

Fig. S1 %*G'UJ cbca]W'XYbh]mcZ Class *Actinobacteria*]gc'UHg

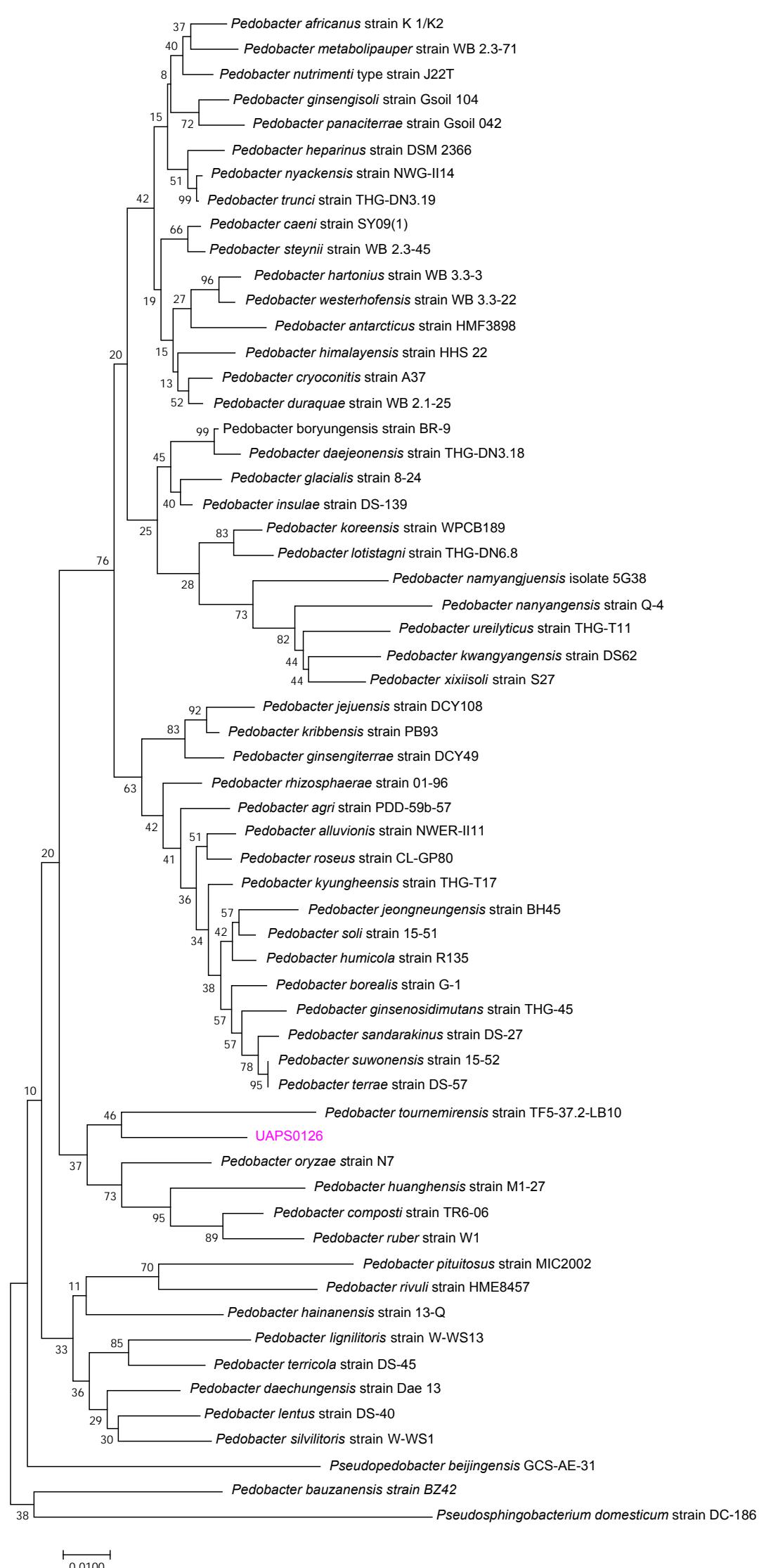


Fig. S1. 16S taxonomical identity of the Class *Sphingobacteria* isolate

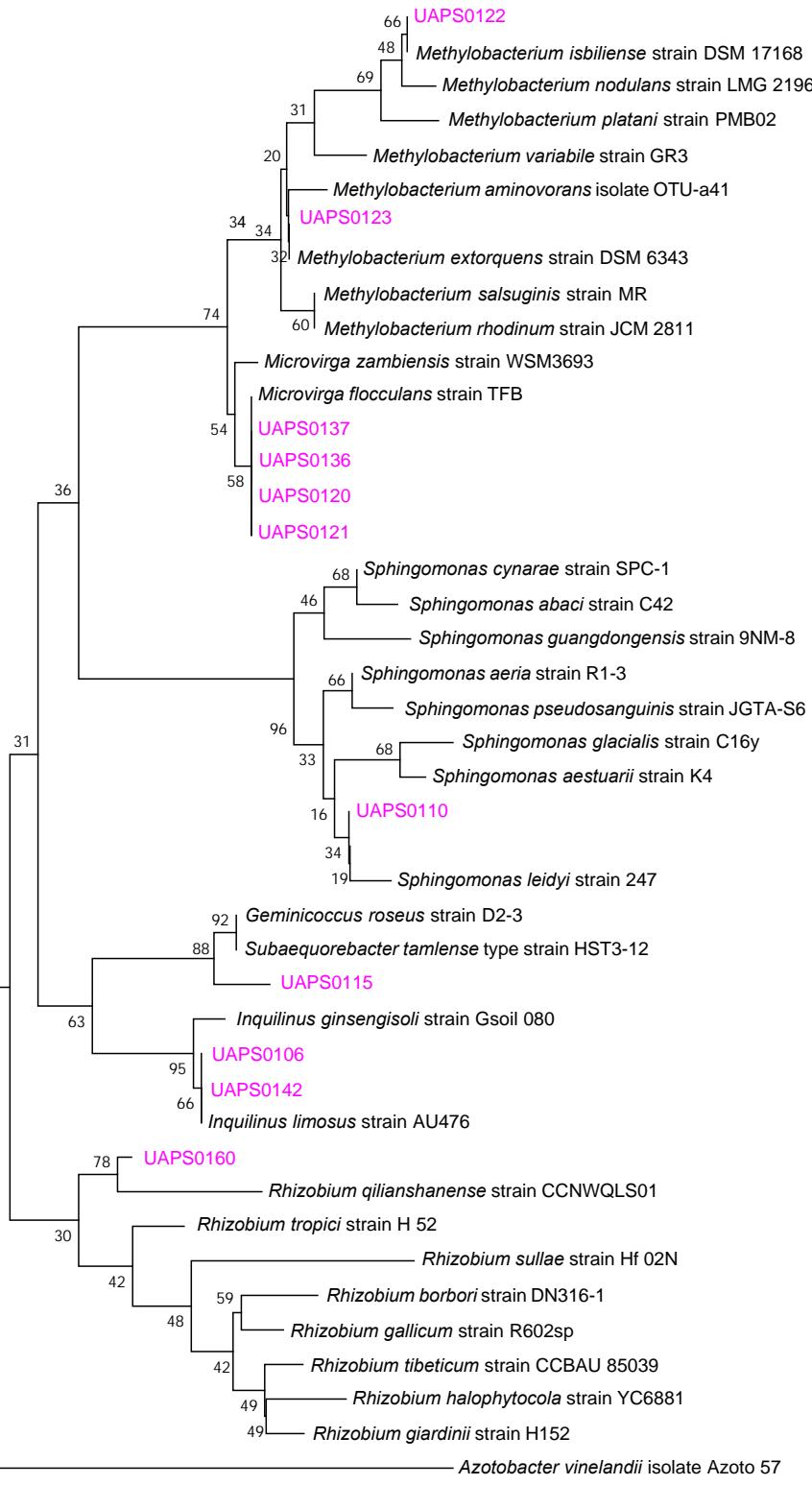
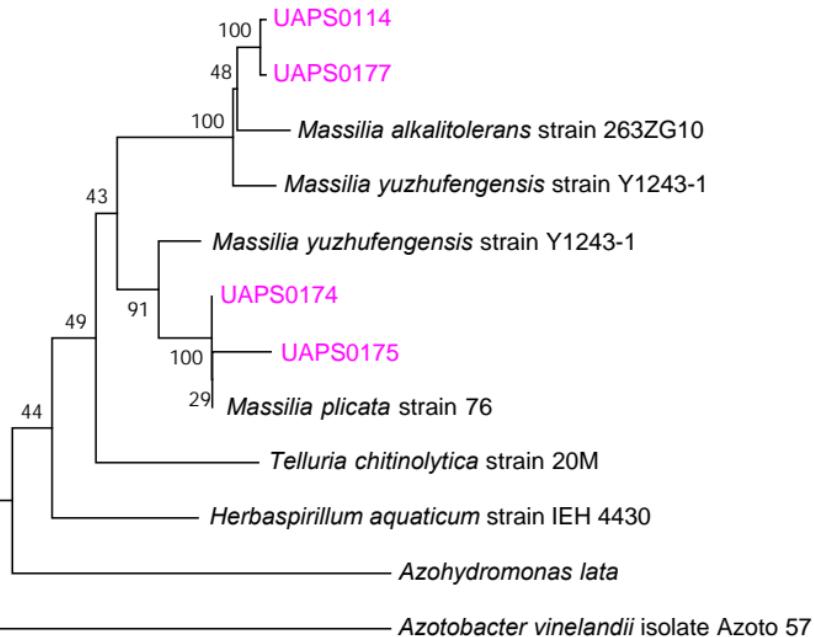


Fig. S1. 16S taxonomical identity of Class *Alphaproteobacteria* isolates

0.0100



0.020

Fig. S1. % G + C content of *cbca* genes from Class *Betaproteobacteria* [gc%]

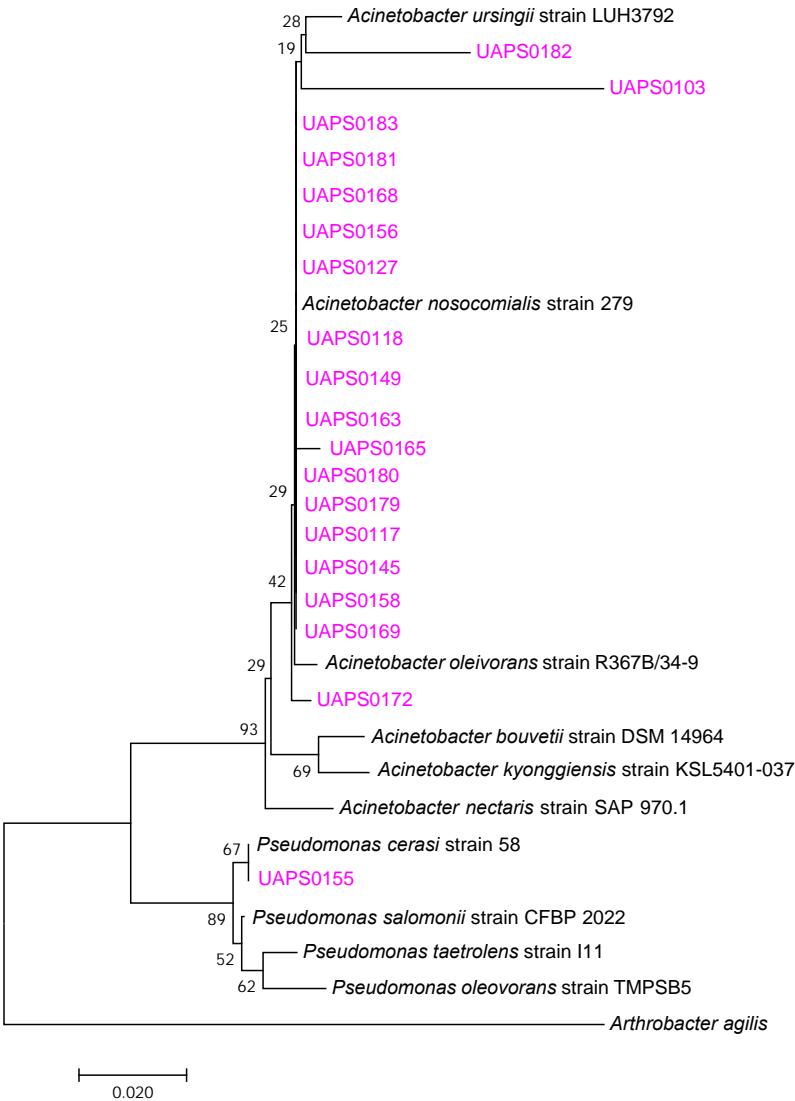
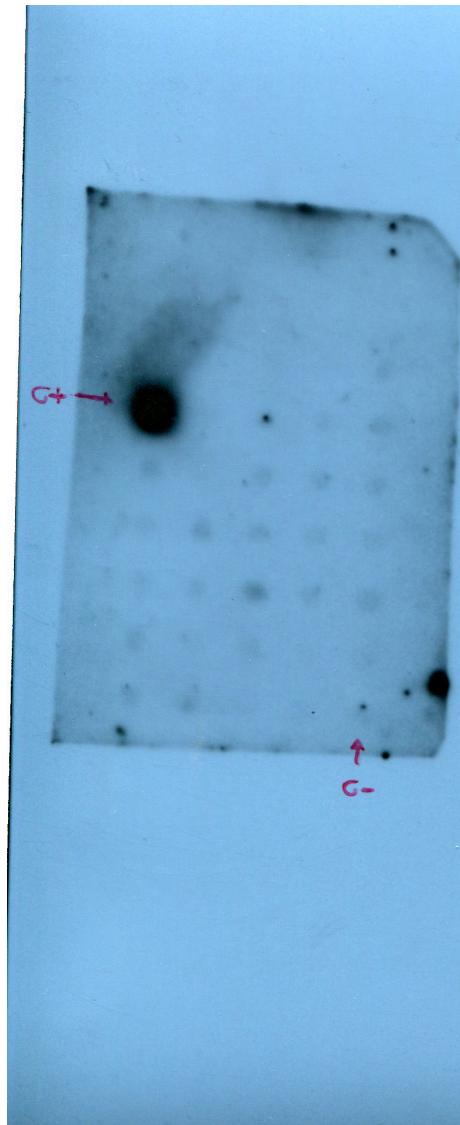


Fig. S1. 16S taxonomical identity of Class *Gammaproteobacteria* isolates

***mxaF* DOT BLOT ARRANGMENT**

C+	blank	77	75	74
72	Ni	69	68	Ni
63	60	58	56	55
49	45	42	Ni	23
22	21	18	17	15
14	Ni	10	06	C-



Positive control **C+** *Methylobacterium extorquens* JCM2802.

Negative control **C-** *U. maydis* 207.

Numbers indicate the reduced name of the isolates. For example, 77 means UAPS07077.

Ni, strain not included in this work.

Fig. S2. *mxaF* dot blot hybridization

Table S1. Methanol:NDMA (N,N'-dimethyl-4-nitrosoaniline oxidoreductase primers.

Primer	Sequence (5'-3')
NDMAY270F	YCC CAA GGA CTA CAA CGT CAT
NDMAGA270F	CCA AGG ACT ACA ACG TCA TGG A
NDMA270F	CCC AAG GAC TAC AAC GTC AT
NDMA850R	CCS AGN CCR CCS GAG TTG AA