Supplementary Information

Table

Table S1 Assignment of T-RFs and analysis of the clone library of *pmoA* transcripts

Phylogenetic lineage	Number of clone	Percentage (%)	Related T-RFs (bp)*
Methylococcus/Methylocaldum	10	18	75
Methylomonas	12	22	438
Methylobacter	8	15	508
Methylocystis/Methylosinus	25	45	208, 244

*: The sizes of the T-RFs retlates to those determined in the T-RFLP analyses; they were sometimes slightly (1-4 bp) different from those determined *in silico* for the clone sequences.

Figure Legends

Fig. S1 Phylogenetic tree of representative *pmoA* transcript clone sequences retrieved from the rhizosphere soil sample of FL treatment on Day 80.

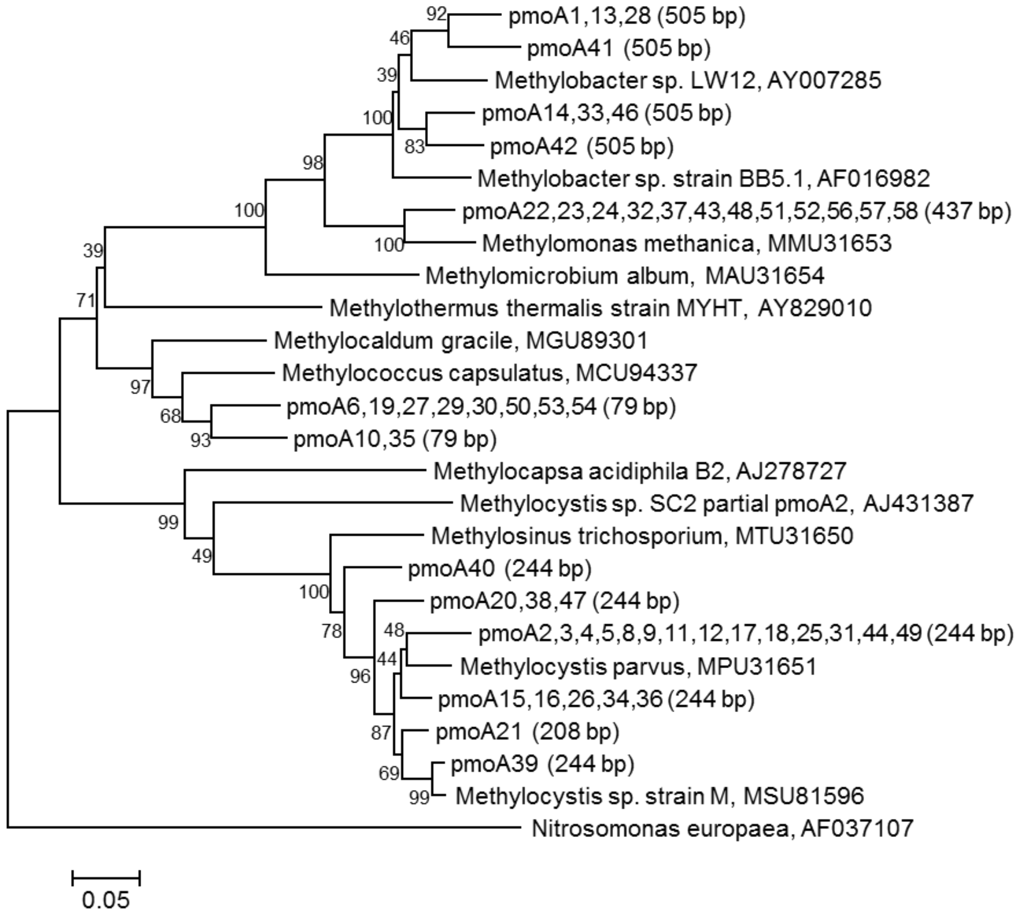

Fig. S2 Correspondence analyses of T-RFLP profiles generated for *pmoA* genes (A, DNA level) and *pmoA* transcripts (B, mRNA level). The eigenvalues of the first and second axes in the two-dimensional ordination diagrams are $\lambda1=0.689$, $\lambda2=0.129$ (DNA), and $\lambda1=0.736$, $\lambda2=0.178$ (mRNA). Different colors denote different sampling dates. Triangle, circle and square indicate surface soil, bulk soil and rhizosphere soil, respectively. At *pmoA* transcripts level (B), the data assigned to the FL and DR treatments are separately circled with blue and red, respectively.