Figure S1 DNA sequences of the upstream region of *catA*

The transcriptional start site of *cat* genes at the thymine residue is enclosed by a square with an arrowhead showing the direction of transcription. The -10 and -35 sequences of the putative promoter for *cat* genes were underlined. A putative inverted repeat sequence of an IS element is indicated by a double line. The possible relic of *catR* gene is indicated by an open arrow along with the deduced amino acid sequences. The amino acid residues corresponding to the CatRs from *Rhodococcus opacus* 1CP and *Rhodococcus erythropolis* ANA-13 were shaded. The sequences are numbered as in the GenBank entry (accession no. AB167712).

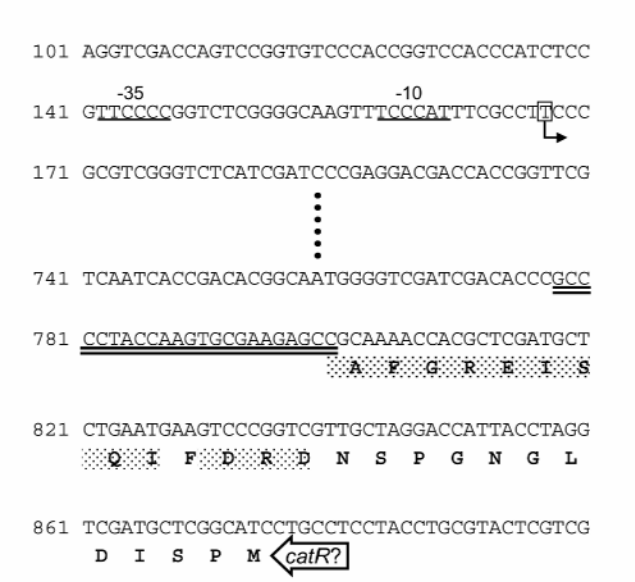

Figure S2 Agarose gel electrophoresis of RT-PCR products

Total RNA prepared from succinate-grown cells of *Rhodococcus* sp. AN-22 was used as a template. On the basis of the nucleotide sequences complementary to those upstream of the *cat* gene cluster, the four primers F1 (5‘-GAAGGACTGAACTATCGGGAAG-3‘), R1 (5‘-CAATCACCGACACGGCAATGG-3‘), R2 (5‘-AACCCTTCGAACGCGTGGAC-3‘) and R3 (5‘-AAGTTTCCCATTTCGCCTTCCC-3‘) were synthesized. cDNA was synthesized with a RevertAid M-MuLV reverse transcriptase (MBI Fermentas) using the F1 primer and the total RNA mentioned above. The cycling of the R1, R2 and R3

primers was performed at 94°C (1 min), 58°C (1 min) and 72°C (1 min) for 30 cycles and additionally at 72°C (2 min) for one cycle to complete the amplifying reaction. Lane 1, markers (100-bp DNA ladder, New England Biolabs); lane 2, a sample amplified with F1 and R3 primers; lane 3, a sample amplified with F1 and R2 primers; and lane 4, a sample amplified with F1 and R1 primers.

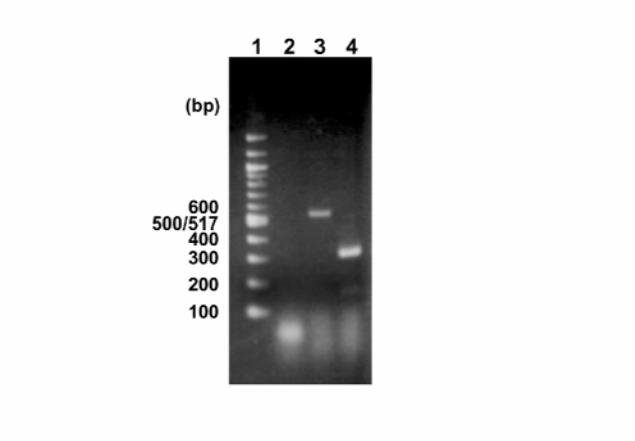

Figure S3 Comparison of organizations of *cat* genes from *Rhodococcus* sp. AN-22 with those from other bacteria reported [6,8,30,31,37]

Open arrows indicate genes and directions of their transcription.