Fig. S1 DGGE analysis of the bacterial population grown under high CO_2 and ambient air. The bacterial diversity of 2 identical inoculate separately incubated under 5% CO_2 (C) and ambient (A) atmospheres at 28° C for 8 h was studied using PCR-DGGE analysis. Conventional samples exhibiting neutral (*a*, *b*, and *c*) and alkaline (*d* and *e*) pH were used for inoculation. The PCR products derived from the original samples (O) were also analysed. *a*, soil of a vegetative field (pH 6.3); *b*, pond sediment (pH 6.8); *c*, soil (pH 6.7); *d*, soil (pH 9.4); *e*, pond water (pH 9.1). Samples were collected at Fujisawa city (*a*, *b*, and *e*) and Atsugi city (*c* and *d*), Kanagawa, Japan. M, DGGE marker II (Wako Pure Chemicals, Tokyo).

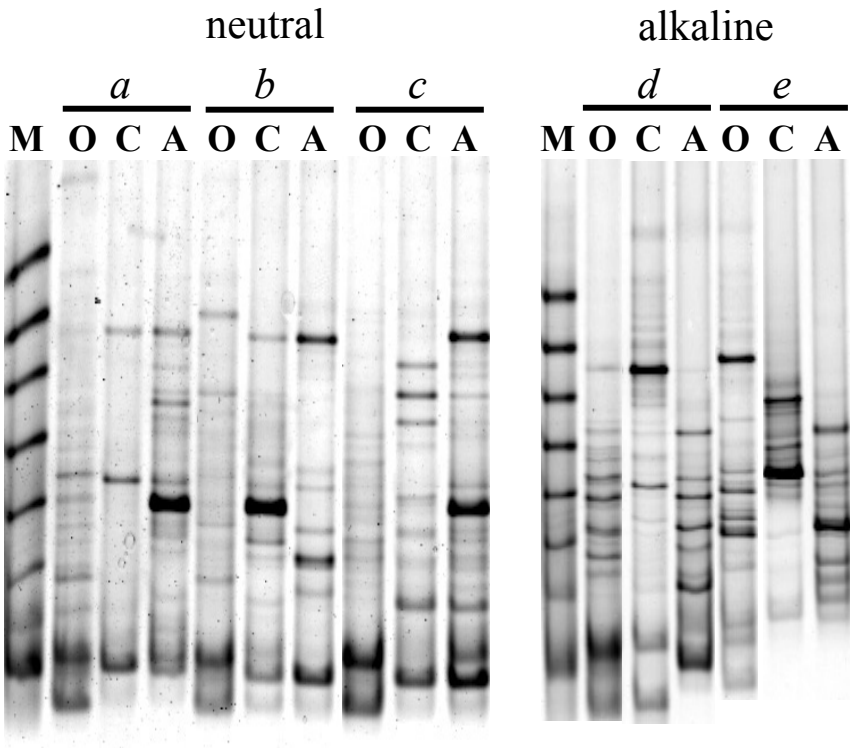
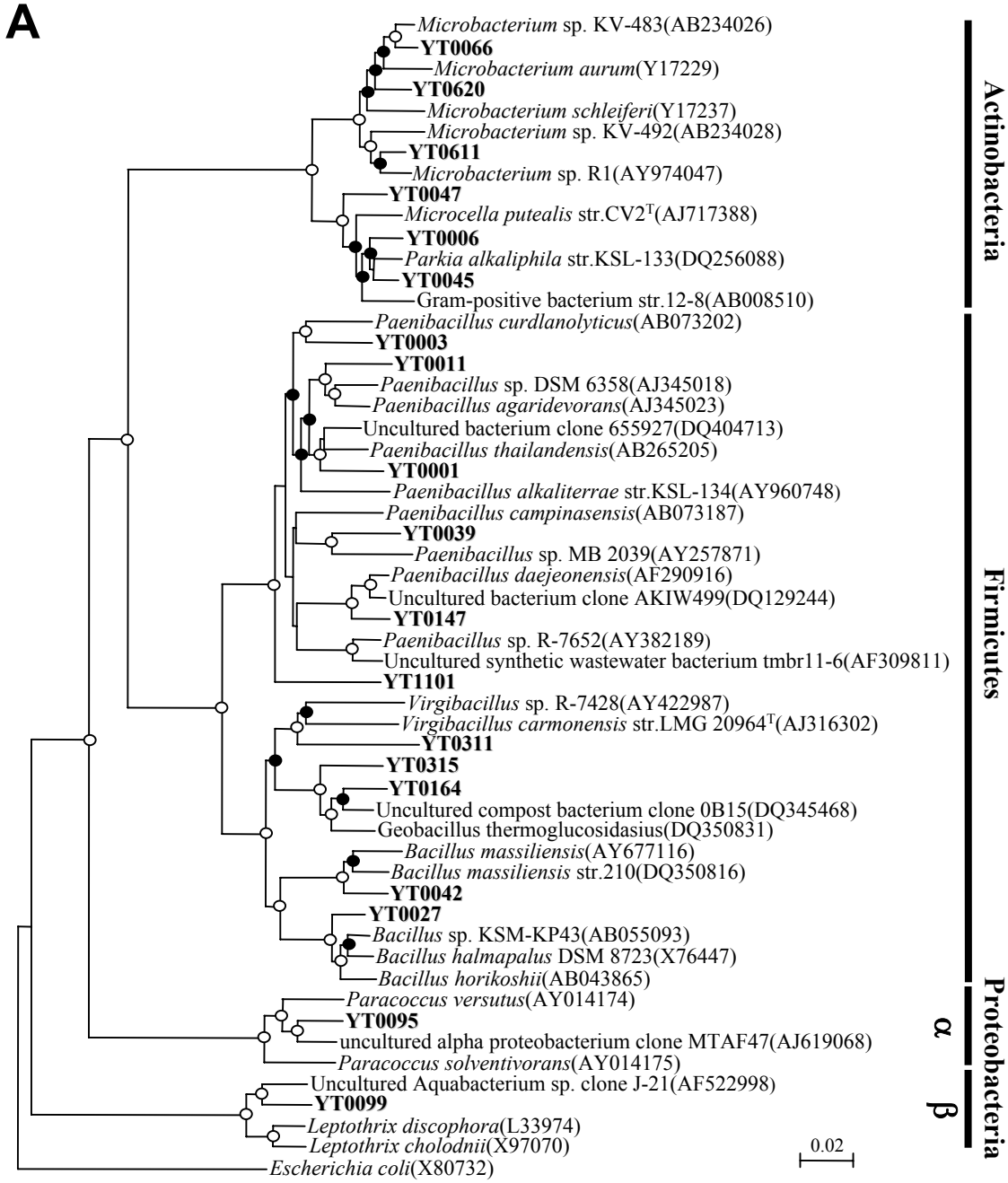
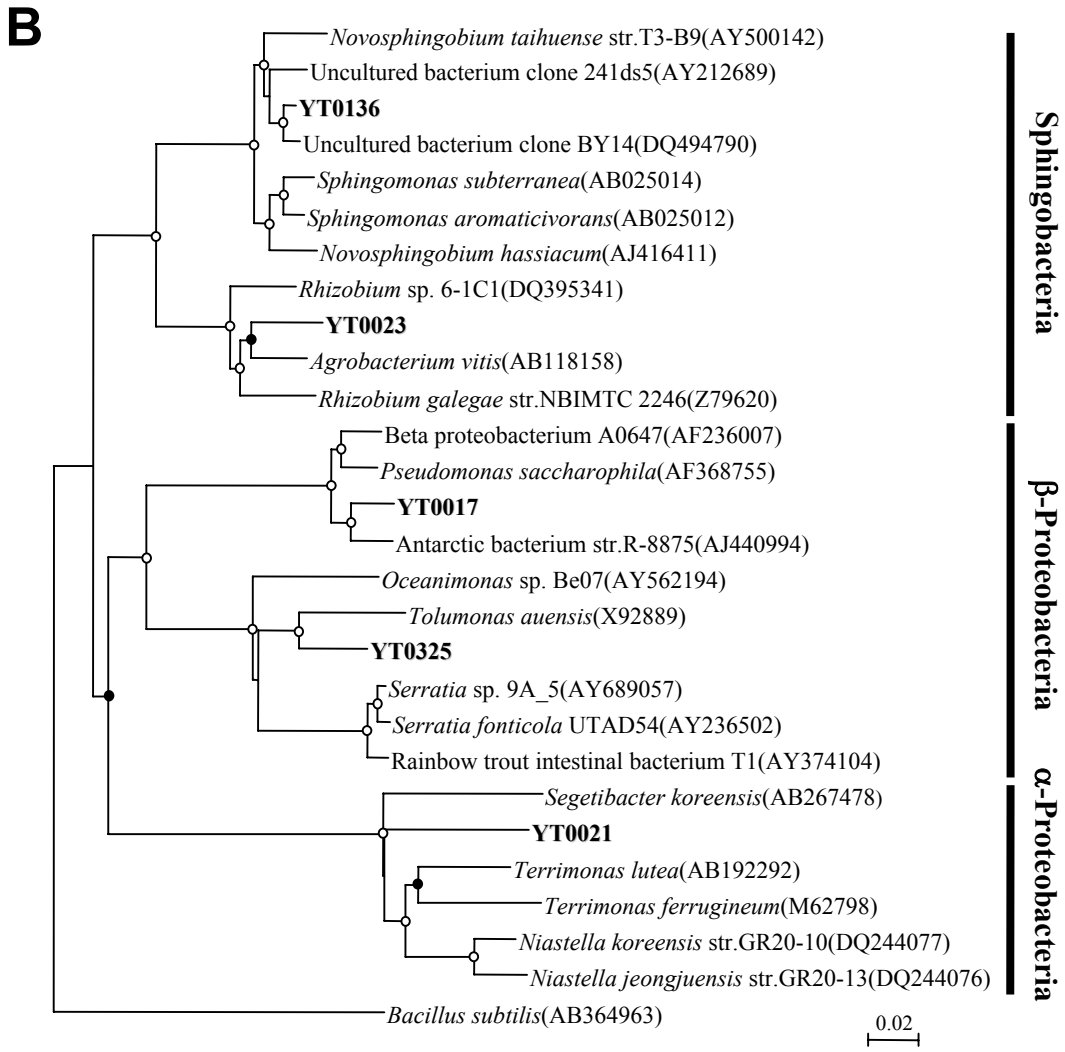


Fig. S2 The 16S rRNA gene-based phylogeny of the high-CO_2-dependent bacteria obtained from alkaline (A) and neutral (B) pH samples. The tree was constructed using the neighbor-joining method. The branching points supported by the 3 analyses (neighbor-joining, maximum-likelihood, and maximum-parsimony methods; based on 1,000 resample datasets) are indicated by closed (>80% bootstrap values) and open (>60% bootstrap values) circles.




B
Novosphingobium taihuense str.T3-B9(AY500142)
Uncultured bacterium clone 241ds5(AY212689)
YT0136
Uncultured bacterium clone BY14(DQ494790)
Sphingomonas subterranea(AB025014)
Sphingomonas aromaticivorans(AB025012)
Novosphingobium hassiacum(AJ416411)
Rhizobium sp. 6-1C1(DQ395341)
YT0023
Agrobacterium vitis(AB118158)
Rhizobium galegae str.NBIMTC 2246(Z79620)
Beta proteobacterium A0647(AF236007)
Pseudomonas saccharophila(AF368755)
YT0017
Antarctic bacterium str.R-8875(AJ440994)
Oceanimonas sp. Be07(AY562194)
Tolumonas auensis(X92889)
YT0325
Serratia sp. 9A_5(AY689057)
Serratia fonticola UTAD54(AY236502)
Rainbow trout intestinal bacterium T1(AY374104)
Segetibacter koreensis(AB267478)
YT0021
Terrimonas lutea(AB192292)
Terrimonas ferrugineum(M62798)
Niastella koreensis str.GR20-10(DQ244077)
Niastella jeongjuensis str.GR20-13(DQ244076)
Bacillus subtilis(AB364963)
0.02
Sphingobacteria
β-Proteobacteria
α-Proteobacteria