6.0 Supplemental Tables and Figures

Table S1. LAMP and qPCR primers used for experiments in this study. Degenerate bases are underlined.

Primer	Start Position	Sequence 5' - 3'
16S rRNA gene targeting *Dehalobacter*		
F3	182	GAGAAGAAAGCTGGCCTCTG
B3	394	GGCCTTCTTCATACACGCG
FIP	258-206	GATCGTCGCCTTGGTAGGCC-TGCTAGCGCTTAGGGATGG
BIP	302-363	GGCCACACTGGGACTGAGACA-TCAGACTTTCGTCCATTGCG
LF	228	CCAACTAGCTAATCAGACGCG
LB	342	AGGCAGCAGTGGGGAATCTTC
rdhA gene		
F3	1171	TTCGGTCCGAGAMWTCGC
B3	1340	TCGGMTACCTCAMMATCCT
FIP	1234-1192	ACTCGCGTACCCCGAATTTTYT-GCCAAAGTCTACACCGACC
BIP	1258-1321	TGCCGCCTGTGCAAAAAATGTG-CTGGCTGCAGAACCTTAGG
LF	1211	TGTCCGGAGCAAGTTCCA
LB	1295	CCCAGGCCATCTCCCAYGA
MIAC luc gene F3		
	1098	AGGACTCTGGTACAAAATCG
B3	1302	ACGTGAATTGCTCAACAGTA
FIP	1166-1120	ACGGATTACCAGGGATTTCAGTC-TTCATTAAAACCGGGAGGT
BIP	1235-1283	TGCACGTTCAAAATTTTTTGCAAC-GAACATTTCGCAGCCTAC
LF	1139	ACACGTTCGTCACATCTCATCT
LB	1259	CCCTTTTTGGAAACAAACACTACG
qPCR rdhA		
Forward		GCAGGAAGATTCTAAAACCTTG
Reverse		CACCGAGGTACTGGAAATGA
qPCR luc		
Forward		TACAACACCCCAACATCTTCGA
Reverse		GGAAGTTCACCGGCGTCAT

Table S2. Testing selected LAMP assay specificity with gDNA from *Dehalobacter* and non-targeted organisms. Percent similarity is based on 16S rRNA gene of organisms or close relative if the 16S rRNA gene was not available in public databases.

16S rRNA gene classification	% Similarity to *Dehalobacter*	Organism	*rdhA* gene	16S rRNA gene
d: Bacteria, c: Clostridia, f: Peptococcaceae 1	-	*Dehalobacter* spp. (in CB&I TCA-20^{TM} culture)	+	+
d: Bacteria, c: Clostridia, f: Peptococcaceae 1	93.2%	*Syntrophobotulus glycolicus* (DSM 8271)	-	+
d: Bacteria, c: Deltaproteobacteria	79.3%	*Desulfacinum infernum* (DSM 9756)	-	-
d: Bacteria, c: Deltaproteobacteria	79.7%	*Desulfobacterium autotrophicum* (DSM 3382)	-	-
d: Bacteria, c: Deltaproteobacteria	82.8%	*Desulfomicrobium baculatum* (DSM 4028)	-	-
d: Bacteria, c: Deltaproteobacteria	85.1%	*Desulfonauticus submarinus* (DSM 15269)	-	-
d: Bacteria, c: Deltaproteobacteria	82.2%	*Syntrophobacter wolinii* (DSM 2805)	-	-
d: Bacteria, c: Thermodesulfobacteria	79.6%	*Thermodesulfobacterium commune* (DSM 2178)	-	-
d: Bacteria, c: Deltaproteobacteria	82.1%	*Thermodesulforhabdus norvegica* (DSM 9990)	-	-
d: Bacteria, c: Nitrospira	77.8%	*Thermodesulfovibrio yellowstonii* (DSM 11347)	-	-
d: Archaea	64.0%	*Methanococcus sp.*(DSM 8766)	-	-
d: Archaea	63.2%	*Methanosarcina sp.* (DSM 4659)	-	-

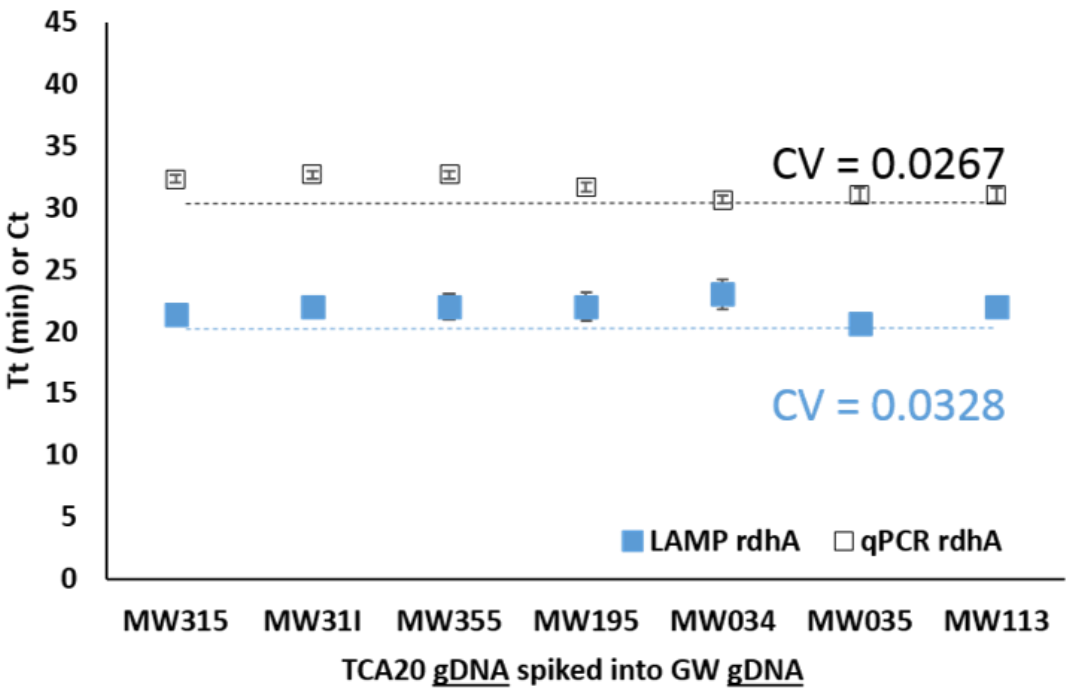

Fig S1. C_t and T_t measured by spiking 5 ng of DNA extracted from TCA-20 into DNA extracted from the groundwater samples. CV indicates the coefficient of variation. Error bars represent standard error of three technical replicates. In some cases error bars are smaller than symbols.

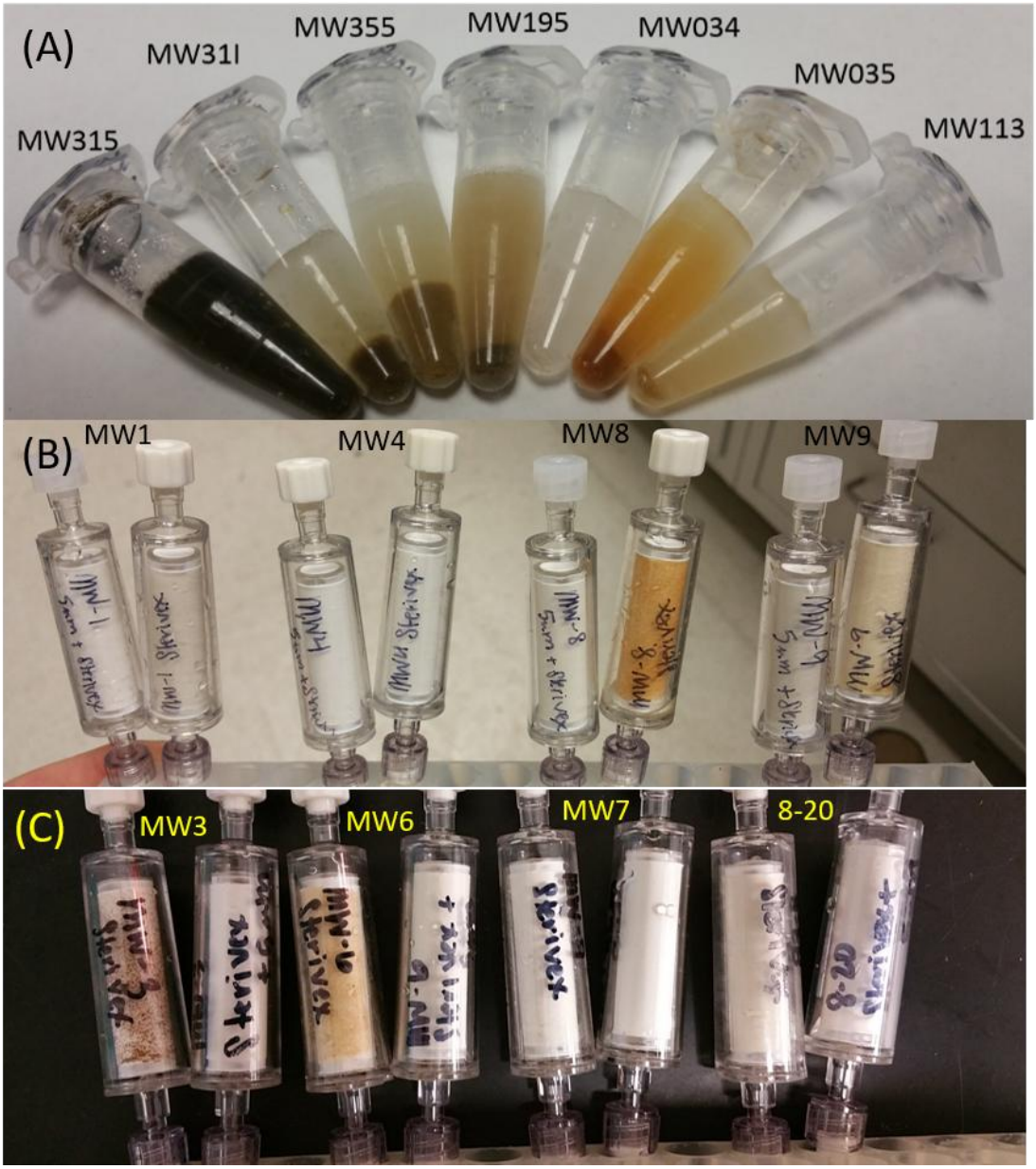

Fig S2. Picture of concentrated groundwater samples collected from remediation sites A) elution collected after concentration with Sterivex filters, B-C) Sterivex filters after passing 200 mL of eight groundwater samples with and without a 5 micron filter to remove suspended solids. In (B) Sterivex filters used after 5 micron filtration are on the left of each pair, in (C) Sterivex filters used after 5 micron filters are on the right side of each pair.