

Fig. S1. RAST assignment of gene distribution in different categories in *D. mccartyi* strain JNA and six other *D. mccartyi* strains

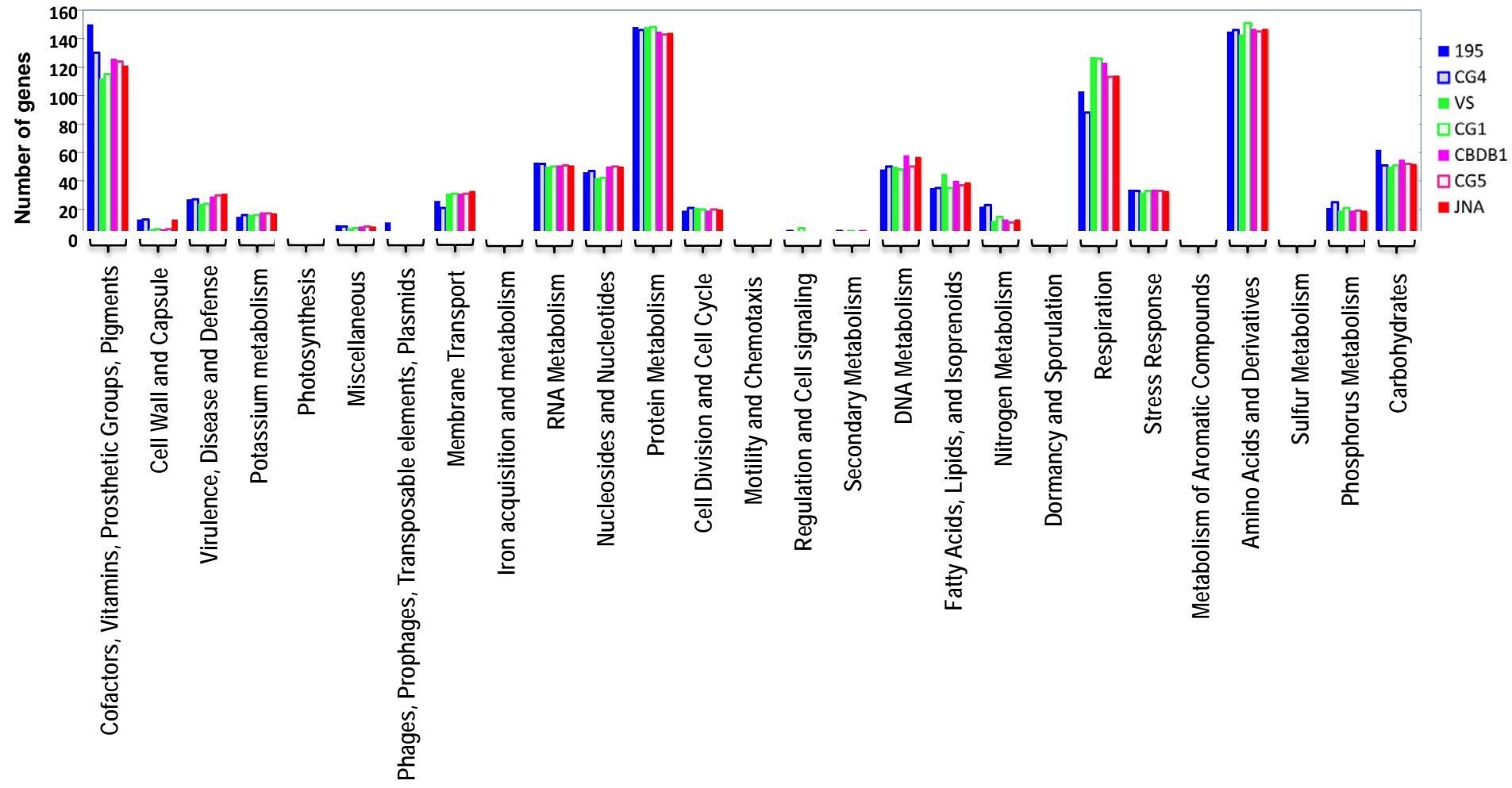


Fig. S2. Relationship of partial *rdhA* gene sequence in JNA genome with two previously identified *rdhA* genes in strain JNA. The only partial RDase gene sequence (396 bp) retrieved from the JNA draft genome shares 100% sequence identity (in red) with the 3' ends of JNA_RD5 (accession ID KJ580603) and JNA_RD6 (accession ID KJ580604) gene sequences.

>JNA_RD5/6 (396 bp)

TTGCTGCCACTCGCCCATAGACTTGGTGCCTACAAATTCTGAAACCTGCGGTATTGCGCGGATGCTTGCCTTCGGGCTTATCCAGAAGGGTACCCCCACCTGGAAAACCCGGCT
TCAGCCAAGTCCGGCATTCACTGGCACATTGAGGGCTGGCAACCAATACCGCAGATTGCTCTACTGCCAACCTGTCAGGGCAGTGCCTTCAACAGCAAACCGGATTCACTCCT
GCATGCTGTGGTTAAGGGCACAGTGCCAATACCCGCTTTAAATAGCTTACAATATGGAAAAGCTATGGATTACGGCGAAAAGACCCGAAGAGTGGTGGATATGGATGAC
TTTACCTACGGTATTGACACCAGTTACTAA

>JNA *rdhA5* (KJ580603) putative reductive dehalogenase (*rdhA5*) and putative reductive dehalogenase membrane anchor protein (*rdhB5*) genes

GCCTGGGGTAGTCGGAGCAGGTTGGTACTATGAGCGCTGCTGCCCTGTTTCCACGATTGGATGAGGTACGTCTCAACCCCTGGTATCAATAAAAATCCTGGTGGTAAAGGAAAG
GGATTTCAGAATCCTACAGTCCCTATAGACTGGTCAAAAGTTACCCGTACGCCGGGTGATTTCAGGGTCTGCCAGACCCACTGTAGCTGATTTCACAAAAGCCGGTTGCGCGGTACTT
CCACTGACCTTGAACCCCTGAAATGGCCCTGACTCTTATGATGCCATGCCAAGGAGTTCCGGGCTGGACTCCCGCTATGCCGTATGGGTGACGTAGGACTACCTCACTGCAATGCT
TCCAAATTATGATGATGGTGCCTGGCCGGCAATATGGAAATGGCGTAAAGGATTAATGTTATGCCGTATTATGCCGCCGGCAGCCCTACCTTACTCCGTGGTGGGGCCTC
AGCTGGATACTACTACCCGTCCCCAGGATTCCGGGCTCCGGTCTGGCAGGGTACTCCGAAGAAAACCTAAACCTGCCCTCTGCCCTCAGATTCTTGGCGCTGGATGTGGGTGCTATT
GAAATTGACGACGATGTTCTAAATTATCCATTCCCAGATTGGCGTAAAGCTGAGTCGTTGAAGACGTAGAGGAAGCTATGAGACCACAACCAAGATGGTTATCCCCGCAAGTGCAAGT
GGATACTTATGTGGAGGCCAGACAGTCACTCGAAGCTACCAGCAGCCAGGCATAACCGAAAGTCATGCTGTTGGTATTATCCCCTCCCAAGGTAGGTGCCAGTCCAGGA
ATTATCCGGGTTGGTTATCAGGCCCTGAATCCGGCATGATGGCTTTGGCTAATCCTTAGCAGCTTAGCCGGTATGGCGAACATGCCGATGCTTCACCCACCATCCTCCAA
ATACGGCACAACTAACCGGGTATGTGGCGTTAACCGACCTGCCATTGCTGCCACTCCGCCATAGACTTGGTGCCTACAAATTCTGAAAACCTGCCGTATTGCGGGATGCTTGCT
CTTCCGGCTTACAGAAGGGTACCCACCTGGAAAACCCGGCTCAGCCAAGTCCGGCATTCACTGGCAGGGCACATTGAGGGCTGGCAACCAATACCGCAGATTGCTCTACTGCCAC
CTGTCAGGGACTTGCCTCAACAGCAAACCGATTCACTGCTGTTAAGGGCACAGTGCCAATACCCGCTTTAAATAGCTTACAATATGGAAAAGCTATGGATTA
CGGGCAAAAGACCCGAAGAGTGGTGGATATGGATGACTTACCTACGGTATTGACACCAGTTACTAATAGCTTAAGGAATTGGAGGTAGGAAGCATGTTTCTGAGACTGGCAGTAGC
AGTCGCCCTGACTGTTGTTGGCTTACCGCCGGCAGCTGGTATAAG

> JNA *rdhA6* (KJ580604) putative reductive dehalogenase (*rdhA6*) and putative reductive dehalogenase membrane anchor protein (*rdhB6*) genes

CTTGGGGTAGTCGGAGCAGGTTGGTACTATGAGCGCTGCTGCCCTGTTTCCACGATTGGATGAGGTACGTCTCAACCCCTGGTATCAATAAAAATCCTGGTGGTAAAGGAAAGGG
ATTCAAAATCCTACCGTACCAATGGATTGGCCCAAATTACCGCCATGCCGGCACGTTAAGACTTACCCAGACCCACTGTAGCTGATTTCACAAAAGCCGGTTGCGCGGTACTTCC
ACTGACCTTGAACCCCTGAAATGGCCCTGACTCTTATGATGCCATGCCAAGGAGTTCCGGGCTGGACTCCGGCTATGCCGTATGGGTGACGTAGGACTACCTCACTGCAATGCTTCC
CAAATTATGATGATGGGTGCCTGGCCGGCAATATGGAAATGGCGTAAAGGATTAATGTTCAAGCGGCTATTATGCCGCCGGCAGCCCTACCTTACTCCGTGGTGGGGCCTCA
GCTGGATACTACTACCCGTCCCCAGGATTCCGGGCTCCGGTCTGGCAGGGTACTCCGAAGAAAACCTAAACCTGCCCTCTGCCCTCAGATTCTTGGCGCTGGATGTGGCAGCCCTG
AACTTGATGACGATATTTGAAGTTTTCACTCTAAATTGGTGGTAAAGACCTGGTTGAAGACGTAGAGGAAGCTTATGAGACCGCAACCAAGATGGTTATCCCCGCAAGTGCAAGTG
GGTACTGATGGAGTGCCAGACAATCTCTGAGGGCACTCGTCGCCAGGCTGGTATAACTGAAAATATGCTGCTGGTATTCTTATTCCGCCCTGCCAAGGTAGGTGTGCAGTCCAGGAA
TTTATCCCGCGTTGGTTATCAGGCCCTGAATCCGGGAATGAAGGGTACCTTACCAAGCCCTGCCGGCTTTCCGGCATGGCGAACATGCCGTATGTCTTACCCACTATCACTCCCAA
TACGGGGTAACCAACCGGGCTATGTGGGCCATGATTACCGACCTGCCCTTGCTGCCACTCCGCCATAGACTTGGTGCCTACAAATTCTGAAAACCTGCCGTATTGCGGGATGCTTGCT
TTTCCGGCTTACAGAAGGGTACCCACCTGGAAAACCCGGCTCAGCCAAGTCCGGCATTCACTGGCAGGGCACATTGAGGGCTGGCAACCAATACCGCAGATTGCTCTACTGCCAC
TGTCACTGCCCTCAACAGCAAACCGGATTCACTGCTGATGCTGTTAAGGGCACAGTGGCAATACCCGCTTTAAATAGCTTACAATATGGAAAAGCTATGGATTAC
GGCGAAAAGACCCGAAGAGTGGTGGATATGGATGACTTACCTACGGTATTGACACCAGTTACTAA

Fig. S3. Phylogeny of RdhA protein sequences in *D. mccartyi* strain JNA and seven other *D. mccartyi* strains. Maximum likelihood tree of deduced amino acid sequences of all full-length RdhAs from the eight strains were analyzed, and the two RDases that potentially catalyze chlorine removal from PCE and PCBs in strain JNA are marked with green solid circles. Scale bar indicates the number of substitutions per site.

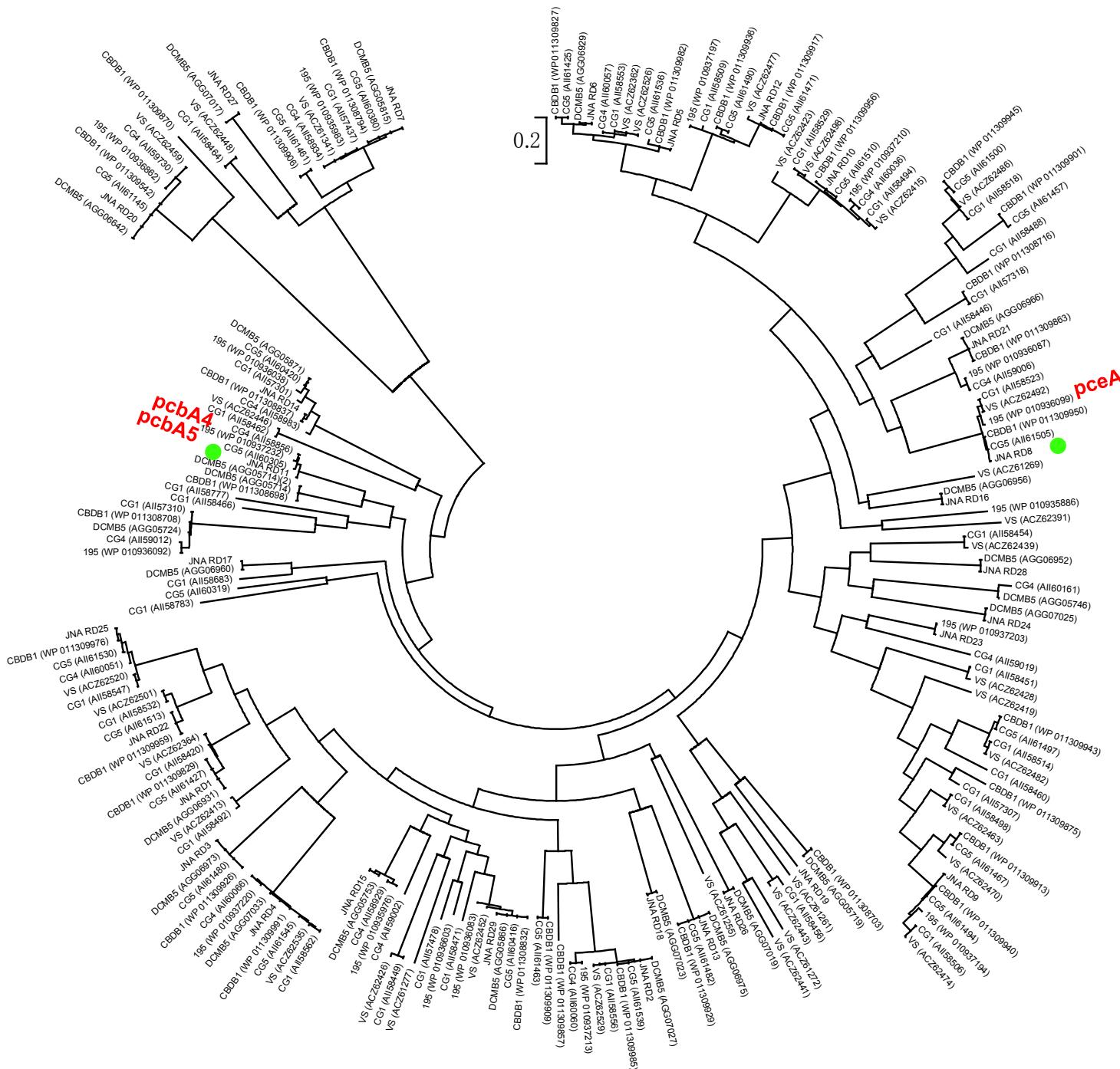


Fig. S4. RT-PCR screening of all *rdhA* genes in strain JNA cells with gene-specific primers to identify which genes are transcribed when JNA is grown on PCE. The cDNA samples converted from RNA at different PCE dechlorination stages (the sampling time can be seen in Fig. 3A) were mixed together for the PCR screening (red labels). Positive control PCR reactions (green labels) were run with genomic DNA as templates, and the negative controls (white labels) without templates.

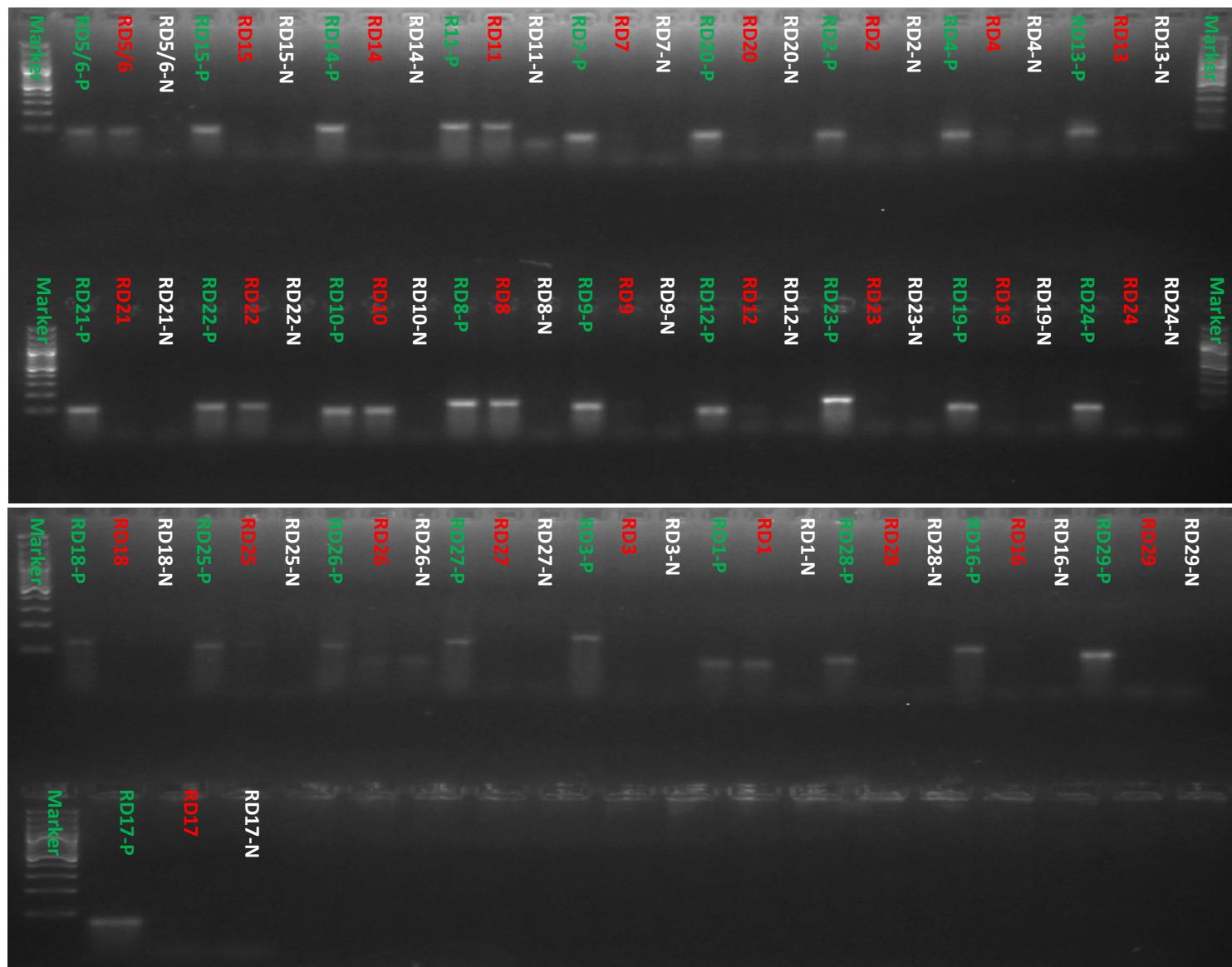


Fig. S5. Transcription of JNA_RD8 and JNA_RD11 genes is associated with PCB dechlorination in *D. mccartyi* strain JNA. (A) Reductive dechlorination of 2345-245-CB to 235-245-CB and 245-245-CB in strain JNA; (B) Transcription profiles of JNA_RD8 and JNA_RD11 genes in strain JNA cells grown with 2345-245-CB. The RNA samples for day 0 were collected 3 hours after inoculation. Cells were not starved, so the transcription at day 0 reflects transcripts for genes involved in the dechlorination of TCE to DCEs. This transcription likely decreased greatly over time because this dechlorination would have been completed by day 30 before the PCB dechlorination began.

