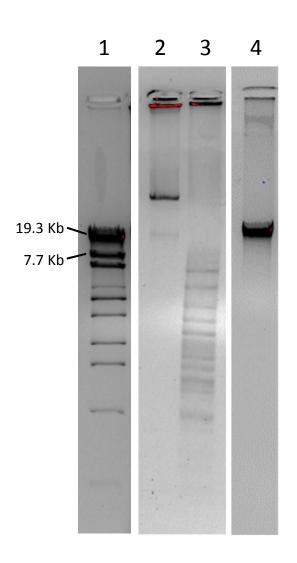
Supplemental document 5: Plasmid maps

- Extraction of plasmid DNA from strain GP59
- Methylophaga nitratireducenticrescens GP59
 - Plasmid pGP32 (GenBank accession # CP021975)
 - Plasmid pGP34 (CP021974)
- Methylophaga frappieri JAM7
 - Plasmid pJAM7-48 (CP003381)

Extraction of plasmid DNA from strain GP59



- 1- Marker
- 2- Undigested plasmid DNA
- 3- Plasmid DNA digested with Rsal
- 4- Genomic DNA

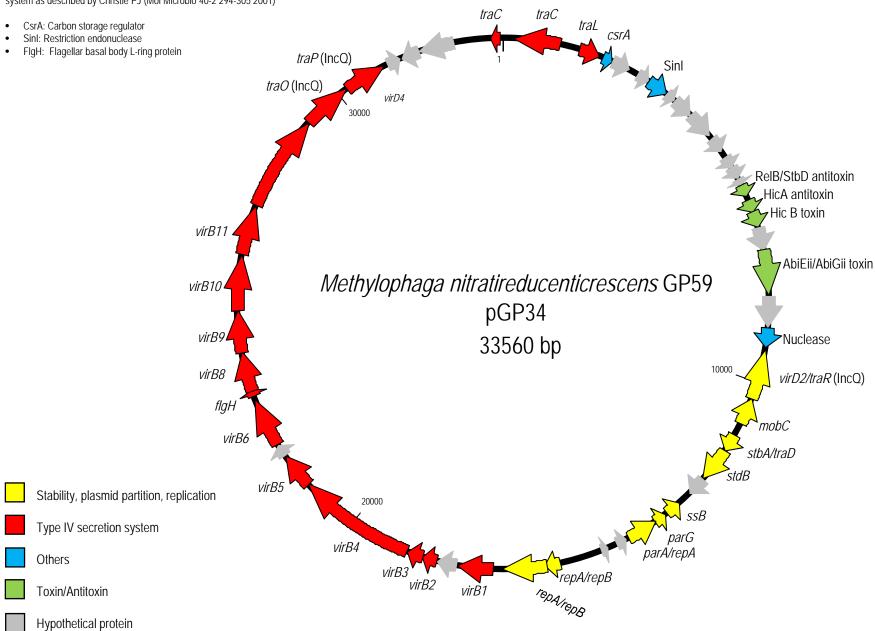
Plasmid DNA was extracted from GP59 cultures by the alkaline lysis protocol, digested with the restriction endonuclease *Rsa*I and ran on a 1% agarose gel electrophoresis. The gel was stained with GelRed to reveal DNA (1).

1-Sambrook JF, Russell DW (ed.). 2001. Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press

Gene annotations were performed by RAST. Further analyses were performed by BLASTP in protein data bases. Type IV secretion system nomenclature (Vir) is based on the T-DNA transfer system as described by Christie PJ (Mol Microbio 40-2 294-305 2001) parA parB putative recombinase CsrA: Carbon storage regulator PilL: conjugative pilus protein FtsH ParAB: plasmid partitioning protein traL RepB: plasmid replication initiator protein virB10 XerD: Site-specific recombinase AraC: transcriptional regulator RadC: DNA repair protein MarR: transcriptional regulator virB9 FtsH: cell division protein, ATP-dependent zinc metalloprotease virB8 **DNA-Cystein** virB6 methyltransferase Methylophaga nitratireducenticrescens GP59 YefM antotoxin YoeB toxin virB5 pGP32 csrA 32421 bp virB4 DNA N6 methyltransferase L virB2 xerD Stability, plasmid partition, replication 20000 virB11 Nuclease Type IV secretion system araC Others MarR toxin/Antitoxin virD4

Hypothetical protein

Gene annotations were performed by RAST. Further analyses were performed by BLASTP, in protein data bases
Type IV secretion system nomenclature (Vir) is based on the T-DNA transfer system as described by Christie PJ (Mol Microbio 40-2 294-305 2001)



Gene annotations were performed by GenBank (NCBI) and by RAST. Further analyses were performed by BLASTP in protein

Gene nomenclature is based on the Pseudomonas aeruginosa IncP alpha plasmid pBS228 (Haines, A.S., Jones, K., Batt, S.M., Kosheleva, I.A. and Thomas, C.M. Sequence of plasmid pBS228 and reconstruction of the Incp-1alpha phylogeny plasmid 58 (1), 76-83 (2007), except for the « Others » which were deduced from protein database analysis (BLASTP).

