

Supplemental Information

Extrachromosomal circular elements targeted by CRISPR-Cas in *Dehalococcoides mccartyi* are linked to mobilization of reductive dehalogenase genes

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References for Supplemental Information

Additional Method Details

Detailed description of enrichment cultures used in the study

The KB-1 set of enrichment cultures originated from microcosms prepared with aquifer materials from a trichloroethene (TCE)-contaminated site in southern Ontario in 1996 as previously described (1). The KB-1 parent enrichment culture, referred to as KB-1/TCE-MeOH, has been maintained in a glass 2L bottle (0.7 L headspace) in anaerobic mineral medium amended with 100 mg/L TCE as electron acceptor and methanol (MeOH) as electron donor, added at 5x the electron equivalents (eeq) required for complete dechlorination, as previously described (1, 2). TCE is completely dechlorinated to ethene prior to refeeding, approximately every 2-4 weeks. Acetogens in the mixed culture ferment added methanol to hydrogen required for energy by *D. mccartyi* and acetate required as carbon source. This parent enrichment culture served as the inoculum for several sub-cultures that were established between 2001 and 2003 and maintained on different chlorinated acceptors, including TCE daughter products *cis*-dichloroethene (cDCE) and vinyl chloride (VC), as well as 1,2-dichloroethane (1,2-DCA). Specifically, in 2001, a sub-culture was created with a 2% transfer into pre-reduced anaerobic mineral medium and maintained on VC and hydrogen as described by Duhamel, Mo (2) and is referred to as KB-1/VC-H₂. This VC enrichment (200 mL) was maintained in a 250 mL glass bottle sealed using a teflon mininert cap and was amended with 55 mg/L VC (supplied as 5mL pure VC gas) and 5x eeq hydrogen gas (supplied as 5mL H₂:CO₂ (80:20) Praxair). The KB-1/VC-H₂ enrichment bottle was also amended with 0.5 mM sodium acetate as a carbon source every ten feedings. In 2003, a 1,2-dichloroethane (DCA)-fed enrichment culture was created (KB-1/1,2-DCA-MeOH culture) fed with 250mg/L 1,2-DCA and 5x MeOH, in a 2L glass pyrex bottle containing 1.6 L culture with 0.7 L headspace). Approximately every 6 months, half of each culture was removed and substituted with fresh pre-reduced anaerobic mineral medium to replenish vitamins and buffer. In all enrichment cultures, chlorinated ethenes, methane and ethene concentrations were monitored using gas chromatography with an FID detector (Agilent 7890A GC system, G1888 auto-sampler, helium used as carrier gas, packed inlet, Agilent GSQ-Plot column 0.53mm x 30m), calibrated with external standards.

Experimental Details for monitoring *vcrA* genomic island

An experiment to specifically monitor the behavior of the *vcrA* genomic island was established using a VC-dechlorinating enrichment culture (KB-1/VC-H₂). This culture was established in 2001 with hydrogen (H₂) as electron donor with a goal towards enriching or isolating a *D. mccartyi* strain (2). This mixed culture dechlorinated VC consistently but more slowly than MeOH-amended cultures. For the experiments described herein, three 250 mL bottles containing 150 mL of anaerobic mineral medium were each inoculated with 50 mL of KB-1/VC-H₂ culture. These triplicate cultures were provided an electron donor mix of MeOH and EtOH as 7.5 x eqq rather than H₂ to boost slow dechlorination rates. Three feedings of VC (~25 mg/L) were each dechlorinated to ethene over ~34 days. The next three dechlorination cycles were intensively monitored for VC depletion and ethene production using gas chromatography and samples (2 mL) were taken for subsequent DNA extraction three times a week. These samples were immediately centrifuged (13,000x g, 15 min, 21°C Eppendorf centrifuge 5417R), decanted and stored frozen at -80°C.

Nucleotide sequence of concatenated *D. mccartyi* gene fragment

This sequence was cloned into a plasmid and used as calibration standard for qPCR.

>*vcrA* – *D.mccartyi* 16s rRNA – *tceA* – *bvcA*

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>AGGCCCTCCAGATGCTCCCTTACATCATGGGGCAATAGGCTTCAGATGAGAATGT
CAGATGAAGAGCAAAGAAGCGAATTTGGCCGCTAAAAAAGAGAGGTTCCCTGGT
TGGGACGGTGGGTTACACGGGAGAGGGGATCAGCGGGCGGATGCACTATTTTACGC
AGTAACTCAACCATTTCCTGGTAGTGGTGAGGAAGGGCACGGATGAACGCTAGCGG
CGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATAGTGGCGAACGG
GTGAGTAACGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAA
GGTAATACCGCATGTGGTGGGCGACATATGTTGGTTCCTAAAGCCGTAAGGCGCT
TGGTGAGGGGCTTGCGTCCGATTAGCTAGTTGGTGGGGTAATGGCCTACCAAGGCTT
CGATCGGTAGCTGGTCTGAGAGGATCCTAATATATGCCGCCACGAATGGCTCACATA
ATTGCTGGGAGAACCCGCTTATGGACGCTATGAAGGTTCTAGGCCTTATCTCTCTA
TGCGAACCATGAATGGAATAAACGGCTTGCATGAATTTGGTCACGCAGATATCAAA
ACCACCAACTACCCGAAGTGGGAGGGTACGCCTGAAGAGAACCTGTTAATCATGCG
CACCGCCGCGCGCTACTTCGGGGCTTCTCCGTTGGCGCCATTAAGATAACGGATAA
CGTGAAGAAAATCTTCTATACCAAAGCCCAGCCCTTATCCTCGGGCCTTGGTATAC
GATTATTATTTAGCGTGGGCAAACAGCAATTTCTGACTGGGAACCAGGAATTAAT
GGCCATGGGCCAACAAGGGACGAAGCTTTATGGTTTGCCTCAAGTACAGGTGGTAT
CGGTAGGTATAGAATTCCTGGTACCCAGCAAATGATGTCCACAATGCGTCTTGACGG
GTCTACTGGTGGTTGGGGTTATTTCAATCAACCACCGGCAGCAGTCTGGGGAGGGAA
ATACCAAGGTGGGAAGGAA
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Supplementary Figures

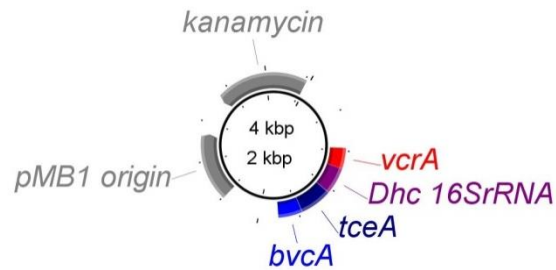


Figure S1. Diagram of the concatenated gene plasmid used as a qPCR standard. The plasmid containing fragments of the *D. mccartyi* 16S rRNA, *vcrA*, *bvCA* and *tceA* genes. Full nucleotide sequence is listed in Additional Method details above.

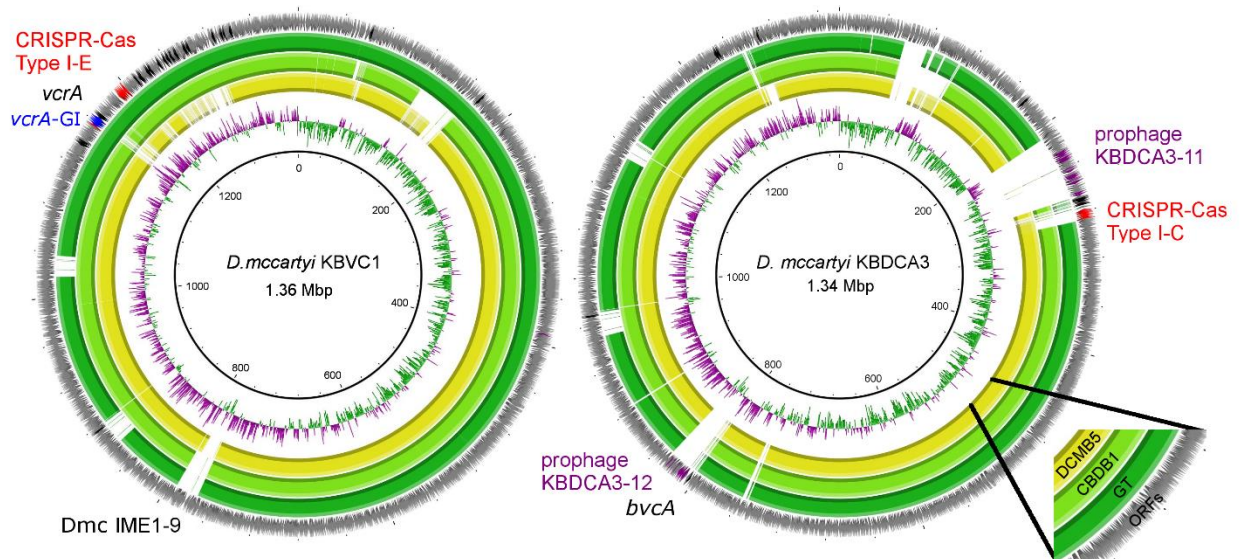


Figure S2. *Dehalococcoides mccartyi* KBVC1 and KBDC3 complete genomes and homology to related genomes. Rings inner to outer: (1) position on genome, (2) GC skew where green (+)/purple (-), (3-5) BLASTN hits (>70% identity) to other *D. mccartyi* strains with CRISPR systems including DCMB5, CBDB1, and GT, (6) open reading frames (ORFs). Predicted prophage genes are highlighted in purple, reductive dehalogenase (*rdhA*) in black, CRISPR-associated proteins in red.

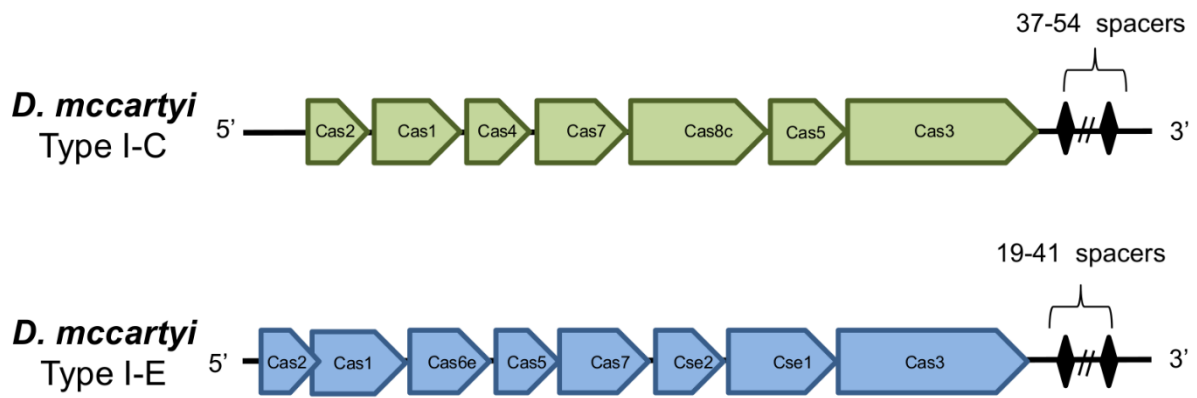


Figure S3. CRISPR-Cas operon from *D. mccartyi* Type I-E and Type I-C. Black diamonds indicate repeats in CRISPR array – which differ based on strain (CBDB1, KBVC1, KBDCA3, GT or DMCB5).

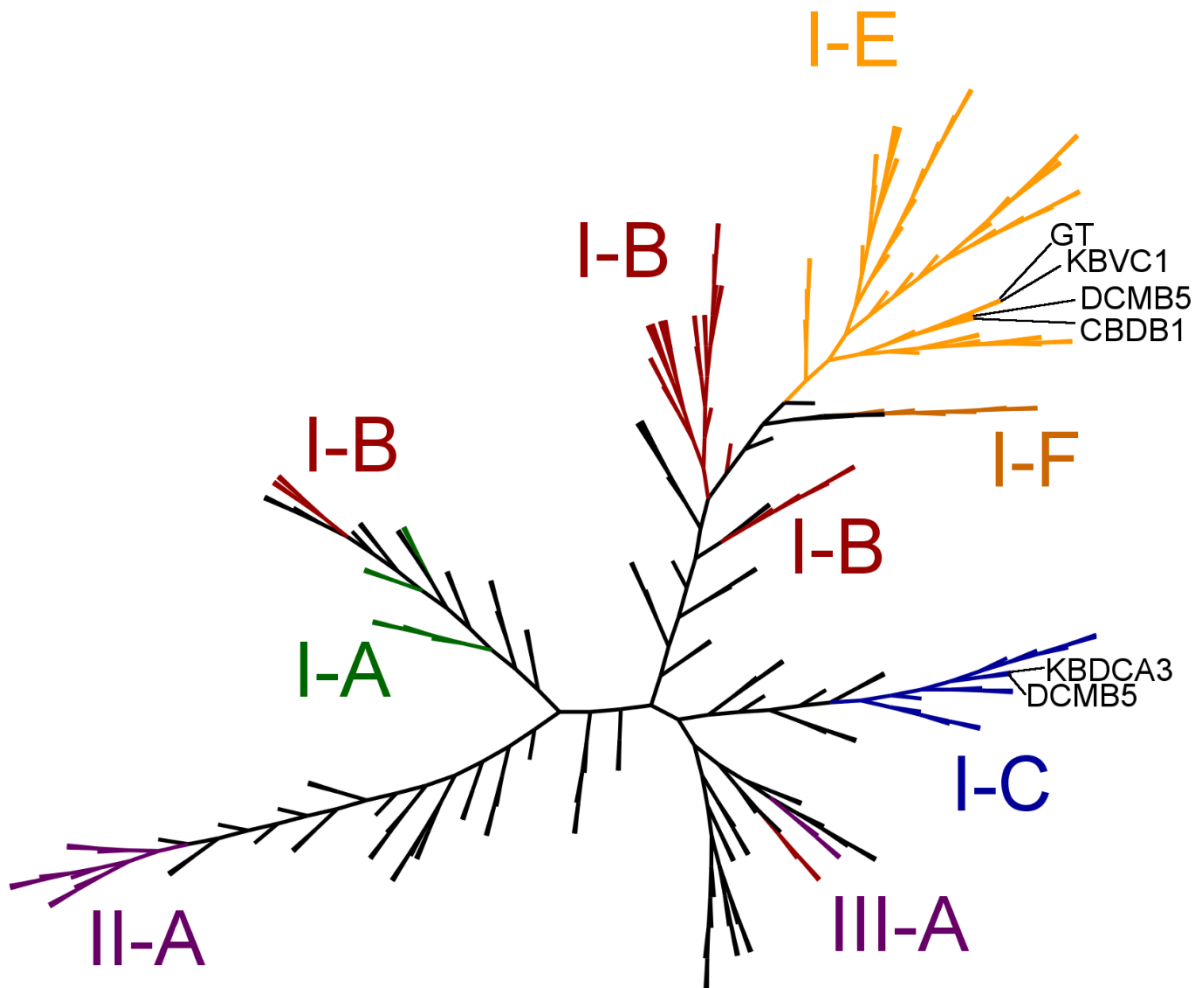


Figure S4. CRISPR Cas1 maximum likelihood tree constructed from an alignment of 227 Cas1 protein sequences. Only Cas1 sequences found in closed genomes were used in the alignment. Cas1 come from different types of CRISPR systems. Systems with clear clades are highlighted in different colours and identified by type. *Dehalococcoides mccartyi* Cas1 are type I-E (orange) and I-C (blue) labeled by strain name. Scale shows number of amino acid substitutions per site. Shown is most likely tree of 100 bootstraps.

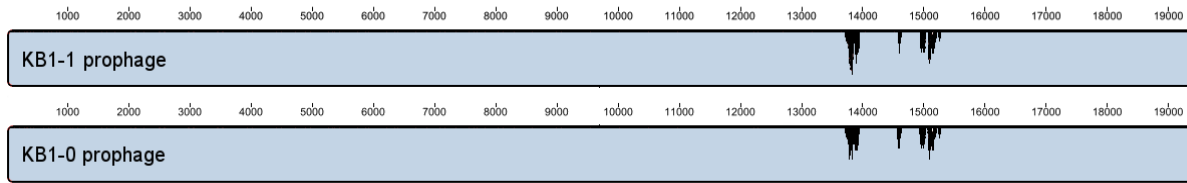


Figure S5. MAUVE nucleotide sequence alignment diagram between two similar KB-1 prophages. Prophage KB1/TCE-0 was found in the KB-1/TCE-MeOH culture in 2007 and prophage KBTCE1/VC2-1 was found in the same culture in 2013. Solid block region indicates sequence homology across entire prophage sequence (blue). Sequence similarity profiles (black) correspond to the average level of conservation in the region. The height of the profile is inversely proportional to the average alignment column change over the alignment. In total 71 of 19,420 bp are different which results in 24 amino acid substitutions (based on predicted open reading frames).

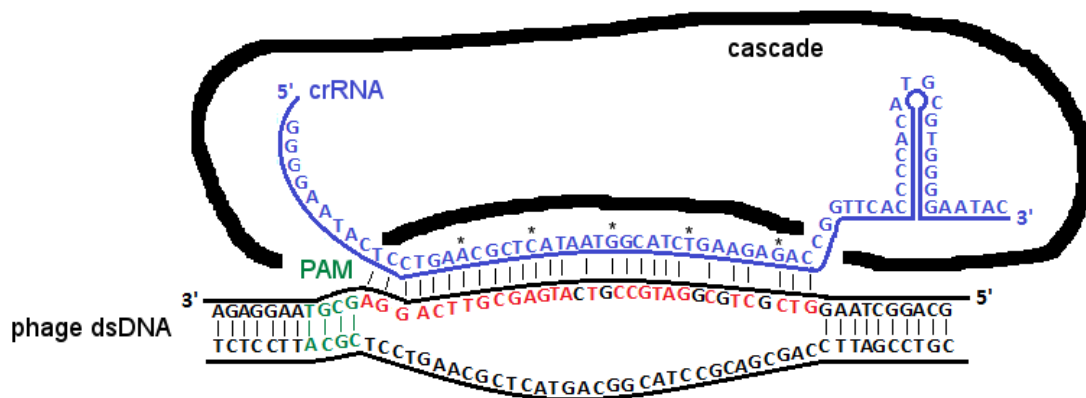


Figure S6. Representation of *Dehalococcoides mccartyi* KBVC1 CRISPR type I-E Cascade action on prophage target. *D. mccartyi* crRNA from the CRISPR array from sequencing information is shown in blue. Protospacer adjacent motif (PAM) is shown in green. Matching DNA sequence from prophage KBDCA3-12 is shown in red. Stars indicate positions that were found to readily tolerate mutations in *E. coli* type I-E CRISPR system (3). Due to the small number of mismatches and none in the PAM or seed regions (seed comprises 8-12 PAM-proximal bases), we expect strain KBVC1 CRISPR system to be able to run interference against this prophage.

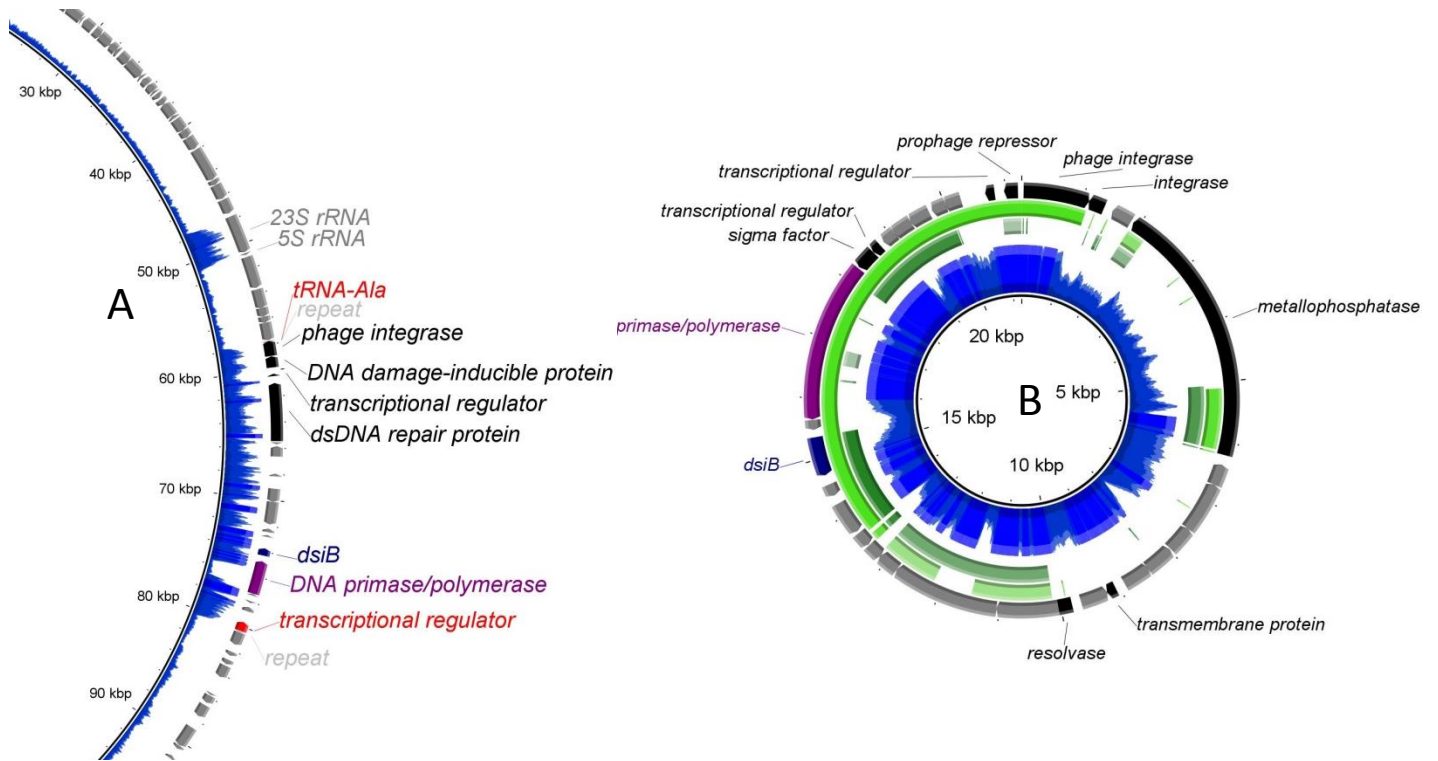


Figure S7. Metagenomic evidence for circular existence of integrative mobilizable elements (IMEs) in *D. mccartyi*. (A) Illustration of partial *D. mccartyi* genome (strain KBTCE2) showing high read depth over IME1-8 region (IME1-8). Strain KBTCE2 has average read depth of 100x with ~700x over IME1-8 region. (B) IME1-1 found circularized from metagenomic data (mate-pair and paired-end reads map only to itself). Read depth is shown in blue ranging from 0 to 1000x. (B) Inner dark green circle indicates significant blast hits to IME1-8 and IME1-2 (70-100% lighter to darker). Coding regions are shown as arrows: colored are annotated genes, in black showing conserved domains (domains annotated individually). In (A) 23S and 5S have high read depth due to multiple strains of *D. mccartyi* in this culture and 100% sequence identity across this region among all strains. See Figure 3a in main text for different IMEs found.

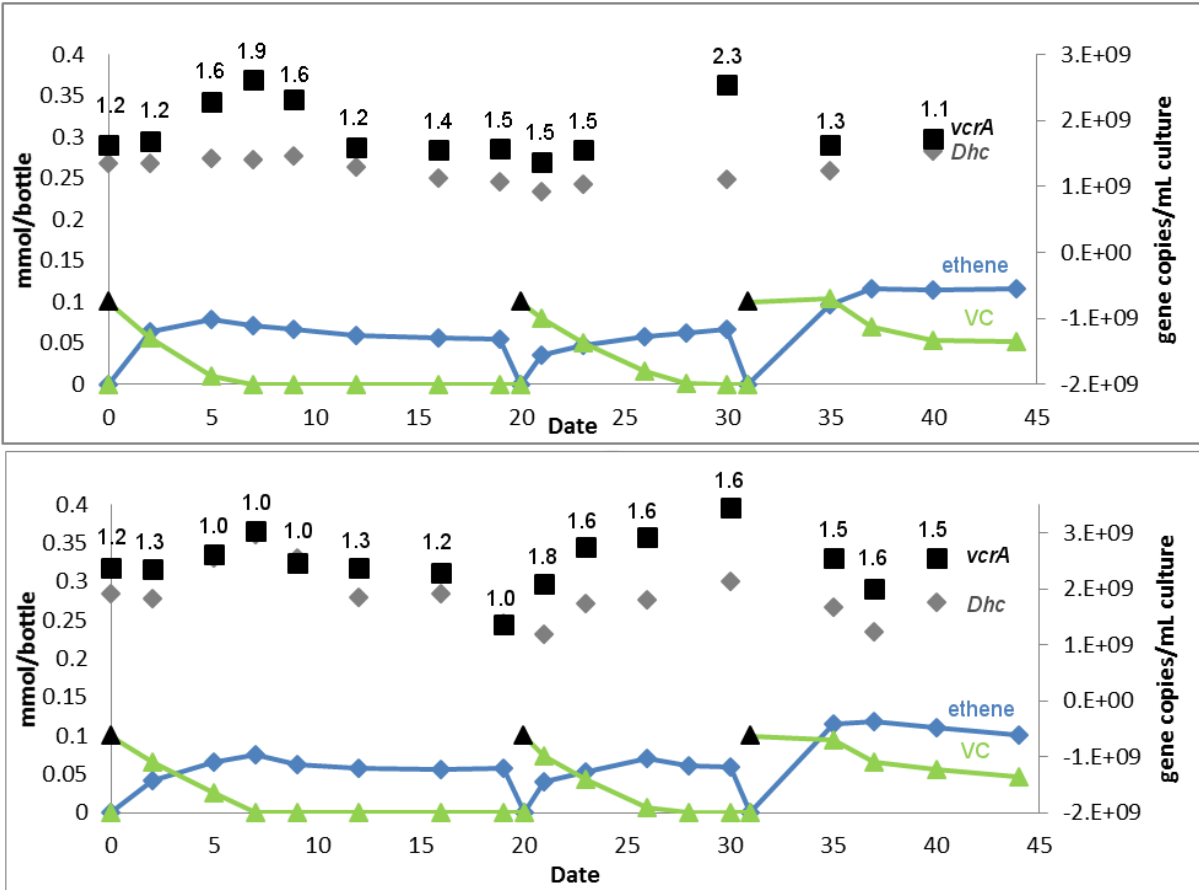


Figure S8. Quantitative PCR (qPCR) and gas chromatography (GC) tracking of two KB-1/VC-H₂ cultures during routine growth. Vinyl chloride (VC) is degraded to ethene (left axes). The number of gene copies of *D. mccartyi* 16S rRNA (*Dhc*, grey triangle) vinyl chloride reductase (*vcrA*, black square) tracked using quantitative qPCR (right axes). Cultures were maintained in batch mode, with periodic purging of gases and re-feeding with VC as indicated on graphs with black triangles. Graphs A and B are two of triplicate cultures studied. The third culture can be found in main text Figure 5. All qPCR raw data is in Table S7, standard curves S8.

Table S1. Primers used in this study

Primer Name	Direction	Sequence	Target	Use	Annealing temp. (°C)	Reference
CRISPR I-E 1f	f	5'-TTGCCCGGTTTCGTCATTA-3'	Annealing outside CRISPR array	PCR	65	This paper
CRISPR I-E 4561r	r	5'-GCCAATCCAACCGACCTT-3'	Annealing outside CRISPR array	PCR	65	This paper
CRISPR I-E 1f	f	5'-TACCTAGGAGTCAAGCATCG-3'	Half of CRISPR array	PCR	59	This paper
CRISPR I-E 1725r	r	5'-AAAACGCAAATTTCTGACAC-3'	Half of CRISPR array	PCR	59	This paper
<i>Dhc</i> 1f	f	5'-GATGAACGCTAGCGGCG-3'	<i>D. mccartyi</i> 16S rRNA gene	qPCR	60	1
<i>Dhc</i> 265r	r	5'-CCTCTCAGACCAGCTACCGATCGAA-3'	<i>D. mccartyi</i> 16S rRNA gene	qPCR	60	1
<i>vcrA</i> 670f	f	5'-GCCCTCCAGATGCTCCCTTTAC-3'	<i>vcrA</i> gene	qPCR	60	2
<i>vcrA</i> 440r	r	5'-TGCCCTTCCTCACCCTACCAG-3'	<i>vcrA</i> gene	qPCR	60	2
<i>vcrA</i> -GI PCR 1 1f	f	5'-CTAGATTCTTAATAAATTCGCGTGT-3'	genome region outside of <i>vcrA</i> -GI	PCR	65	This paper
<i>vcrA</i> -GI PCR 1 19361r	r	5'-AAATAACAAATGAGCTCTCAGAAAA-3'	genome region outside of <i>vcrA</i> -GI	PCR	65	This paper
<i>vcrA</i> GI PCR 2 1f	f	5'-GTA AAACTTACCGGGTTGAT-3'	circular <i>vcrA</i> genomic island	PCR	59.5	This paper
<i>vcrA</i> GI PCR 2 10426r	r	5'-TTGTTGCTAACACGACTGTT-3'	circular <i>vcrA</i> genomic island	PCR	59.5	This paper
seq-1	f	5'-ACAGGAACGAAGACGAACGGGG-3'	100 bp before CRISPR	sequencing	n/a	This paper
seq-2	f	5'-AGTGCCTACCCTACGAGCAAGG-3'	31 bp before CRISPR	sequencing	n/a	This paper
seq-3	f	5'-ATCGCTAGGGCTTGCCGAACT-3'	spacer # 6	sequencing	n/a	This paper
seq-1	r	5'-ACGCTTCGTTCTGGTGGAA-3'	spacer # 16	sequencing	n/a	This paper
seq-2	r	5'-GGCGTTTAGACCATTTTCACGC-3'	spacer # 27	sequencing	n/a	This paper
seq-3	r	5'-GCGAGTCGTA CTGTATTGAGG-3'	spacer # 33	sequencing	n/a	This paper
seq-4	r	5'-ACCAGCACTATCAAAAACGCA-3'	48 bp after the end of CRISPR	sequencing	n/a	This paper
seq-T3-1348-1f	f	5'-GAGATCTCTCCATGCCCAGC3-3'	300 bp after <i>vcrA</i> -GI	sequencing	n/a	This paper
seq-T1-1572r	r	5'-GAGCAGGCTGGGAAACTCAT-3'	233 bp after <i>vcrA</i> -GI	sequencing	n/a	This paper

¹ Hendrickson et al. (2002) AEM 68, 485-495, ² Molenda et al. (2016) AEM 82,40-50

Table S2. General features of *Dehalococcoides mccartyi* genomes. Genomes closed from KB-1 derived enrichment cultures compared with other CRISPR-Cas containing strains GT, CBDB1 and DCMB5.

Strain	KBVC1	GT	CBDB1	DCMB5	KBDC3
Origin	KB-1VC enrichment S.Ontario, CAN	Cont. aquifer, Cottage Grove, WI, USA	Saale river near Jena, GER	Bitterfeld region, GER	KB-1 1,2-DCA enrichment S. Ontario, CAN
Genome size (Mbp)	1.39	1.36	1.4	1.43	1.34
G+C content (%)	47.3	47	47	47.1	47.6
Protein coding genes	1468	1416	1460	1458	1404
Hypothetical genes (%)	31.1	18.6	28.7	25.4	29.1
tRNA	47	46	47	46	46
Number of Recombinases	4	7	4	7	4
Sub-group/Clade	Pinellas	Pinellas	Pinellas	Pinellas	Pinellas
Chlorinated substrate	VC	TCE	1,2,3-TCB ¹ & 1,2,4-	1,2,3-TCB	1,2-DCA
CRISPR-Cas type	I-E	I-E	I-E	I-E & I-C	I-C
<i>rdhA</i> genes	22	20	32	23	9
Characterized² RDases	VcrA, PceA	VcrA, PceA	MbrA, CbrA, PceA	MbrA, CbrA	BvcA
Genomic position of CRISPR-Cas (kbp)	1208	1176	1201	1318 (I-E)	276
				97 (I-C)	
No. of CRISPR spacers	41	37	19	28 (I-E)	38
				54 (I-C)	
NCBI accession number	CP019968	CP001924	AJ965256	CP004079	CP019946

¹1,2,3-trichlorobenzene (1,2,3-TCB). 1,2,4-trichlorobenzene (1,2,4-TCB) ² *characterized* indicates any RDase which has been at least partially biochemically characterized, not what is being expressed in culture by each strain.

Table S3. Potential targets of *Dehalococcoides mccartyi* KBVC1, KBDCA3, CBDB1, GT and DCMB5 CRISPRs. Results from BLAST searches: (1) against a database of KB-1 prophages and all *D. mccartyi* prophages from NCBI closed genomes and (2) against a database of all *D. mccartyi* genomes. A fasta file with all spacer sequences is provided in supplemental information separately from this excel file. GI: Genomic Island. Hit was listed in table if e-value < 1e⁻¹. *rdhA*-containing genomic islands (GI) are highlighted in red. New spacers acquired between 2002 and 2013 are highlighted in blue.

strain	CRISPR type	spacer #	FASTA name of spacer	spacer length (bp)	Type of mobile DNA which matched to spacer	<i>D.mccartyi</i> Mobile DNA name	BLAST hit length	% pairwise identity	e-value	Gene annotation of BLAST hit	best assignment for spacer
CBDB1	I-E	1	CBDB1_AJ965256_spacer_1	33	prophage	KBTCE1/KBVC2-12 prophage	16	93.8	3.22E-01	hypothetical protein	*
CBDB1	I-E	2	CBDB1_AJ965256_spacer_2	33	prophage	KBTCE1/KBVC2-12 prophage	13	100	3.03E-01	CBS-domain containing protein	*
CBDB1	I-E	3	CBDB1_AJ965256_spacer_3	34	IME1	IME1-13	32	96.9	2.50E-08	hypothetical protein	*
CBDB1	I-E	4	CBDB1_AJ965256_spacer_4	33	prophage	BTF08 prophage	13	100	3.03E-01	hypothetical protein	*
CBDB1	I-E	4	CBDB1_AJ965256_spacer_4	33	prophage	KBTCE1/KBVC2-12 prophage	13	100	3.03E-01	hypothetical protein	*
CBDB1	I-E	5	CBDB1_AJ965256_spacer_5	33	no hits						*
CBDB1	I-E	6	CBDB1_AJ965256_spacer_6	33	prophage	CG1 prophage	32	93.8	7.60E-09	endolysin	*
CBDB1	I-E	6	CBDB1_AJ965256_spacer_6	33	prophage	195 prophage	18	88.9	3.03E-01	hypothetical protein	*
CBDB1	I-E	6	CBDB1_AJ965256_spacer_6	33	prophage	195 prophage	21	85.7	3.03E-01	hypothetical protein	*
CBDB1	I-E	7	CBDB1_AJ965256_spacer_7	33	no hits						*
CBDB1	I-E	8	CBDB1_AJ965256_spacer_8	33	no hits						*
CBDB1	I-E	9	CBDB1_AJ965256_spacer_9	34	IME1	IME1-9	33	97	7.81E-09	hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	BTF08 prophage	25	96	3.94E-06	hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	CG1 prophage	33	97	1.79E-10	hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	pg11a5 prophage	25	96	3.94E-06	hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	KB1/cDCE-4 prophage	33	87.9	1.13E-06	non-coding hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	KB1/TCE-0 prophage	33	87.9	1.13E-06	hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	KBDCA1/KBDCA2-6 prophage	33	87.9	1.13E-06	hypothetical protein	*
CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	KBTCE1/KBVC2-1 prophage	33	87.9	1.13E-06	hypothetical protein	*

CBDB1	I-E	10	CBDB1_AJ965256_spacer_10	33	prophage	KBTCE1/KBVC2-5 prophage	33	87.9	1.13E-06	hypothetical protein	
CBDB1	I-E	11	CBDB1_AJ965256_spacer_11	34	prophage	CG1 prophage	27	92.6	1.61E-04	hypothetical protein	*
CBDB1	I-E	12	CBDB1_AJ965256_spacer_12	34	prophage	KBTCE1/KBVC2-11 prophage	13	100	3.22E-01	phage antirepressor	*
CBDB1	I-E	13	CBDB1_AJ965256_spacer_13	33	prophage	CG3 prophage	32	96.9	6.24E-10	non-coding	
CBDB1	I-E	13	CBDB1_AJ965256_spacer_13	33	prophage	KB1/cDCE-8 prophage	33	100	4.10E-12	hypothetical protein	*
CBDB1	I-E	14	CBDB1_AJ965256_spacer_14	33	no hits						*
CBDB1	I-E	15	CBDB1_AJ965256_spacer_15	33	no hits						*
CBDB1	I-E	16	CBDB1_AJ965256_spacer_16	33	prophage	KBTCE1/KBVC2-10 prophage	13	100	3.03E-01	phage tail protein	*
CBDB1	I-E	17	CBDB1_AJ965256_spacer_17	33	prophage	WBC-2 prophage	13	100	3.03E-01	non-coding	*
CBDB1	I-E	17	CBDB1_AJ965256_spacer_17	33	prophage	KBDCA1-9 prophage	13	100	3.03E-01	RNA polymerase	
CBDB1	I-E	17	CBDB1_AJ965256_spacer_17	33	prophage	KBTCE1/KBVC2-10 prophage	13	100	3.03E-01	RNA polymerase	
CBDB1	I-E	18	CBDB1_AJ965256_spacer_18	33	IME1	IME1-10	33	93.9	8.22E-08	non-coding	
CBDB1	I-E	18	CBDB1_AJ965256_spacer_18	33	IME1	IME1-11	33	93.9	8.22E-08	hypothetical protein	
CBDB1	I-E	18	CBDB1_AJ965256_spacer_18	33	IME1	IME1-12	33	97	8.22E-08	non-coding	
CBDB1	I-E	18	CBDB1_AJ965256_spacer_18	33	IME1	IME1-13	33	100	6.74E-09	non-coding	*
CBDB1	I-E	19	CBDB1_AJ965256_spacer_19	33	prophage	pg1a5 prophage	33	100	4.2E-12	hypothetical protein	
CBDB1	I-E	19	CBDB1_AJ965256_spacer_19	33	prophage	KB1/TCE-0 prophage	33	100	4.2E-12	hypothetical protein	*
CBDB1	I-E	19	CBDB1_AJ965256_spacer_19	33	prophage	KBDCA1/KBDCA2-6 prophage	33	100	4.2E-12	hypothetical protein	
CBDB1	I-E	19	CBDB1_AJ965256_spacer_19	33	prophage	KBTCE1/KBVC2-1 prophage	33	100	4.2E-12	hypothetical protein	
CBDB1	I-E	19	CBDB1_AJ965256_spacer_19	33	prophage	KBTCE1/KBVC2-5 prophage	33	100	4.2E-12	hypothetical protein	
DCMB5	I-C	1	DCMB5_CP004079_I-C_spacer_1	36	prophage	KBTCE1/KBVC2-12 prophage	25	84	2.95E-02	non-coding	*
DCMB5	I-E	1	DCMB5_CP004079_I-E_spacer_1	33	no hits						*
DCMB5	I-C	2	DCMB5_CP004079_I-C_spacer_2	35	no hits						*
DCMB5	I-E	2	DCMB5_CP004079_I-E_spacer_2	33	no hits						*
DCMB5	I-C	3	DCMB5_CP004079_I-C_spacer_3	33	no hits						*
DCMB5	I-E	3	DCMB5_CP004079_I-E_spacer_3	33	no hits						*
DCMB5	I-C	4	DCMB5_CP004079_I-C_spacer_4	34	no hits						*
DCMB5	I-E	4	DCMB5_CP004079_I-E_spacer_4	33	no hits						*
DCMB5	I-E	5	DCMB5_CP004079_I-E_spacer_5	33	IME1	IME1-13	32	100	7.70E-02	hypothetical protein	*
DCMB5	I-C	5	DCMB5_CP004079_I-C_spacer_5	34	no hits						*

DCMB5	I-E	6	DCMB5_CP004079_I-E_spacer_6	33	prophage	KB1/cDCE-4 prophage	33	100	4.20E-12	phage tail tape measure	
DCMB5	I-E	6	DCMB5_CP004079_I-E_spacer_6	33	prophage	KB1/cDCE-7 prophage	33	100	4.20E-12	phage tail tape measure	
DCMB5	I-E	6	DCMB5_CP004079_I-E_spacer_6	33	prophage	KB1/TCE-0 prophage	33	100	4.20E-12	phage tail tape measure	*
DCMB5	I-E	6	DCMB5_CP004079_I-E_spacer_6	33	prophage	KBDCA1/KBDCA2-6 prophage	33	100	4.20E-12	phage tail tape measure	
DCMB5	I-E	6	DCMB5_CP004079_I-E_spacer_6	33	prophage	KBTC1/KBVC2-1 prophage	33	100	4.20E-12	phage tail tape measure	
DCMB5	I-E	6	DCMB5_CP004079_I-E_spacer_6	33	prophage	KBTC1/KBVC2-5 prophage	33	100	4.20E-12	phage tail tape measure	
DCMB5	I-C	6	DCMB5_CP004079_I-C_spacer_6	34	no hits						*
DCMB5	I-C	7	DCMB5_CP004079_I-C_spacer_7	32	prophage	WBC-2 prophage	13	100	2.84E-01	s-adenosylmethionine synthetase	*
DCMB5	I-C	7	DCMB5_CP004079_I-C_spacer_7	32	prophage	KBTC1/KBVC2-12 prophage	12	100	9.90E-01	phage integrase	
DCMB5	I-C	7	DCMB5_CP004079_I-C_spacer_7	32	prophage	KBTC2-2 prophage	12	100	9.90E-01	phage terminase	
DCMB5	I-C	7	DCMB5_CP004079_I-C_spacer_7	32	prophage	KBTC3-3 prophage	12	100	9.90E-01	phage terminase	
DCMB5	I-E	7	DCMB5_CP004079_I-E_spacer_7	33	no hits						*
DCMB5	I-E	8	DCMB5_CP004079_I-E_spacer_8	33	prophage	KB1/cDCE-8 prophage	33	100	4.20E-12	hypothetical protein	*
DCMB5	I-C	8	DCMB5_CP004079_I-C_spacer_8	35	no hits						*
DCMB5	I-E	9	DCMB5_CP004079_I-E_spacer_9	33	IME1	IME1-12	33	100	1.59E-10	hypothetical protein	*
DCMB5	I-E	9	DCMB5_CP004079_I-E_spacer_9	33	IME1	IME1-8	31	100	1.93E-09	non-coding	
DCMB5	I-E	9	DCMB5_CP004079_I-E_spacer_9	33	IME1	IME1-9	33	100	1.59E-10	hypothetical protein	
DCMB5	I-E	9	DCMB5_CP004079_I-E_spacer_9	33	IME1	IME1-13	33	100	1.59E-10	hypothetical protein	
DCMB5	I-C	9	DCMB5_CP004079_I-C_spacer_9	35	prophage	BTF08 prophage	13	100	3.40E-01	DNA polymerase	*
DCMB5	I-E	9	DCMB5_CP004079_I-E_spacer_9	33	no hits						*
DCMB5	I-E	10	DCMB5_CP004079_I-E_spacer_10	33	prophage	KBTC2-2 prophage	13	13	3.03E-01	phage intergrase	*
DCMB5	I-E	10	DCMB5_CP004079_I-E_spacer_10	33	prophage	KBTC3-3 prophage	13	13	3.03E-01	phage intergrase	
DCMB5	I-C	10	DCMB5_CP004079_I-C_spacer_10	35	IME1	IME1-10	35	100	1.41E-11	hypothetical protein	*
DCMB5	I-C	10	DCMB5_CP004079_I-C_spacer_10	35	IME1	IME1-8	35	100	1.41E-11	hypothetical protein	
DCMB5	I-C	10	DCMB5_CP004079_I-C_spacer_10	35	IME1	IME1-8	17	100	8.34E-02	hypothetical protein	
DCMB5	I-C	10	DCMB5_CP004079_I-C_spacer_10	35	IME1	IME1-13	35	100	1.41E-11	hypothetical protein	
DCMB5	I-C	11	DCMB5_CP004079_I-C_spacer_11	32	no hits						*

DCMB5	I-E	11	DCMB5_CP004079_I-E_spacer_11	33	no hits						*
DCMB5	I-E	12	DCMB5_CP004079_I-E_spacer_12	33	prophage	BTF08 prophage	31	83.9	5.84E-04	portal protein	*
				33		KBTCE1/KBVC2-12				hypothetical	
DCMB5	I-E	12	DCMB5_CP004079_I-E_spacer_12	33	prophage	prophage	31	83.9	5.84E-04	protein	*
DCMB5	I-C	12	DCMB5_CP004079_I-C_spacer_12	30	no hits						*
				33		KBTCE1/KBVC2-11					
DCMB5	I-E	13	DCMB5_CP004079_I-E_spacer_13	33	prophage	prophage	12	100	3.03E-01	DNA primase	*
DCMB5	I-C	13	DCMB5_CP004079_I-C_spacer_13	34	no hits						*
DCMB5	I-E	14	DCMB5_CP004079_I-E_spacer_14	33	prophage	BTF08 prophage	21	90.5	8.67E-02	nuclease	
DCMB5	I-E	14	DCMB5_CP004079_I-E_spacer_14	33	prophage	KBDCA1-9 prophage	13	100	3.03E-01	nuclease	
				33		KBTCE1/KBVC2-10				hypothetical	
DCMB5	I-E	14	DCMB5_CP004079_I-E_spacer_14	33	prophage	prophage	13	100	3.03E-01	protein	*
DCMB5	I-C	14	DCMB5_CP004079_I-C_spacer_14	34	no hits						*
				34		KB1/cDCE-4 prophage	13	100	3.22E-01	hypothetical	
DCMB5	I-C	15	DCMB5_CP004079_I-C_spacer_15	34	prophage	prophage	13	100	3.22E-01	protein	*
				34		KB1/cDCE-7 prophage	13	100	3.22E-01	hypothetical	
DCMB5	I-C	15	DCMB5_CP004079_I-C_spacer_15	34	prophage	prophage	13	100	3.22E-01	protein	*
DCMB5	I-E	15	DCMB5_CP004079_I-E_spacer_15	33	no hits						*
DCMB5	I-C	16	DCMB5_CP004079_I-C_spacer_16	35	no hits						*
DCMB5	I-E	16	DCMB5_CP004079_I-E_spacer_16	33	no hits						*
				33		BTF08 prophage	18	94.4	2.48E-02	DNA polymerase	
DCMB5	I-E	17	DCMB5_CP004079_I-E_spacer_17	33	prophage	CG1 prophage	33	93.9	2.18E-09	phage terminase	
DCMB5	I-E	17	DCMB5_CP004079_I-E_spacer_17	33	prophage	CG3 prophage	33	93.9	2.18E-09	protein	
DCMB5	I-E	17	DCMB5_CP004079_I-E_spacer_17	33	IME- <i>vrA</i>	IME- <i>vrA</i> GT	13	100	5.36E-02	dsiB	*
DCMB5	I-E	17	DCMB5_CP004079_I-E_spacer_17	33	IME- <i>vrA</i>	IME- <i>vrA</i> KBVC1	13	100	5.36E-02	dsiB	
DCMB5	I-E	17	DCMB5_CP004079_I-E_spacer_17	33	IME- <i>vrA</i>	IME- <i>vrA</i> VS	13	100	5.36E-02	dsiB	
DCMB5	I-C	17	DCMB5_CP004079_I-C_spacer_17	37	no hits						*
DCMB5	I-C	18	DCMB5_CP004079_I-C_spacer_18	36	no hits						*
DCMB5	I-E	18	DCMB5_CP004079_I-E_spacer_18	33	no hits						*
DCMB5	I-C	19	DCMB5_CP004079_I-C_spacer_19	37	no hits						*
DCMB5	I-E	19	DCMB5_CP004079_I-E_spacer_19	33	no hits						*
				34		KBTCE1/KBVC2-1				hypothetical	
DCMB5	I-E	20	DCMB5_CP004079_I-E_spacer_20	34	prophage	prophage	34	100	4.92E-11	protein	
				34		KBTCE1/KBVC2-11				hypothetical	
DCMB5	I-E	20	DCMB5_CP004079_I-E_spacer_20	34	prophage	prophage	34	100	4.92E-11	protein	
				36		IME1-10	36	91.7	9.59E-08	hypothetical	
DCMB5	I-C	20	DCMB5_CP004079_I-C_spacer_20	36	IME1	IME1-10	36	91.7	9.59E-08	protein	*
				36		IME1-11	36	91.7	9.59E-08	hypothetical	
DCMB5	I-C	20	DCMB5_CP004079_I-C_spacer_20	36	IME1	IME1-11	36	91.7	9.59E-08	protein	
				36		IME1-10	36	91.7	9.59E-08	hypothetical	
DCMB5	I-C	20	DCMB5_CP004079_I-C_spacer_20	36	IME1	IME1-10	36	91.7	9.59E-08	protein	
DCMB5	I-C	21	DCMB5_CP004079_I-C_spacer_21	33	no hits						*
DCMB5	I-E	21	DCMB5_CP004079_I-E_spacer_21	34	no hits						*

DCMB5	I-E	22	DCMB5_CP004079_I-E_spacer_22	33	prophage	CG1 prophage	31	100	5.12E-11	prohead protease	*
DCMB5	I-E	22	DCMB5_CP004079_I-E_spacer_22	33	prophage	CG3 prophage	26	88.5	5.84E-04	hypothetical protein	*
DCMB5	I-C	22	DCMB5_CP004079_I-C_spacer_22	33	no hits						*
DCMB5	I-C	23	DCMB5_CP004079_I-C_spacer_23	33	unknown GI	KBDCA1	27	85.2	7.70E-01	hypothetical protein	*
DCMB5	I-C	23	DCMB5_CP004079_I-C_spacer_23	33	unknown GI	KBDCA2	27	85.2	7.70E-01	hypothetical protein	*
DCMB5	I-E	23	DCMB5_CP004079_I-E_spacer_23	33	no hits						*
DCMB5	I-C	24	DCMB5_CP004079_I-C_spacer_24	32	IME-OG19	IME-OG19 CG1	22	90.9	7.05E-02	<i>rdhA</i> OG19	*
DCMB5	I-C	24	DCMB5_CP004079_I-C_spacer_24	32	IME-OG19	IME-OG19 VS	22	90.9	7.05E-02	<i>rdhA</i> OG19	*
DCMB5	I-E	24	DCMB5_CP004079_I-E_spacer_24	33	no hits						*
DCMB5	I-E	25	DCMB5_CP004079_I-E_spacer_25	33	prophage	KBDCA1-9 prophage	25	84	3.03E-01	hypothetical protein	
DCMB5	I-E	25	DCMB5_CP004079_I-E_spacer_25	33	prophage	KBTCE1/KBVC2-10 prophage	25	84	3.03E-01	hypothetical protein	
DCMB5	I-E	25	DCMB5_CP004079_I-E_spacer_25	33	prophage	KBTCE1/KBVC2-11 prophage	25	84	3.03E-01	hypothetical protein	
DCMB5	I-E	25	DCMB5_CP004079_I-E_spacer_25	33	IME- <i>vrA</i>	IME- <i>vrA</i> KBVC1	12	100	1.87E-01	hypr-nap	*
DCMB5	I-C	25	DCMB5_CP004079_I-C_spacer_25	34	prophage	195 prophage	13	100	3.22E-01	phage terminase	*
DCMB5	I-C	26	DCMB5_CP004079_I-C_spacer_26	34	no hits						*
DCMB5	I-E	26	DCMB5_CP004079_I-E_spacer_26	33	no hits						*
DCMB5	I-E	27	DCMB5_CP004079_I-E_spacer_27	33	prophage	CG3 prophage	32	90.6	3.32E-07	hypothetical protein	
DCMB5	I-C	27	DCMB5_CP004079_I-C_spacer_27	34	prophage	KBTCE1/KBVC2-10 prophage	18	94.4	3.22E-01	non-coding	*
DCMB5	I-E	28	DCMB5_CP004079_I-E_spacer_28	33	prophage	CG1 prophage	33	90.6	9.26E-08	portal protein	*
DCMB5	I-C	28	DCMB5_CP004079_I-C_spacer_28	36	no hits						*
DCMB5	I-C	29	DCMB5_CP004079_I-C_spacer_29	33	prophage	KBTCE1/KBVC2-11 prophage	13	100	3.03E-01	hypothetical protein	*
DCMB5	I-C	30	DCMB5_CP004079_I-C_spacer_30	35	prophage	BTF08 prophage	13	100	3.40E-01	hypothetical protein	*
DCMB5	I-C	31	DCMB5_CP004079_I-C_spacer_31	34	no hits						*
DCMB5	I-C	32	DCMB5_CP004079_I-C_spacer_32	35	IME1	IME1-10	35	85.7	1.61E-04	hypothetical protein	*
DCMB5	I-C	32	DCMB5_CP004079_I-C_spacer_32	35	IME1	IME1-8	35	85.7	1.61E-04	hypothetical protein	*
DCMB5	I-C	32	DCMB5_CP004079_I-C_spacer_32	35	IME1	IME1-13	35	85.7	1.61E-04	hypothetical protein	*
DCMB5	I-C	33	DCMB5_CP004079_I-C_spacer_33	36	unknown GI	GT	18	100	2.57E-02	peptidase	
DCMB5	I-C	33	DCMB5_CP004079_I-C_spacer_33	36	unknown target	WBC-2	18	100	2.57E-02	TldD	
DCMB5	I-C	33	DCMB5_CP004079_I-C_spacer_33	36	unknown GI	11a5-GI	18	100	2.57E-02	TldD	*
DCMB5	I-C	34	DCMB5_CP004079_I-C_spacer_34	35	no hits						*
DCMB5	I-C	35	DCMB5_CP004079_I-C_spacer_35	34	no hits						*

DCMB5	I-C	36	DCMB5_CP004079_I-C_spacer_36	32	prophage	KB1/cDCE-7 prophage	18	94.4	2.84E-01	hypothetical protein	
DCMB5	I-C	36	DCMB5_CP004079_I-C_spacer_36	32	prophage	KB1/TCE-0 prophage	18	94.4	2.84E-01	hypothetical protein	
DCMB5	I-C	36	DCMB5_CP004079_I-C_spacer_36	32	prophage	KBDCA1/KBDCA2-6 prophage	18	94.4	2.84E-01	hypothetical protein	
DCMB5	I-C	36	DCMB5_CP004079_I-C_spacer_36	32	prophage	KBTCE1/KBVC2-1 prophage	18	94.4	2.84E-01	AMP-binding protein	
DCMB5	I-C	36	DCMB5_CP004079_I-C_spacer_36	32	prophage	KBTCE1/KBVC2-12 prophage	13	100	2.84E-01	hypothetical protein	*
DCMB5	I-C	36	DCMB5_CP004079_I-C_spacer_36	32	prophage	KBTCE1/KBVC2-5 prophage	18	94.4	2.84E-01	hypothetical protein	
DCMB5	I-C	37	DCMB5_CP004079_I-C_spacer_37	35	IME1	IME1-13	23	100	4.61E-05	hypothetical protein	*
DCMB5	I-C	38	DCMB5_CP004079_I-C_spacer_38	35	no hits						*
DCMB5	I-C	39	DCMB5_CP004079_I-C_spacer_39	34	no hits						*
DCMB5	I-C	40	DCMB5_CP004079_I-C_spacer_40	32	prophage	pg11a5 prophage	18	94.4	2.84E-01	hypothetical protein	*
DCMB5	I-C	41	DCMB5_CP004079_I-C_spacer_41	33	IME1	IME1-10	30	80	9.37E-01	hypothetical protein	*
DCMB5	I-C	41	DCMB5_CP004079_I-C_spacer_41	33	IME1	IME1-8	30	80	9.37E-01	hypothetical protein	
DCMB5	I-C	42	DCMB5_CP004079_I-C_spacer_42	32	prophage	BTF08 prophage	17	88.2	9.90E-01	hypothetical protein	*
DCMB5	I-C	42	DCMB5_CP004079_I-C_spacer_42	32	prophage	WBC-2 prophage	17	88.2	9.90E-01	hypothetical protein	
DCMB5	I-C	43	DCMB5_CP004079_I-C_spacer_43	31	prophage	BTF08 prophage	16	93.8	2.65E-01	hypothetical protein	*
DCMB5	I-C	43	DCMB5_CP004079_I-C_spacer_43	31	prophage	KBTCE2-2 prophage	16	93.8	2.65E-01	hypothetical protein	
DCMB5	I-C	43	DCMB5_CP004079_I-C_spacer_43	31	prophage	KBTCE3-3 prophage	16	93.8	2.65E-01	hypothetical protein	
DCMB5	I-C	44	DCMB5_CP004079_I-C_spacer_44	36	prophage	195 prophage	13	100	3.59E-01	adenine-specific methyltransferase	*
DCMB5	I-C	45	DCMB5_CP004079_I-C_spacer_45	35	no hits						*
DCMB5	I-C	46	DCMB5_CP004079_I-C_spacer_46	36	prophage	pg11a5 prophage	36	97.2	4.99E-12	hypothetical protein	*
DCMB5	I-C	46	DCMB5_CP004079_I-C_spacer_46	36	prophage	KB1/cDCE-4 prophage	36	97.2	4.99E-12	hypothetical protein	
DCMB5	I-C	46	DCMB5_CP004079_I-C_spacer_46	36	prophage	KB1/cDCE-7 prophage	36	97.2	4.99E-12	hypothetical protein	
DCMB5	I-C	47	DCMB5_CP004079_I-C_spacer_47	35	prophage	CG1 prophage	31	87.1	1.55E-05	hypothetical protein	

DCMB5	I-C	47	DCMB5_CP004079_I-C_spacer_47	35	prophage	CG3 prophage	32	87.5	4.43E-06	phage major capsid hypothetical	
DCMB5	I-C	47	DCMB5_CP004079_I-C_spacer_47	35	prophage	195 prophage	13	100	3.40E-01	protein	*
DCMB5	I-C	48	DCMB5_CP004079_I-C_spacer_48	34	no hits						*
DCMB5	I-C	49	DCMB5_CP004079_I-C_spacer_49	35	no hits						*
DCMB5	I-C	50	DCMB5_CP004079_I-C_spacer_50	37	no hits						*
DCMB5	I-C	51	DCMB5_CP004079_I-C_spacer_51	32	no hits						*
						KBTCE1/KBVC2-11 prophage				hypothetical protein	
DCMB5	I-C	52	DCMB5_CP004079_I-C_spacer_52	30	prophage		12	100	8.58E-01		*
DCMB5	I-C	53	DCMB5_CP004079_I-C_spacer_53	35	no hits						*
										hypothetical protein	
DCMB5	I-C	54	DCMB5_CP004079_I-C_spacer_54	36	prophage	CG3 prophage	13	100	3.59E-01	phage tape measure	*
GT	I-E	1	GT_CP001924_spacer_1	31	prophage	195 prophage	17	88.2	9.24E-01		*
GT	I-E	2	GT_CP001924_spacer_2	32	no hits						*
										hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	pg11a5 prophage	12	100	9.90E-01	protease	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KB1/cDCE-4 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KB1/cDCE-7 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KB1/TCE-0 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KBDCA1/KBDCA2-6 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KBTCE1/KBVC2-1 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KBTCE1/KBVC2-11 prophage	21	85.7	2.84E-01	hypothetical protein	*
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KBTCE1/KBVC2-5 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KBTCE2-2 prophage	12	100	9.90E-01	hypothetical protein	
GT	I-E	3	GT_CP001924_spacer_3	32	prophage	KBTCE3-3 prophage	12	100	9.90E-01	protease	
GT	I-E	4	GT_CP001924_spacer_4	33	no hits						*
GT	I-E	5	GT_CP001924_spacer_5	32	prophage	CG1 prophage	32	90.6	3.03E-07	phage terminase hypothetical	*
GT	I-E	5	GT_CP001924_spacer_5	32	prophage	CG3 prophage	32	90.6	3.03E-07	protein	
GT	I-E	6	GT_CP001924_spacer_6	32	no hits						*
										hypothetical protein	
GT	I-E	7	GT_CP001924_spacer_7	32	prophage	KBTCE2-2 prophage	12	100	9.90E-01	hypothetical protein	*
GT	I-E	7	GT_CP001924_spacer_7	32	prophage	KBTCE3-3 prophage	12	100	9.90E-01	protein	
GT	I-E	8	GT_CP001924_spacer_8	32	no hits						*
GT	I-E	9	GT_CP001924_spacer_9	32	prophage	KB1/cDCE-8 prophage	32	100	1.38E-11	non-coding	*

GT	I-E	10	GT_CP001924_spacer_10	32	prophage	CG3 prophage	12	100	9.90E-01	hypothetical protein	*
GT	I-E	11	GT_CP001924_spacer_11	32	prophage	WBC-2 prophage	14	100	8.13E-02	hypothetical protein	*
GT	I-E	11	GT_CP001924_spacer_11	32	prophage	KBDCA1-9 prophage	14	100	8.13E-02	phage terminase	
GT	I-E	11	GT_CP001924_spacer_11	32	prophage	KBTCE1/KBVC2-10 prophage	14	100	8.13E-02	phage terminase	
GT	I-E	11	GT_CP001924_spacer_11	32	prophage	KBTCE1/KBVC2-11 prophage	14	100	8.13E-02	phage terminase	
GT	I-E	12	GT_CP001924_spacer_12	32	IME- <i>vcrA</i>	IME- <i>vcrA</i> KBVC2	14	92.9	6.19E-01	dsiB	*
GT	I-E	13	GT_CP001924_spacer_13	32	prophage	195 prophage	12	100	9.90E-01	phage integrase	*
GT	I-E	14	GT_CP001924_spacer_14	32	unknown GI	CG1 GI	24	87.5	2.46E-01	hypothetical protein	*
GT	I-E	15	GT_CP001924_spacer_15	32	prophage	BTF08 prophage	32	84.4	1.57E-04	hypothetical protein	*
GT	I-E	15	GT_CP001924_spacer_15	32	prophage	KBDCA1-9 prophage	16	93.8	2.84E-01	non-coding	
GT	I-E	15	GT_CP001924_spacer_15	32	prophage	KBTCE1/KBVC2-10 prophage	16	93.8	2.84E-01	phage terminase	
GT	I-E	15	GT_CP001924_spacer_15	32	prophage	KBTCE1/KBVC2-11 prophage	16	93.8	2.84E-01	non-coding	
GT	I-E	15	GT_CP001924_spacer_15	32	prophage	KBTCE1/KBVC2-12 prophage	32	84.4	1.57E-04	non-coding	
GT	I-E	16	GT_CP001924_spacer_16	33	prophage	CG1 prophage	33	87.9	1.13E-06	phage terminase	*
GT	I-E	16	GT_CP001924_spacer_16	33	prophage	CG3 prophage	33	87.9	1.13E-06	hypothetical protein	
GT	I-E	17	GT_CP001924_spacer_17	33	unknown GI	BAV1 GI	22	90.9	7.70E-02	hypothetical protein	*
GT	I-E	18	GT_CP001924_spacer_18	32	no hits						*
GT	I-E	19	GT_CP001924_spacer_19	32	prophage	BTF08 prophage	18	94.4	2.33E-02	DNA polymerase	
GT	I-E	19	GT_CP001924_spacer_19	32	prophage	CG1 prophage	32	93.8	7.12E-09	phage terminase	*
GT	I-E	19	GT_CP001924_spacer_19	32	prophage	CG3 prophage	32	93.8	7.12E-09	hypothetical protein	
GT	I-E	20	GT_CP001924_spacer_20	32	IME1	IME1-14	32	94.4	8.59E-01	hypothetical protein	*
GT	I-E	21	GT_CP001924_spacer_21	32	no hits						*
GT	I-E	22	GT_CP001924_spacer_22	32	prophage	BTF08 prophage	21	90.5	8.13E-02	nuclease	
GT	I-E	22	GT_CP001924_spacer_22	32	prophage	KBDCA1-9 prophage	13	100	2.84E-01	nuclease	
GT	I-E	22	GT_CP001924_spacer_22	32	prophage	KBTCE1/KBVC2-10 prophage	13	100	2.84E-01	hypothetical protein	*
GT	I-E	23	GT_CP001924_spacer_23	32	prophage	KBTCE1/KBVC2-11 prophage	13	100	2.84E-01	DNA primase	*
GT	I-E	24	GT_CP001924_spacer_24	32	prophage	BTF08 prophage	28	85.7	5.84E-04	DNA polymerase I	

GT	I-E	24	GT_CP001924_spacer_24	32	prophage	KBTCE1/KBVC2-12 prophage	28	85.7	5.84E-04	DNA polymerase I	
GT	I-E	24	GT_CP001924_spacer_24	32	prophage	KBTCE2-2 prophage	15	93.3	9.90E-01	phage portal protein	*
GT	I-E	24	GT_CP001924_spacer_24	32	prophage	KBTCE3-3 prophage	15	93.3	9.90E-01	phage portal protein	
GT	I-E	25	GT_CP001924_spacer_25	32	no hits						*
GT	I-E	26	GT_CP001924_spacer_26	32	prophage	KBTCE2-2 prophage	13	100	2.84E-01	phage integrase	*
GT	I-E	26	GT_CP001924_spacer_26	32	prophage	KBTCE3-3 prophage	13	100	2.84E-01	phage integrase	
GT	I-E	27	GT_CP001924_spacer_27	32	IME1	IME1-13	32	100	5.07E-10	hypothetical protein	*
GT	I-E	28	GT_CP001924_spacer_28	32	no hits						*
GT	I-E	29	GT_CP001924_spacer_29	33	no hits						*
GT	I-E	30	GT_CP001924_spacer_30	32	no hits						*
GT	I-E	31	GT_CP001924_spacer_31	32	prophage	KBTCE1/KBVC2-12 prophage	13	100	2.84E-01	non-coding	*
GT	I-E	32	GT_CP001924_spacer_32	33	no hits						*
GT	I-E	33	GT_CP001924_spacer_33	33	IME1	IME1-13	33	100	1.59E-10	hypothetical protein	*
GT	I-E	34	GT_CP001924_spacer_34	32	no hits						*
GT	I-E	35	GT_CP001924_spacer_35	31	prophage	KBTCE1/KBVC2-10 prophage	13	100	2.65E-01	hypothetical protein	
GT	I-E	35	GT_CP001924_spacer_35	31	prophage	KBTCE2-2 prophage	12	100	9.24E-01	hypothetical protein	
GT	I-E	35	GT_CP001924_spacer_35	31	prophage	KBTCE3-3 prophage	12	100	9.24E-01	hypothetical protein	
GT	I-E	35	GT_CP001924_spacer_35	32	prophage	KBDCA1-9 prophage	13	100	2.65E-01	hypothetical protein	*
GT	I-E	36	GT_CP001924_spacer_36	32	no hits						*
GT	I-E	37	GT_CP001924_spacer_37	32	prophage	CG3 prophage	12	100	9.90E-01	hypothetical protein	*
KBDCA3	I-C	1	KBDCA3_CP019946_spacer_1	34	no hits						*
KBDCA3	I-C	2	KBDCA3_CP019946_spacer_2	34	prophage	KBTCE2-2 prophage	12	100	8.01E-01	phage protein	*
KBDCA3	I-C	2	KBDCA3_CP019946_spacer_2	34	prophage	KBTCE3-3 prophage	12	100	8.01E-01	phage protein	
KBDCA3	I-C	3	KBDCA3_CP019946_spacer_3	34	prophage	KBDCA1/KBDCA2-6 prophage	12	100	8.01E-01	phage tape measure	
KBDCA3	I-C	3	KBDCA3_CP019946_spacer_3	34	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.01E-01	phage tape measure	*
KBDCA3	I-C	3	KBDCA3_CP019946_spacer_3	34	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.01E-01	phage tape measure	
KBDCA3	I-C	3	KBDCA3_CP019946_spacer_3	34	prophage	KBTCE1/KBVC2-5 prophage	12	100	8.01E-01	hypothetical protein	
KBDCA3	I-C	4	KBDCA3_CP019946_spacer_4	31	no hits						*
KBDCA3	I-C	5	KBDCA3_CP019946_spacer_5	33	prophage	pg11a5 prophage	12	100	7.56E-01	hypothetical protein	*

KBDCA3	I-C	5	KBDCA3_CP019946_spacer_5	33	prophage	195 prophage	12	100	7.56E-01	phage protein	
KBDCA3	I-C	5	KBDCA3_CP019946_spacer_5	33	prophage	KBTC1/KBVC2-1 prophage	12	100	7.56E-01	hypothetical protein	
KBDCA3	I-C	6	KBDCA3_CP019946_spacer_6	35	unknown GI	BTF08 GI	25	92	1.96E-03	transcriptional repressor LexA	
KBDCA3	I-C	6	KBDCA3_CP019946_spacer_6	35	prophage	CG1 prophage	24	91.7	6.84E-03	transcriptional regulator	*
KBDCA3	I-C	6	KBDCA3_CP019946_spacer_6	35	prophage	CG1 prophage	12	100	8.45E-01	hypothetical protein	
KBDCA3	I-C	6	KBDCA3_CP019946_spacer_6	35	unknown GI	11a5-GI	25	92	1.96E-03	phage tape	
KBDCA3	I-C	7	KBDCA3_CP019946_spacer_7	35	prophage	195 prophage	15	93.3	8.45E-01	measure reductive dehalogenase OG	*
KBDCA3	I-C	8	KBDCA3_CP019946_spacer_8	34	IME-OG49	DCMB5 GI <i>rdhA</i> containing	29	90.9	8.34E-02	49	*
KBDCA3	I-C	9	KBDCA3_CP019946_spacer_9	34	IME- <i>vcrA</i>	IME- <i>vcrA</i> KBVC2	12	100	1.87E-01	parBc	*
KBDCA3	I-C	10	KBDCA3_CP019946_spacer_10	35	no hits						*
KBDCA3	I-C	11	KBDCA3_CP019946_spacer_11	34	prophage	pg11a5 prophage	26	84.6	6.57E-02	phage terminase	*
KBDCA3	I-C	12	KBDCA3_CP019946_spacer_12	34	no hits						*
KBDCA3	I-C	13	KBDCA3_CP019946_spacer_13	35	IME1	IME1-11	18	94.4	8.73E-01	DsiB	*
KBDCA3	I-C	13	KBDCA3_CP019946_spacer_13	35	IME1	IME1-8	18	94.4	8.73E-01	DsiB	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	195 prophage	12	100	8.90E-01	hypothetical protein	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	IME1	IME1-13	35	94.3	7.87E-09	hypothetical protein	*
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KB1/cDCE-4 prophage	22	86.4	2.55E-01	non-coding hypothetical	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBDCA1/KBDCA2-6 prophage	22	86.4	2.55E-01	hypothetical protein	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-1 prophage	17	88.2	8.90E-01	hypothetical protein	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-1 prophage	22	86.4	2.55E-01	hypothetical protein	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-1 prophage	22	86.4	2.55E-01	hypothetical protein	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-10 prophage	15	93.3	8.90E-01	hypothetical protein	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-11 prophage	15	93.3	8.90E-01	phage tape	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-11 prophage	15	93.3	8.90E-01	measure phage tape	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	prophage	KBTC1/KBVC2-5 prophage	22	86.4	2.55E-01	measure phage tape	
KBDCA3	I-C	14	KBDCA3_CP019946_spacer_14	36	IME- <i>tceA</i>	IME- <i>tceA</i>	36	91.7	9.59E-08	phage portal protein	
KBDCA3	I-C	15	KBDCA3_CP019946_spacer_15	34	no hits						*

KBDC A3	I-C	16	KBDC A3_CP019946_spacer_16	34	prophage	KBTC E2-2 prophage	12	100	8.01E-01	site-specific recombinase	*
KBDC A3	I-C	16	KBDC A3_CP019946_spacer_16	34	prophage	KBTC E3-3 prophage	12	100	8.01E-01	site-specific recombinase	
KBDC A3	I-C	17	KBDC A3_CP019946_spacer_17	35	no hits						*
KBDC A3	I-C	18	KBDC A3_CP019946_spacer_18	34	prophage	CG1 prophage	12	100	8.01E-01	major capsid protein	*
KBDC A3	I-C	19	KBDC A3_CP019946_spacer_19	34	no hits						*
KBDC A3	I-C	20	KBDC A3_CP019946_spacer_20	33	prophage	KB1/cDCE-4 prophage	33	87.9	8.08E-07	hypothetical protein	
KBDC A3	I-C	20	KBDC A3_CP019946_spacer_20	33	prophage	KBDC A1/KBDC A2-6 prophage	33	87.9	8.08E-07	hypothetical protein	
KBDC A3	I-C	20	KBDC A3_CP019946_spacer_20	33	prophage	KBTC E1/KBVC2-1 prophage	33	87.9	8.08E-07	hypothetical protein	*
KBDC A3	I-C	20	KBDC A3_CP019946_spacer_20	33	prophage	KBTC E1/KBVC2-1 prophage	33	87.9	8.08E-07	hypothetical protein	
KBDC A3	I-C	21	KBDC A3_CP019946_spacer_21	34	IME1	IME1-9	34	100	4.92E-11	hypothetical protein	*
KBDC A3	I-C	21	KBDC A3_CP019946_spacer_21	34	prophage	KBDC A1/KBDC A2-6 prophage	12	100	8.01E-01	phage prohead protease	
KBDC A3	I-C	21	KBDC A3_CP019946_spacer_21	34	prophage	KBTC E1/KBVC2-1 prophage	12	100	8.01E-01	phage prohead protease	
KBDC A3	I-C	21	KBDC A3_CP019946_spacer_21	34	prophage	KBTC E1/KBVC2-1 prophage	12	100	8.01E-01	phage prohead protease	
KBDC A3	I-C	21	KBDC A3_CP019946_spacer_21	34	prophage	KBTC E1/KBVC2-5 prophage	12	100	8.01E-01	phage prohead protease	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	unknown GI	195 GI	35	85.7	1.60E-04	DNA primase	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-14	35	85.7	1.60E-04	dsiB	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-10	35	100	1.41E-11	hypothetical protein	*
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-11	35	85.7	1.60E-04	phage tape measure	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-8	35	100	1.41E-11	hypothetical protein	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-8	35	85.7	1.60E-04	phage tape measure	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-9	35	85.7	1.60E-04	phage tape measure	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-13	35	100	1.41E-11	hypothetical protein	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	IME1	IME1-13	35	85.7	1.60E-04	hypothetical protein	
KBDC A3	I-C	22	KBDC A3_CP019946_spacer_22	35	prophage	KBDC A1/KBDC A2-6 prophage	12	100	8.45E-01	hypothetical protein	

KBDCA3	I-C	22	KBDCA3_CP019946_spacer_22	35	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.45E-01	hypothetical protein	
KBDCA3	I-C	22	KBDCA3_CP019946_spacer_22	35	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.45E-01	hypothetical protein	
KBDCA3	I-C	22	KBDCA3_CP019946_spacer_22	35	prophage	KBTCE1/KBVC2-5 prophage	12	100	8.45E-01	hypothetical protein	
KBDCA3	I-C	22	KBDCA3_CP019946_spacer_22	35	IME- <i>vcrA</i>	IME- <i>vcrA</i> GT	14	92.9	6.88E-01	hypothetical protein	
KBDCA3	I-C	22	KBDCA3_CP019946_spacer_22	35	IME- <i>vcrA</i>	IME- <i>vcrA</i> KBVC1	14	92.9	6.88E-01	dsiB	
KBDCA3	I-C	22	KBDCA3_CP019946_spacer_22	35	IME- <i>vcrA</i>	IME- <i>vcrA</i> WBC-2	14	92.9	6.88E-01	dsiB	
KBDCA3	I-C	23	KBDCA3_CP019946_spacer_23	36	prophage	KBTCE2-2 prophage	16	100	6.00E-03	hypothetical protein	*
KBDCA3	I-C	23	KBDCA3_CP019946_spacer_23	36	prophage	KBTCE3-3 prophage	16	100	6.00E-03	hypothetical protein	
KBDCA3	I-C	24	KBDCA3_CP019946_spacer_24	36	prophage	BTF08 prophage	12	100	7.65E-01	phage tape measure	
KBDCA3	I-C	24	KBDCA3_CP019946_spacer_24	36	prophage	KBTCE1/KBVC2-12 prophage	12	100	8.90E-01	non-coding hypothetical protein	
KBDCA3	I-C	24	KBDCA3_CP019946_spacer_24	36	prophage	KBTCE2-2 prophage	14	100	7.30E-02	hypothetical protein	*
KBDCA3	I-C	24	KBDCA3_CP019946_spacer_24	36	prophage	KBTCE2-2 prophage	15	93.3	8.90E-01	non-coding hypothetical protein	
KBDCA3	I-C	24	KBDCA3_CP019946_spacer_24	36	prophage	KBTCE3-3 prophage	14	100	7.30E-02	hypothetical protein	
KBDCA3	I-C	24	KBDCA3_CP019946_spacer_24	36	prophage	KBTCE3-3 prophage	15	93.3	8.90E-01	hypothetical protein	
KBDCA3	I-C	25	KBDCA3_CP019946_spacer_25	36	no hits						*
KBDCA3	I-C	26	KBDCA3_CP019946_spacer_26	34	prophage	195 prophage	12	100	8.01E-01	hypothetical protein	
KBDCA3	I-C	26	KBDCA3_CP019946_spacer_26	34	IME1	IME1-9	20	90	9.35E-01	phage DNA helicase	*
KBDCA3	I-C	27	KBDCA3_CP019946_spacer_27	32	IME1	IME1-13	32	100	5.07E-10	hypothetical protein	*
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	pg11a5 prophage	12	100	7.12E-01	hypothetical protein	*
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KB1/cDCE-4 prophage	12	100	7.12E-01	hypothetical protein	
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KBDCA1/KBDCA2-6 prophage	12	100	7.12E-01	hypothetical protein	
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KBTCE1/KBVC2-1 prophage	12	100	7.12E-01	hypothetical protein	
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KBTCE1/KBVC2-1 prophage	12	100	7.12E-01	hypothetical protein	
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KBTCE1/KBVC2-5 prophage	12	100	7.12E-01	hypothetical protein	
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KBTCE1/KBVC2-5 prophage	12	100	7.12E-01	hypothetical protein	
KBDCA3	I-C	28	KBDCA3_CP019946_spacer_28	32	prophage	KBTCE2-2 prophage	12	100	7.12E-01	phage terminase	

KBDC A3	I-C	28	KBDC A3_CP019946_spacer_28	32	prophage	KBTCE3-3 prophage	12	100	7.12E-01	phage terminase	
KBDC A3	I-C	29	KBDC A3_CP019946_spacer_29	34	prophage	KB1/cDCE-4 prophage	12	100	8.01E-01	hypothetical protein	
KBDC A3	I-C	29	KBDC A3_CP019946_spacer_29	34	prophage	KBDC A1/KBDC A2-6 prophage	12	100	8.01E-01	phage related protein	
KBDC A3	I-C	29	KBDC A3_CP019946_spacer_29	34	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.01E-01	hypothetical protein	*
KBDC A3	I-C	29	KBDC A3_CP019946_spacer_29	34	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.01E-01	hypothetical protein	
KBDC A3	I-C	30	KBDC A3_CP019946_spacer_30	35	prophage	KB1/cDCE-4 prophage	12	100	8.45E-01	hypothetical protein	
KBDC A3	I-C	30	KBDC A3_CP019946_spacer_30	35	prophage	KBDC A1/KBDC A2-6 prophage	12	100	8.45E-01	phage related protein	
KBDC A3	I-C	30	KBDC A3_CP019946_spacer_30	35	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.45E-01	hypothetical protein	*
KBDC A3	I-C	30	KBDC A3_CP019946_spacer_30	35	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.45E-01	hypothetical protein	
KBDC A3	I-C	31	KBDC A3_CP019946_spacer_31	36	IME1	IME1-10	36	100	3.72E-12	hypothetical protein	*
KBDC A3	I-C	31	KBDC A3_CP019946_spacer_31	36	IME1	IME1-8	36	100	3.72E-12	hypothetical protein	
KBDC A3	I-C	32	KBDC A3_CP019946_spacer_32	35	IME1	IME1-10	26	88.5	2.05E-02	hypothetical protein	*
KBDC A3	I-C	32	KBDC A3_CP019946_spacer_32	35	IME1	IME1-11	26	88.5	2.05E-02	hypothetical protein	
KBDC A3	I-C	32	KBDC A3_CP019946_spacer_32	35	IME1	IME1-9	26	88.5	2.05E-02	hypothetical protein	
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	IME1	IME1-8	33	97	6.28E-09	phage protein	*
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	prophage	KBDC A1/KBDC A2-6 prophage	12	100	8.45E-01	phage protein	
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.45E-01	non-coding	
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	prophage	KBTCE1/KBVC2-1 prophage	12	100	8.45E-01	phage portal protein	
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	prophage	KBTCE1/KBVC2-5 prophage	12	100	8.45E-01	phage portal protein	
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	prophage	KBTCE2-2 prophage	27	81.5	8.45E-01	phage portal protein	
KBDC A3	I-C	33	KBDC A3_CP019946_spacer_33	35	prophage	KBTCE3-3 prophage	27	81.5	8.45E-01	phage portal protein	
KBDC A3	I-C	34	KBDC A3_CP019946_spacer_34	34	prophage	KBTCE2-2 prophage	16	93.8	1.97E-01	phage tape measure	*
KBDC A3	I-C	34	KBDC A3_CP019946_spacer_34	34	prophage	KBTCE3-3 prophage	16	93.8	1.97E-01	phage tape measure	
KBDC A3	I-C	35	KBDC A3_CP019946_spacer_35	35	no hits						*

KBVC1	I-E	9	KBVC1_CP019968_spacer_9	32	IME1	IME1-13	32	100	5.07E-10	hypothetical protein	
KBVC1	I-E	9	KBVC1_CP019968_spacer_9	32	prophage	KBTCE2-2 prophage	12	100	7.12E-01	hypothetical protein	
KBVC1	I-E	9	KBVC1_CP019968_spacer_9	32	prophage	KBTCE3-3 prophage	12	100	7.12E-01	hypothetical protein	
KBVC1	I-E	10	KBVC1_CP019968_spacer_10	32	IME1	IME1-11	32	96.6	1.72E-08	hypothetical protein	
KBVC1	I-E	10	KBVC1_CP019968_spacer_10	32	IME1	IME1-8	32	100	4.05E-10	hypothetical protein	*
KBVC1	I-E	11	KBVC1_CP019968_spacer_11	32	prophage	CG1 prophage	31	96.8	7.53E-08	hypothetical protein	
KBVC1	I-E	11	KBVC1_CP019968_spacer_11	32	prophage	KB1/cDCE-8 prophage	32	100	9.89E-12	hypothetical protein	*
KBVC1	I-E	12	KBVC1_CP019968_spacer_12	32	no hits						*
KBVC1	I-E	13	KBVC1_CP019968_spacer_13	32	no hits						*
KBVC1	I-E	14	KBVC1_CP019968_spacer_14	32	no hits						*
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	prophage	195 prophage	12	100	7.12E-01	hypothetical protein	
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME1	IME1-10	32	96.9	2.16E-08	hypothetical protein	*
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME1	IME1-10	32	93.8	2.63E-07	hypothetical protein	
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME1	IME1-8	32	93.8	2.63E-07	hypothetical protein	
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME1	IME1-8	32	93.8	2.63E-07	hypothetical protein	
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME1	IME1-8	32	93.8	2.63E-07	hypothetical protein	
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME1	IME1-13	32	90.6	1.12E-05	phage integrase	
KBVC1	I-E	15	KBVC1_CP019968_spacer_15	32	IME- <i>tceA</i>	IME- <i>tceA</i>	32	93.8	2.63E-07	hypothetical protein	
KBVC1	I-E	16	KBVC1_CP019968_spacer_16	32	IME1	IME1-10	32	96.6	1.72E-08	non-coding	
KBVC1	I-E	16	KBVC1_CP019968_spacer_16	32	IME1	IME1-8	32	96.6	1.72E-08	non-coding	
KBVC1	I-E	16	KBVC1_CP019968_spacer_16	32	IME1	IME1-8	32	93.8	2.10E-07	non-coding	*
KBVC1	I-E	17	KBVC1_CP019968_spacer_17	32	prophage	BTF08-2 prophage	32	84.4	1.13E-04	hypothetical protein	*
KBVC1	I-E	17	KBVC1_CP019968_spacer_17	32	prophage	KBTCE1/KBVC2-10 prophage	16	93.8	2.04E-01	hypothetical protein	
KBVC1	I-E	17	KBVC1_CP019968_spacer_17	32	prophage	KBTCE1/KBVC2-11 prophage	16	93.8	2.04E-01	hypothetical protein	
KBVC1	I-E	17	KBVC1_CP019968_spacer_17	32	prophage	KBTCE1/KBVC2-12 prophage	32	84.4	1.13E-04	hypothetical protein	
KBVC1	I-E	17	KBVC1_CP019968_spacer_17	32	prophage	KBTCE1/KBVC2-12 prophage	32	84.4	1.13E-04	phage terminase	

KBVC1	I-E	18	KBVC1_CP019968_spacer_18	33	prophage	CG1 prophage	33	87.9	8.08E-07	major capsid protein	*
KBVC1	I-E	18	KBVC1_CP019968_spacer_18	33	prophage	KBDCA1/KBDCA2-6 prophage	15	93.3	7.56E-01	major capsid protein	
KBVC1	I-E	18	KBVC1_CP019968_spacer_18	33	prophage	KBTC1/KBVC2-1 prophage	15	93.3	7.56E-01	phage terminase	
KBVC1	I-E	18	KBVC1_CP019968_spacer_18	33	prophage	KBTC1/KBVC2-1 prophage	15	93.3	7.56E-01	major capsid protein	
KBVC1	I-E	18	KBVC1_CP019968_spacer_18	33	prophage	KBTC1/KBVC2-5 prophage	15	93.3	7.56E-01	major capsid protein	
KBVC1	I-E	19	KBVC1_CP019968_spacer_19	33	unknown GI	BAV1 GI	22	90.9	7.70E-02	hypothetical protein	*
KBVC1	I-E	20	KBVC1_CP019968_spacer_20	32	prophage	KBTC2-2 prophage	12	100	7.12E-01	phage portal protein	*
KBVC1	I-E	20	KBVC1_CP019968_spacer_20	32	prophage	KBTC3-3 prophage	12	100	7.12E-01	phage portal protein	
KBVC1	I-E	21	KBVC1_CP019968_spacer_21	32	no hits						*
KBVC1	I-E	22	KBVC1_CP019968_spacer_22	32	prophage	CG1 prophage	32	93.8	5.12E-09	phage terminase	*
KBVC1	I-E	22	KBVC1_CP019968_spacer_22	32	prophage	CG1 prophage	32	93.8	2.63E-07	terminase	
KBVC1	I-E	22	KBVC1_CP019968_spacer_22	32	IME- <i>vcrA</i>	IME- <i>vcrA</i> GT	13	100	5.08E-02	dsiB	
KBVC1	I-E	22	KBVC1_CP019968_spacer_22	32	IME- <i>vcrA</i>	IME- <i>vcrA</i> KBVC1	13	100	5.08E-02	dsiB	
KBVC1	I-E	23	KBVC1_CP019968_spacer_23	32	no hits						*
KBVC1	I-E	24	KBVC1_CP019968_spacer_24	32	no hits						*
KBVC1	I-E	25	KBVC1_CP019968_spacer_25	32	no hits						*
KBVC1	I-E	26	KBVC1_CP019968_spacer_26	32	no hits						*
KBVC1	I-E	27	KBVC1_CP019968_spacer_27	32	prophage	BTF08-2 prophage	28	85.7	3.94E-04	hypothetical protein	*
KBVC1	I-E	27	KBVC1_CP019968_spacer_27	32	prophage	KBTC1/KBVC2-12 prophage	28	85.7	3.94E-04	DNA polymerase I	
KBVC1	I-E	27	KBVC1_CP019968_spacer_27	32	prophage	KBTC1/KBVC2-12 prophage	28	85.7	3.94E-04	DNA polymerase I	
KBVC1	I-E	27	KBVC1_CP019968_spacer_27	32	prophage	KBTC2-2 prophage	15	93.3	7.12E-01	hypothetical protein	
KBVC1	I-E	27	KBVC1_CP019968_spacer_27	32	prophage	KBTC3-3 prophage	15	93.3	7.12E-01	phage portal protein	
KBVC1	I-E	28	KBVC1_CP019968_spacer_28	32	no hits						*
KBVC1	I-E	29	KBVC1_CP019968_spacer_30	32	prophage	KBTC2-2 prophage	13	100	2.04E-01	phage integrase	
KBVC1	I-E	29	KBVC1_CP019968_spacer_29	32	no hits						*
KBVC1	I-E	30	KBVC1_CP019968_spacer_30	32	IME1	IME1-13	32	100	5.07E-10	hypothetical protein	*
KBVC1	I-E	30	KBVC1_CP019968_spacer_30	32	prophage	KBTC3-3 prophage	13	100	2.04E-01	phage integrase	
KBVC1	I-E	31	KBVC1_CP019968_spacer_31	32	no hits						*
KBVC1	I-E	32	KBVC1_CP019968_spacer_32	33	no hits						*
KBVC1	I-E	33	KBVC1_CP019968_spacer_33	32	IME- <i>vcrA</i>	IME- <i>vcrA</i> GT	19	89.5	1.46E-02	dsiB	*
KBVC1	I-E	33	KBVC1_CP019968_spacer_33	32	IME- <i>vcrA</i>	IME- <i>vcrA</i> KBVC1	19	89.5	1.46E-02	dsiB	

KBVC1	I-E	33	KBVC1_CP019968_spacer_33	32	IME- <i>verA</i>	IME- <i>verA</i> WBC-2	19	89.5	1.46E-02	dsiB	
KBVC1	I-E	34	KBVC1_CP019968_spacer_34	32	no hits						*
KBVC1	I-E	35	KBVC1_CP019968_spacer_35	33	no hits						*
KBVC1	I-E	36	KBVC1_CP019968_spacer_36	33	IME1	IME1-13	33	100	1.59E-10	hypothetical protein	*
KBVC1	I-E	37	KBVC1_CP019968_spacer_37	32	no hits						*
KBVC1	I-E	38	KBVC1_CP019968_spacer_38	31	prophage	KBTCE2-2 prophage	12	100	6.67E-01	hypothetical protein	*
KBVC1	I-E	38	KBVC1_CP019968_spacer_38	31	prophage	KBTCE3-3 prophage	12	100	6.67E-01	hypothetical protein	*
KBVC1	I-E	39	KBVC1_CP019968_spacer_39	32	no hits						*
KBVC1	I-E	40	KBVC1_CP019968_spacer_40	32	no hits						*
KBVC1	I-E	41	KBVC1_CP019968_spacer_41	34	no hits						*

Table S5. Integrative Mobilizable Elements (IMEs) found targeted by the CRISPR systems of *D. mccartyi* KBVC1 and KBDCA3. Nucleotide sequences in File S5.

<i>D. mccartyi</i> host strain	circularized?	evidence for circularization	type	name	notes
<i>D. mccartyi</i> contigs from metagenome	yes	Illumina sequencing: mate-pair and paired-end	IME1	Dmc IME1-1	
<i>D. mccartyi</i> contigs from metagenome	yes	Illumina sequencing: mate-pair and paired-end	IME1	Dmc IME1-2	
<i>D. mccartyi</i> contigs from metagenome			IME1	Dmc IME1-3	
<i>D. mccartyi</i> contigs from metagenome			IME1	Dmc IME1-4	
<i>D. mccartyi</i> contigs from metagenome			IME1	Dmc IME1-5	
<i>D. mccartyi</i> contigs from metagenome			IME1	Dmc IME1-6	
<i>D. mccartyi</i> contigs from metagenome			IME1	Dmc IME1-7	
KBTCE2			IME1	Dmc IME1-8	
KBVC1	yes	Illumina sequencing: mate-pair and paired-end	IME1	Dmc IME1-9	
KBDCA1			IME1	Dmc IME1-10	
KBDCA1			IME1	Dmc IME1-11	
KBDCA2			IME1	Dmc IME1-12	
WBC-2			IME1	Dmc IME1-13	
BAV1			IME1	Dmc IME1-14	
195	yes	published as tandem repeat	IME1	Dmc IME1-15	
11a5			IME2	Dmc IME2	no <i>rdhA</i>
BAV1			<i>rdhA</i> containing IME	Dmc IME-OG24	<i>rdhA</i> containing
DCMB5			<i>rdhA</i> containing IME	Dmc IME-OG49	<i>rdhA</i> containing
KBVC1, KBVC2, KBTCE1, WBC-2	yes	1) Illumina sequencing: mate-pair and paired-end 2) qPCR plus PCR	<i>rdhA</i> containing IME	Dmc IME-vcrA	<i>rdhA</i> containing
195, KBTCE2, KBTCE3		sequence alignments indicate mobilization in last 100 years	<i>rdhA</i> containing IME	Dmc IME-tceA	<i>rdhA</i> containing

Table S6. IME1-like constructs found in other bacteria whose genomes are available in NCBI

Phylum	Class	Species	NCBI Accession	# plasmids published on NCBI	# IME1-like constructs in genome	is IME1-like construct adjacent to prophage	CRISPR type if present	Do CRISPR spacers have matches to IME1-like sequence?
Proteo.	Betaproteo.	<i>Nitrosomonas communis</i>	NZ_CP011451.1	0	1	no		
Proteo.	Betaproteo.	<i>Paucibacter</i> sp. KCTC	NZ_CP013692.1	0	1	yes		
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> FJACT-1458	NZ_CP016554.1	1 MP	3	no		
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> FJAT-91	NZ_CP016612.1	1 MP	4	no		
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> CMR15	NC_017559.1	1+ 1 MP	1	no		
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> p082	NC_017574.1	1 MP	1	yes	CAS-I-E	yes
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> pS107	NC_014311.1	1 MP	1	yes		
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> GM1000	NC_003295.1	1 MP	2	yes		
Proteo.	Betaproteo.	<i>Ralstonia solanacearum</i> OE1-1	NZ_CP009764.1	1 MP	1	yes		
Proteo.	Betaproteo.	<i>Hydrogenophaga</i> sp. PBC	NZ_CP017311.1	0	2	tandem duplicate		
Proteo.	Betaproteo.	<i>Rugosibacter aromaticivorans</i>	CP010554.1	0	1	yes		
Proteo.	Betaproteo.	<i>Janthinobacterium marseille</i>	NC_009659.1	0	1	yes		
Proteo.	Betaproteo.	<i>Acidovorax ebreus</i>	NC_011992.1	0	1	yes		
Proteo.	Betaproteo.	<i>Burkholderiales bacterium</i> GJ-E10	NZ_AP014683.1	0	1	yes		
Proteo.	Betaproteo.	<i>Comamonadaceae bacterium</i> B1	NZ_AP014569.1	1	1	yes		
Proteo.	Betaproteo.	<i>Cupriavidus gilardii</i>	NZ_CP010516.1	0	1	yes		
Proteo.	Betaproteo.	<i>Polyangium brachysporum</i>	NZ_CP011371.1	0	1	yes		
Proteo.	Betaproteo.	<i>Variovorax</i> sp. HW608	NZ_LT607803.1	0	1	yes		
Proteo.	Betaproteo.	<i>Alicyclophilus denitrificans</i> K601	NC_015422.1	1	1	yes	CAS-II-C	no
Proteo.	Betaproteo.	<i>Burkholderia vietnamiensis</i> G4	CP000614.1	5	1	yes		
Proteo.	Gammaproteo.	<i>Hahella chejunsis</i>	NC_007645.1	0	1	yes	CAS-I-C	no
Proteo.	Gammaproteo.	<i>Stenotrophomonas maltophilia</i> K279a	NC_010943.1	2	1	yes		
Proteo.	Gammaproteo.	<i>Lysobacter gummosus</i>	NZ_CP011131.1	0	1	yes		
Proteo.	Gammaproteo.	<i>Xanthomonas albilineans</i>	NC_013722.1	3	1	yes	CAS-I-C and I-F	yes
Proteo.	Deltaproteo.	<i>Desulfovibrio vulgaris</i> DP4	NC_008751.1	1	1	yes		

Proteo.	Deltaproteo.	<i>Desulfarculus baarsii</i>	NC_014365.1	0	1	yes	CAS-I-C and III-D CAS-I-E	no
Proteo.	Deltaproteo.	<i>Geobacter sulfurreducens</i> AM-1	NZ_CP010430.1	0	1	yes	and I-U	no
Proteo.	Acidithiobacillia	<i>Acidithiobacillus caldus</i> ATCC 51756	NZ_CP005986.1	2 + 1 MP	1	yes	CAS-IV-A	no
Nitro.	Nitrospira	<i>Nitrospira defluvii</i>	NC_014355.1	0	1	yes	CAS-I-E	no

Proteo-Proteobacteria, Nitro-Nitrospirae, MP- Megaplasmid

Table S7. Quantitative PCR (qPCR) raw data used to make Figure 5 & S8. *Dhc* - *Dehalococcoides mccartyi*. DNA extracts from 2mL culture.

Sub-culture	Day	See Figure in text	number of qPCR reactions <i>vcrA</i>	number of qPCR reactions <i>Dhc</i>	Raw data - Mean Starting Quantity (copies/uL) or calculated as range if from 2 qPCR reactions		Concentration in culture (copies/mL culture)		Ratio
					<i>vcrA</i>	<i>Dhc</i> 16S rRNA	<i>vcrA</i>	<i>Dhc</i> 16S rRNA	<i>vcrA/Dhc</i>
KB1/VC-ME b	0	5	3	2	3.98E+06	3.33E+06	1.99E+09	1.67E+09	1.2
KB1/VC-ME b	2	5	2	3	3.06E+06	2.54E+06	1.53E+09	1.27E+09	1.2
KB1/VC-ME b	5	5	3	2	4.52E+06	3.35E+06	2.26E+09	1.67E+09	1.3
KB1/VC-ME b	7	5	3	3	4.33E+06	3.64E+06	2.17E+09	1.82E+09	1.2
KB1/VC-ME b	9	5	2	3	4.47E+06	3.62E+06	2.23E+09	1.81E+09	1.2
KB1/VC-ME b	12	5	2	3	3.49E+06	2.97E+06	1.75E+09	1.48E+09	1.2
KB1/VC-ME b	16	5	3	3	3.76E+06	3.20E+06	1.88E+09	1.60E+09	1.2
KB1/VC-ME b	19	5	3	2	3.99E+06	3.37E+06	2.00E+09	1.69E+09	1.2
KB1/VC-ME b	21	5	3	2	3.72E+06	3.19E+06	1.86E+09	1.59E+09	1.2
KB1/VC-ME b	23	5	3	2	6.28E+06	3.31E+06	3.14E+09	1.66E+09	1.9
KB1/VC-ME b	26	5	2	2	7.32E+06	3.49E+06	3.66E+09	1.75E+09	2.1
KB1/VC-ME b	30	5	3	3	5.64E+06	3.39E+06	2.82E+09	1.70E+09	1.7
KB1/VC-ME b	35	5	2	2	5.30E+06	3.32E+06	2.65E+09	1.66E+09	1.6
KB1/VC-ME b	37	5	3	3	5.68E+06	3.79E+06	2.84E+09	1.90E+09	1.5
KB1/VC-ME b	40	5	3	3	4.50E+06	3.46E+06	2.25E+09	1.73E+09	1.3
KB1/VC-ME c	0	S8 (b)	3	3	4.76E+06	3.82E+06	2.38E+09	1.91E+09	1.2
KB1/VC-ME c	2	S8 (b)	3	3	4.72E+06	3.65E+06	2.36E+09	1.82E+09	1.3
KB1/VC-ME c	5	S8 (b)	3	2	5.25E+06	5.08E+06	2.62E+09	2.54E+09	1.0
KB1/VC-ME c	7	S8 (b)	3	2	6.06E+06	5.91E+06	3.03E+09	2.96E+09	1.0
KB1/VC-ME c	9	S8 (b)	3	3	4.94E+06	5.08E+06	2.47E+09	2.54E+09	1.0
KB1/VC-ME c	12	S8 (b)	3	2	4.76E+06	3.70E+06	2.38E+09	1.85E+09	1.3
KB1/VC-ME c	16	S8 (b)	3	3	4.57E+06	3.83E+06	2.28E+09	1.91E+09	1.2
KB1/VC-ME c	19	S8 (b)	3	3	2.75E+06	2.76E+06	1.37E+09	1.38E+09	1.0

KB1/VC-ME c	21	S8 (b)	3	3	4.17E+06	2.37E+06	2.09E+09	1.19E+09	1.8
KB1/VC-ME c	23	S8 (b)	3	3	5.48E+06	3.49E+06	2.74E+09	1.74E+09	1.6
KB1/VC-ME c	26	S8 (b)	3	3	5.85E+06	3.58E+06	2.93E+09	1.79E+09	1.6
KB1/VC-ME c	30	S8 (b)	3	3	6.91E+06	4.26E+06	3.45E+09	2.13E+09	1.6
KB1/VC-ME c	35	S8 (b)	3	3	5.08E+06	3.35E+06	2.54E+09	1.68E+09	1.5
KB1/VC-ME c	37	S8 (b)	3	3	3.99E+06	2.46E+06	1.99E+09	1.23E+09	1.6
KB1/VC-ME c	40	S8 (b)	3	3	5.10E+06	3.50E+06	2.55E+09	1.75E+09	1.5
KB1/VC-ME a	0	S8 (a)	3	3	3.26E+06	2.71E+06	1.63E+09	1.36E+09	1.2
KB1/VC-ME a	2	S8 (a)	3	2	3.36E+06	2.72E+06	1.68E+09	1.36E+09	1.2
KB1/VC-ME a	5	S8 (a)	3	3	4.56E+06	2.87E+06	2.28E+09	1.44E+09	1.6
KB1/VC-ME a	7	S8 (a)	3	2	5.24E+06	2.81E+06	2.62E+09	1.40E+09	1.9
KB1/VC-ME a	9	S8 (a)	3	2	4.63E+06	2.94E+06	2.31E+09	1.47E+09	1.6
KB1/VC-ME a	12	S8 (a)	3	3	3.19E+06	2.58E+06	1.59E+09	1.29E+09	1.2
KB1/VC-ME a	16	S8 (a)	3	2	3.13E+06	2.24E+06	1.56E+09	1.12E+09	1.4
KB1/VC-ME a	19	S8 (a)	3	2	3.16E+06	2.14E+06	1.58E+09	1.07E+09	1.5
KB1/VC-ME a	21	S8 (a)	3	3	2.74E+06	1.86E+06	1.37E+09	9.32E+08	1.5
KB1/VC-ME a	23	S8 (a)	3	3	3.13E+06	2.09E+06	1.56E+09	1.05E+09	1.5
KB1/VC-ME a	30	S8 (a)	3	3	5.08E+06	2.24E+06	2.54E+09	1.12E+09	2.3
KB1/VC-ME a	35	S8 (a)	3	2	3.26E+06	2.49E+06	1.63E+09	1.25E+09	1.3
KB1/VC-ME a	40	S8 (a)	3	2	3.44E+06	3.06E+06	1.72E+09	1.53E+09	1.1

Table S8. Details of standard curves generated for qPCR including slope, efficiency, R2, and Y-intercepts. *Dhc* - *Dehalococcoides mccartyi*

Run #	Samples quantified	gene target	slope	y-intercept	efficiency	R ²
1	KB1/VC-ME a day 0-12	<i>Dhc</i> 16S rRNA	-3.905	38.2	80.3	0.997
1	KB1/VC-ME a day 0-12	<i>vcrA</i>	-3.910	39.9	80.2	0.998
2	KB1/VC-ME a day 16-40	<i>Dhc</i> 16S rRNA	-3.918	39.0	80.0	0.999
2	KB1/VC-ME a day 16-40	<i>vcrA</i>	-3.908	39.7	80.3	0.993
3	KB1/VC-ME b day 0-40	<i>Dhc</i> 16S rRNA	-3.916	41.4	80.0	0.998
3	KB1/VC-ME b day 0-40	<i>vcrA</i>	-3.907	43.4	80.3	1.000
4	KB1/VC-ME c day 0-16	<i>Dhc</i> 16S rRNA	-3.841	39.5	80.7	1.000
4	KB1/VC-ME c day 0-16	<i>vcrA</i>	-3.917	40.3	80.0	0.999
5	KB1/VC-ME c day 19-40	<i>Dhc</i> 16S rRNA	-3.912	40.7	80.1	0.996
5	KB1/VC-ME c day 19-40	<i>vcrA</i>	-3.741	42.6	85.0	0.996

References for Supplemental Information

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3. Fineran PC, Gerritzen MJH, Suárez-Diez M, Künne T, Boekhorst J, van Hijum SAFT, Staals RHJ, Brouns SJJ. Degenerate target sites mediate rapid primed CRISPR adaptation. *Proc Natl Acad Sci USA.* 2014;111(16):E1629-E38.