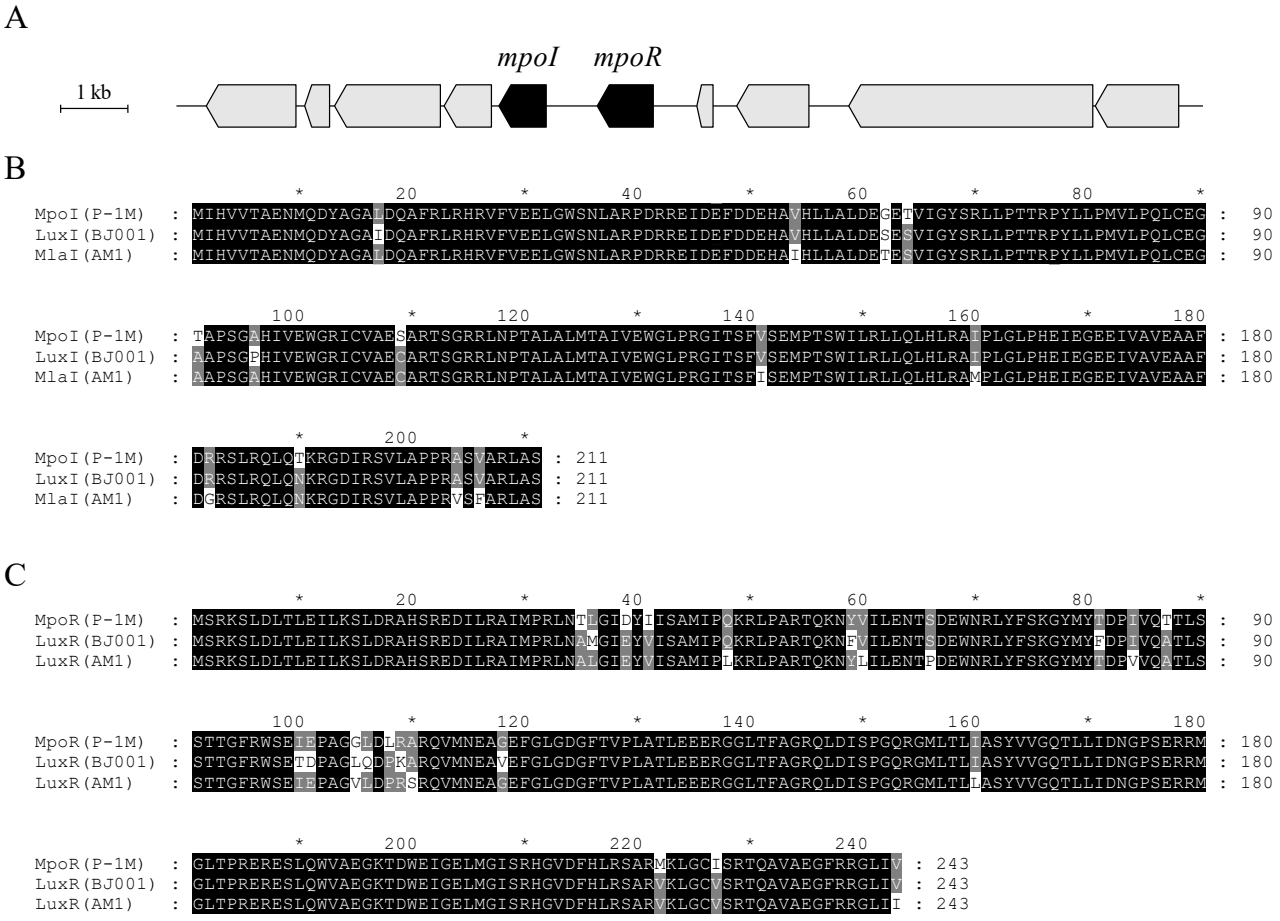

Figure S1. (A) Arrangement of the ORFs upstream and downstream of the *mpoI* and *mpoR* genes in the genome of *Methylobacterium populi* P-1M. Scale bar = 1 kb. (B) Multiple sequence alignment of MpoI from P-1M, LuxI from *M. populi* BJ001, and MlaI from *M. extorquens* AM1. (C) Multiple sequence alignment of MpoR from P-1M and LuxR from *M. populi* BJ001 and *M. extorquens* AM1. Sequences were aligned with ClustalW (Thompson et al. 1994) and shaded using GeneDoc software (Nicholas et al. 1997). Residues that are conserved across all three sequences are shaded black; residues that are conserved across two sequences are shaded light gray.

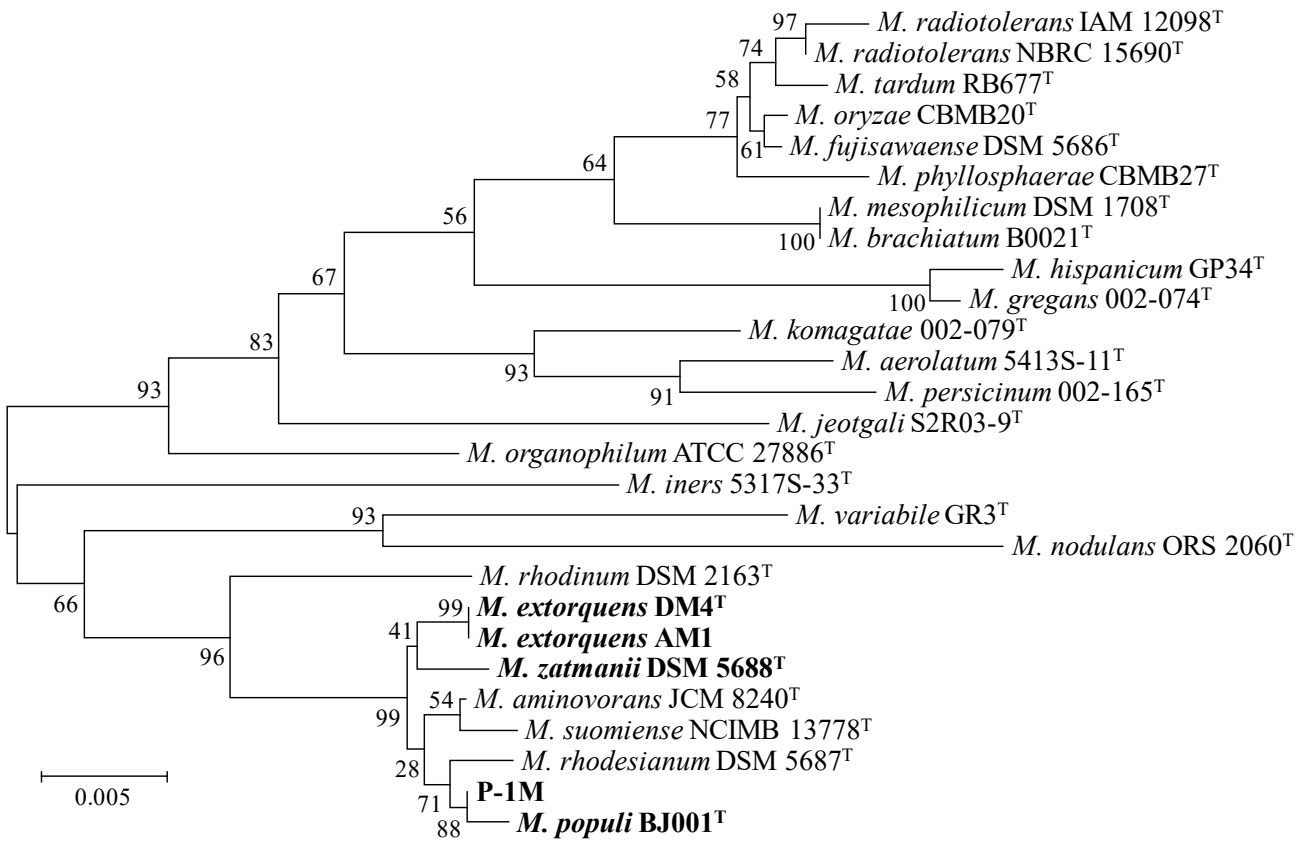

Figure S2. Phylogenetic tree of 16S rRNA gene sequences from *Methylobacterium* strains. The phylogenetic tree was constructed by the neighbor-joining method with the ClustalW program of MEGA software. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The scale bar represents 0.005 substitutions per nucleotide position. *Methylobacterium* strains that contain *mpoIR* quorum-sensing system in the reported complete genome sequence are shown in bold.

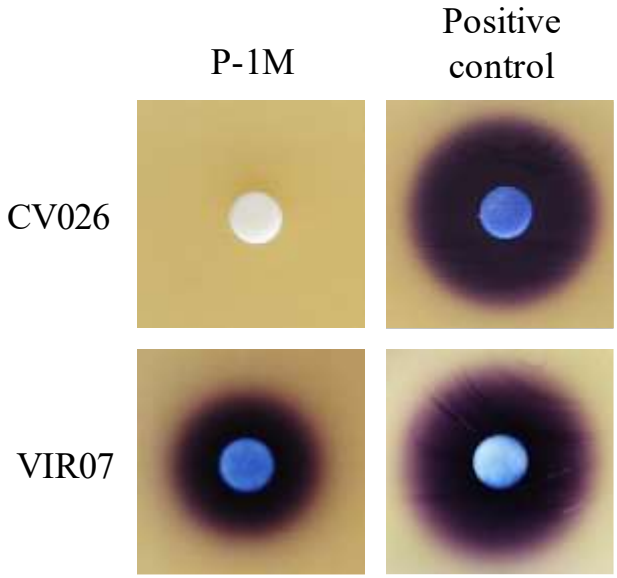

Figure S3. Identification of the AHLs produced by P-1M. P-1M was grown in MB medium for 48 h at 30°C. Then, AHLs in ethyl acetate extract of culture supernatant were detected by spotting onto disks that were placed onto LB agar plates inoculated with one of the AHL-reporter strains (*C. violaceum* CV026 or VIR07). After incubation for 24 h at 30°C, the presence of AHLs was confirmed by the production of purple pigment. C6-HSL and *N*-decanoyl-L-homoserine lactone (C10-HSL) were used as positive controls for CV026 and VIR07, respectively.