McbG, a LysR family transcriptional regulator activates the *mcbBCDEF* gene cluster involved in the upstream pathway of carbaryl degradation in *Pseudomonas* sp. XWY-1

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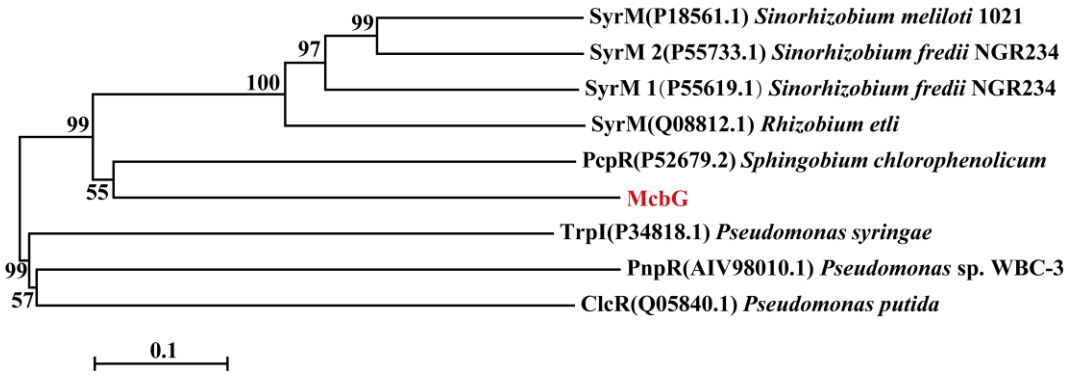

FIG S1 Phylogenetic analysis of McbG and related protein by neighbor-joining method. Bootstrap values (%) are indicated at the nodes, the scale bar represents 0.1 substitutions per site.

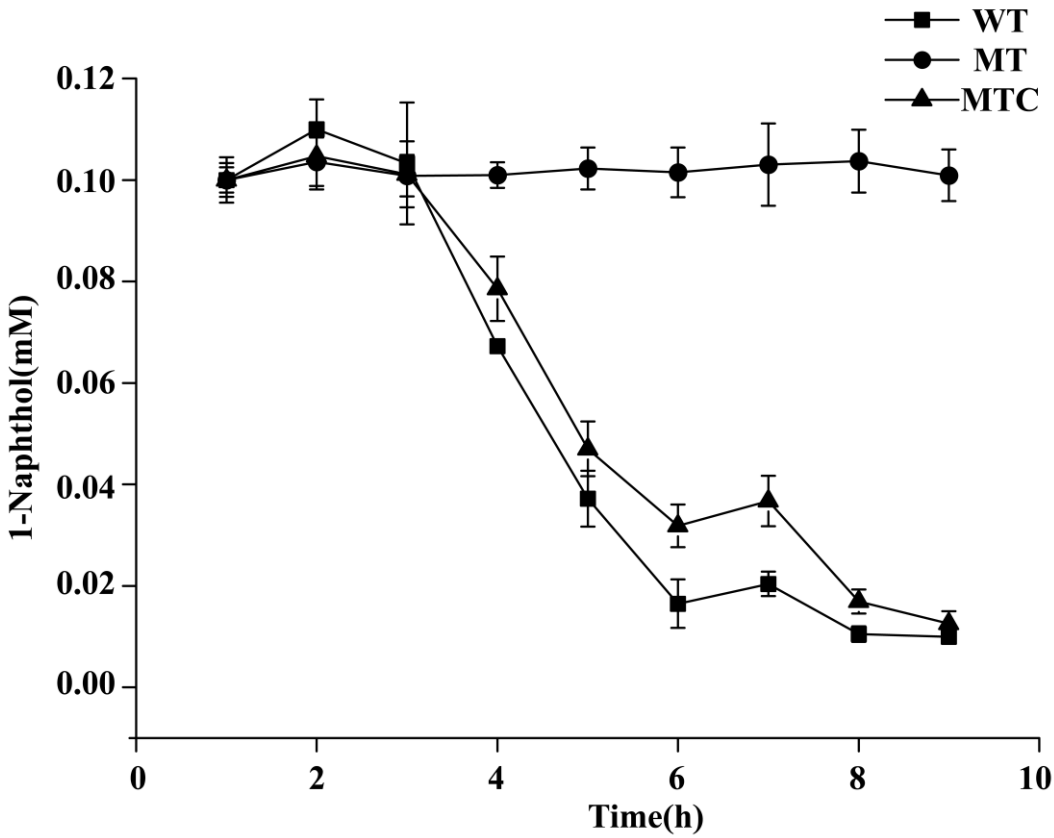

FIG S2 Degradation of 1-naphthol by wild-type strain XWY-1 (WT), the *mcbG* knockout mutant strain (MT) and the *mcbG*-complemented strain (MTC).

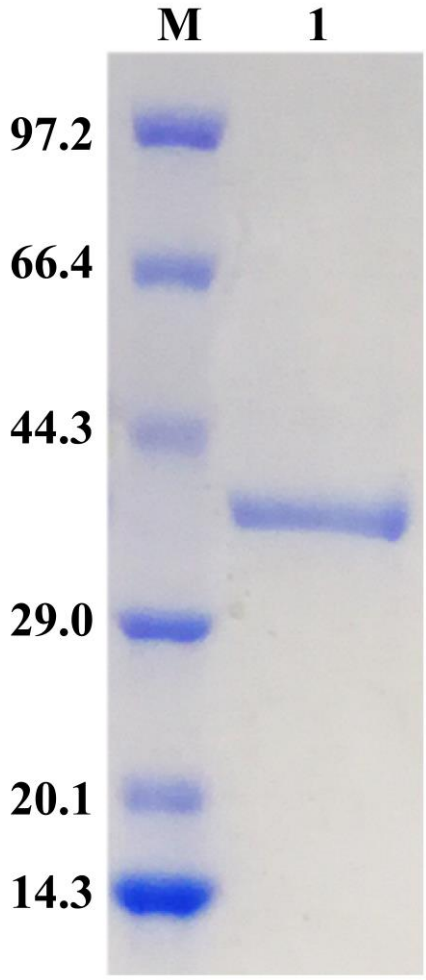

FIG S3 SDS-PAGE analysis of the purified McbG stained with Coomassie Brilliant Blue. Lane M contains protein standards and lane 1 contains purified N-terminal His8-tagged McbG.

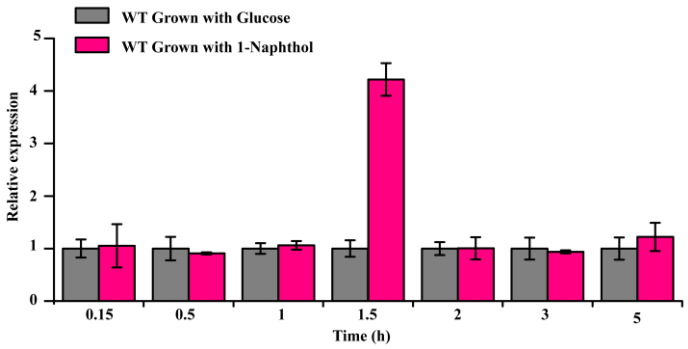

Fig S4 The transcriptional level of *mcbG* in strain XWY-1 (WT) in the presence of 0.1 mM glucose or 0.1 mM 1-naphthol. The transcriptional level of the 16S rRNA gene was used as an internal standard, and the data in each column were calculated by the $2^{-\Delta\Delta CT}$ threshold cycle (C_T) method using 3 replicates. The samples were taken at 0.15 h, 0.5 h, 1 h, 1.5 h, 2 h, 3 h and 5 h.

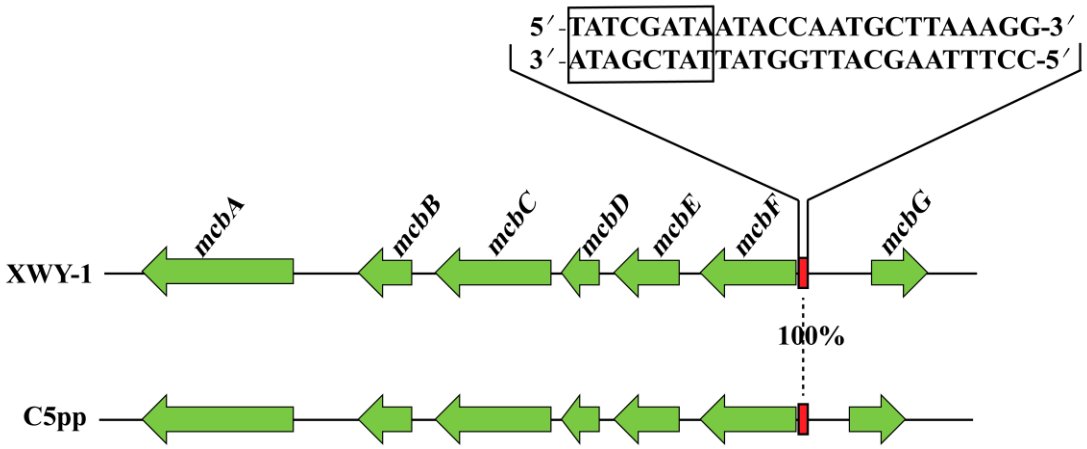

FIG S5 Comparison analysis of the *mcbABCDEFG* cluster in strains XWY-1 and C5pp. The sequence shows that McbG binding site is identical in strains C5pp and XWY-1.

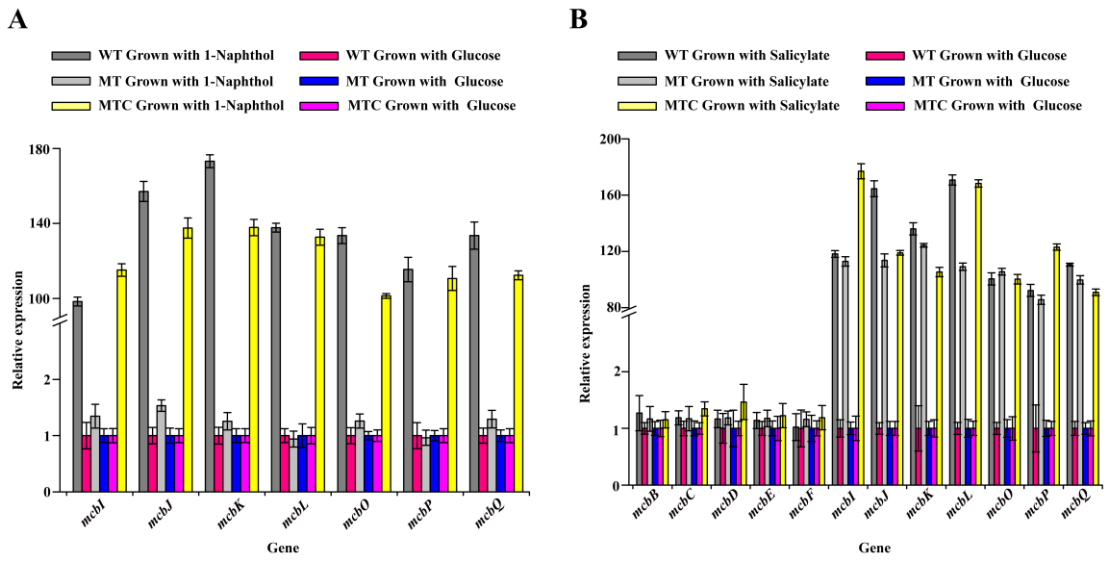

FIG S6 (A) Transcriptional analysis of *mcbIJKL* and *mcbOPQ* gene clusters in the XWY-1 (WT), the *mcbG* knockout mutant (MT), and the *mcbG*-complemented strain (MTC) in the presence of 0.1 mM glucose or 0.1 mM 1-naphthol. The transcriptional level of the 16S rRNA gene was used as an internal standard, and the data in each column were calculated by the $2^{-\Delta\Delta CT}$ threshold cycle (C_T) method using 3 replicates. (B) Transcriptional analysis of *mcbBCDEF*, *mcbIJKL* and *mcbOPQ* gene clusters in the XWY-1 (WT), the *mcbG* knockout mutant (MT), and the *mcbG*-complemented strain (MTC) in the presence of 0.1 mM glucose or 0.1 mM salicylate. The transcriptional level of the 16S rRNA gene was used as an internal standard, and the data in each column were calculated by the $2^{-\Delta\Delta CT}$ threshold cycle (C_T) method using 3 replicates.