	<i>pceA, vcrA</i>	CP019968
KBVC2	<i>pceA, vcrA</i>	CP019969
KBTCE1	<i>pceA, vcrA</i>	CP019999
KBTCE2	<i>tceA</i>	CP019865
KBTCE3	<i>tceA</i>	CP019866
KBDCA1	<i>bvcA</i>	CP019867
KBDCA2	<i>bvcA</i>	CP019867
KBDCA3	<i>bvcA</i>	CP019946