1 ***Oceanobacillus alkalisoli* sp. nov., an alkaliphilic bacterium isolated**

2 **from saline-alkaline soil**

3 **Pin-jiao Jin[1], Lei Sun[1], Manik Prabhu Narsing Rao[2], Jian-yu Jiao[2], Xiu-jun Sun[1],**

4 **Wen-Jun Li[2,3], Shuang Wang[1,3]***

5 **[1] Heilongjiang Academy of Black Soil Conservation & Utilization, Heilongjiang**

6 **Academy of Agricultural Sciences/Key Lab of Soil Environment and Plant**

7 **Nutrition of Heilongjiang Province/Heilongjiang Fertilizer Engineering Research**

8 **Center, Harbin 150086, PR China**

9 **[2] State Key Laboratory of Biocontrol and Guangdong Key Laboratory of Plant**

10 **Resources, School of Life Sciences, Sun Yat-Sen University, Guangzhou 510275,**
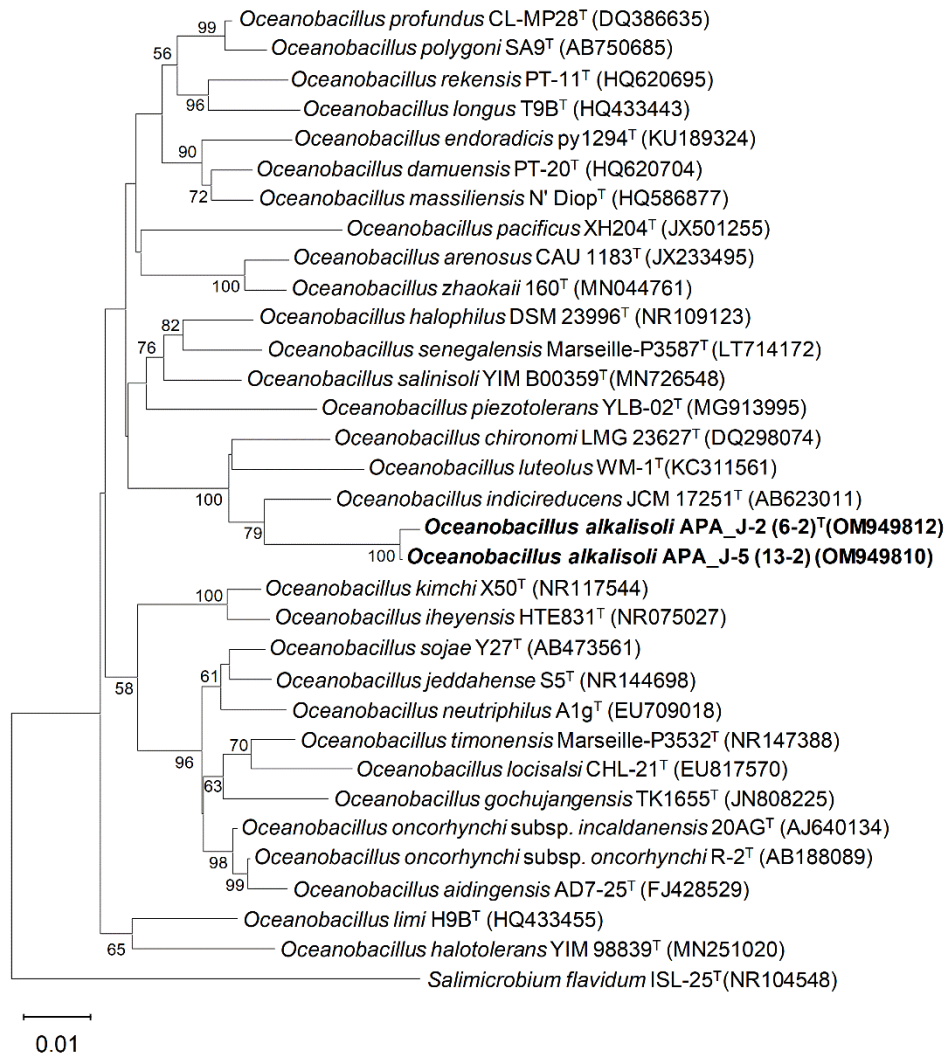
11 **PR China**

12 **[3] State Key Laboratory of Desert and Oasis Ecology, Xinjiang Institute of Ecology**

13 **and Geography, Chinese Academy of Sciences, Urumqi 830011, PR China**

14 ***Authors for correspondence:**

15 **Shuang Wang**

16 **Tel & Fax: +86 0451-86668726**

17 **E-mail: wangshuang0726@163.com**

Fig. S1 Minimum-evolution phylogenetic tree based on 16S rRNA gene sequences of strains APA_J-2 (6-2)^{T}, APA_J-5 (13-2) and other closest relatives. Bootstrap values ($\geqslant$ 50%) based on 1000 replications are shown at branch nodes. *Salimicrobium flavidum* ISL-25^{T} (NR104548) is used as the outgroup. Bar, 0.01 represents substitutions per nucleotide position.
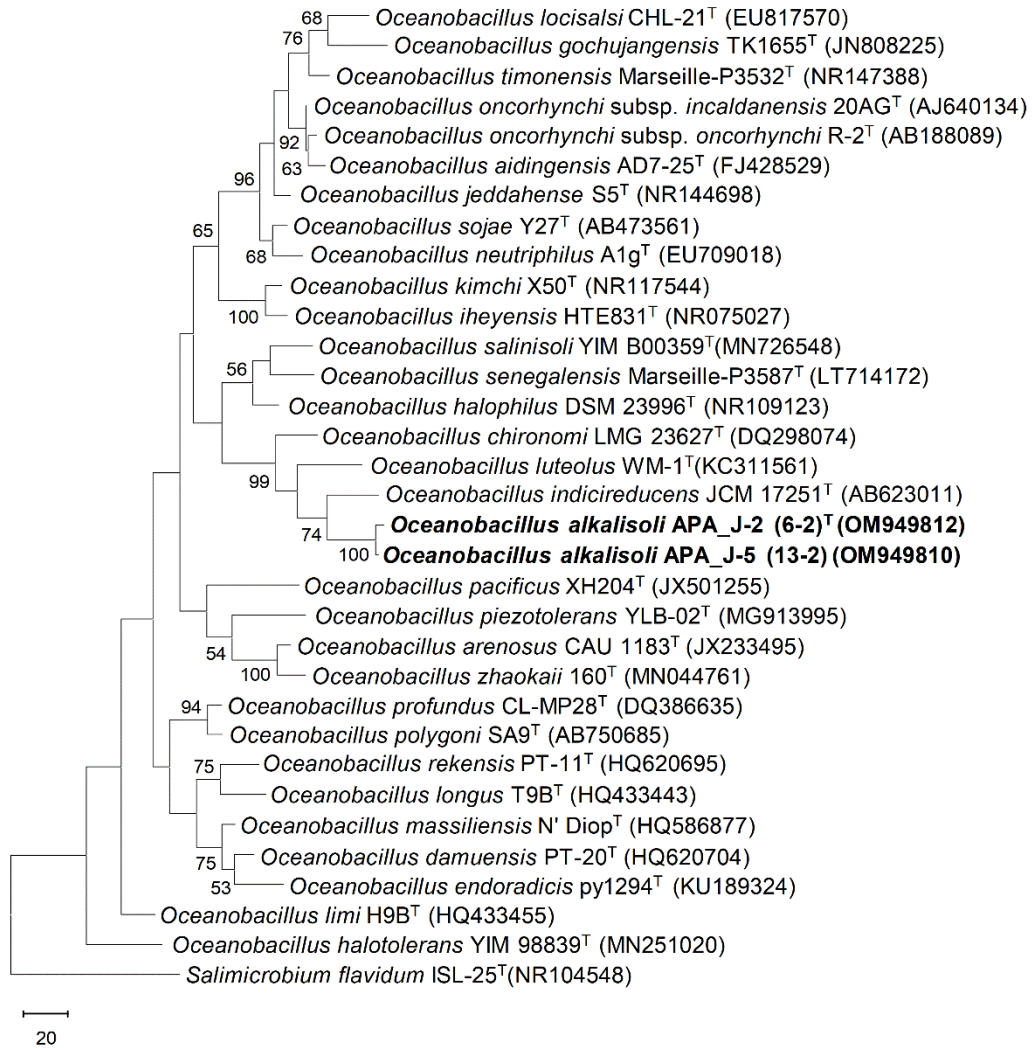
Fig. S2 Maximum-parsimony phylogenetic tree based on 16S rRNA gene sequences of strains APA_J-2 (6-2)^T, APA_J-5 (13-2) and other closest relatives. Bootstrap values ($\geqslant 50\%$) based on 1000 replications are shown at branch nodes. *Salimicrobium flavidum* ISL-25^T (NR104548) is used as the outgroup. Bar, 20 represents substitutions per nucleotide position.
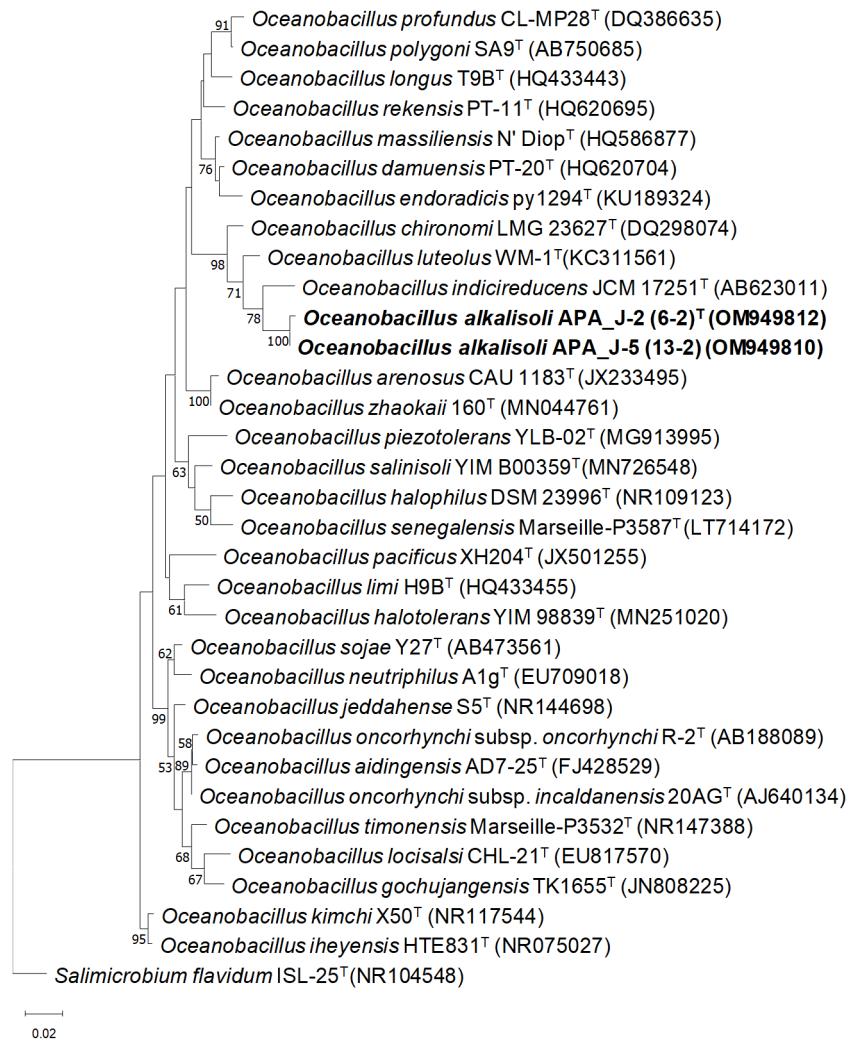
Fig. S3 Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences of strains APA_J-2 (6-2)^T, APA_J-5 (13-2) and other closest relatives. Bootstrap values ($\geqslant$ 50%) based on 1000 replications are shown at branch nodes. *Salimicrobium flavidum* ISL-25^T (NR104548) is used as the outgroup. Bar, 0.02 represents substitutions per nucleotide position.
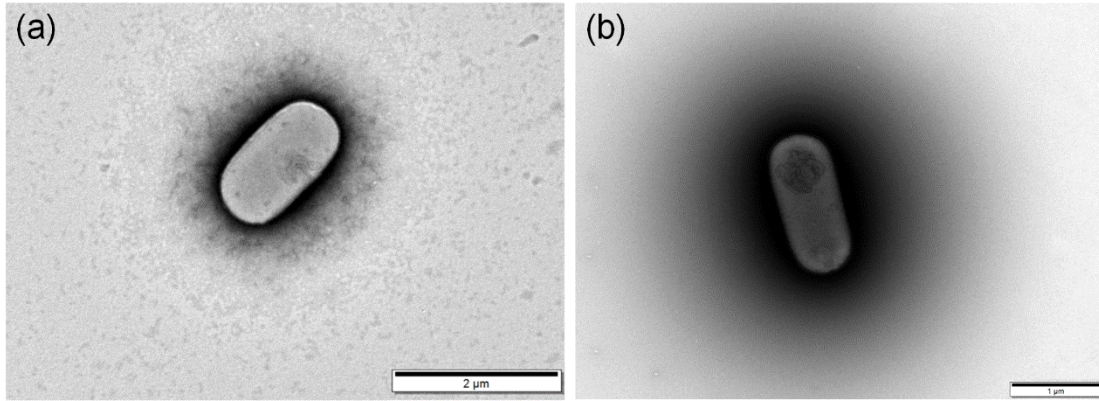
34   **Fig. S4** Transmission electronic micrographs of strains (a) APA_J-2 (6-2)^{T} and (b)

35   APA_J-5 (13-2) grown on R2A agar at 28 ºC for 3 days. Bars, (a) 2 µm, (b) 1 µm.
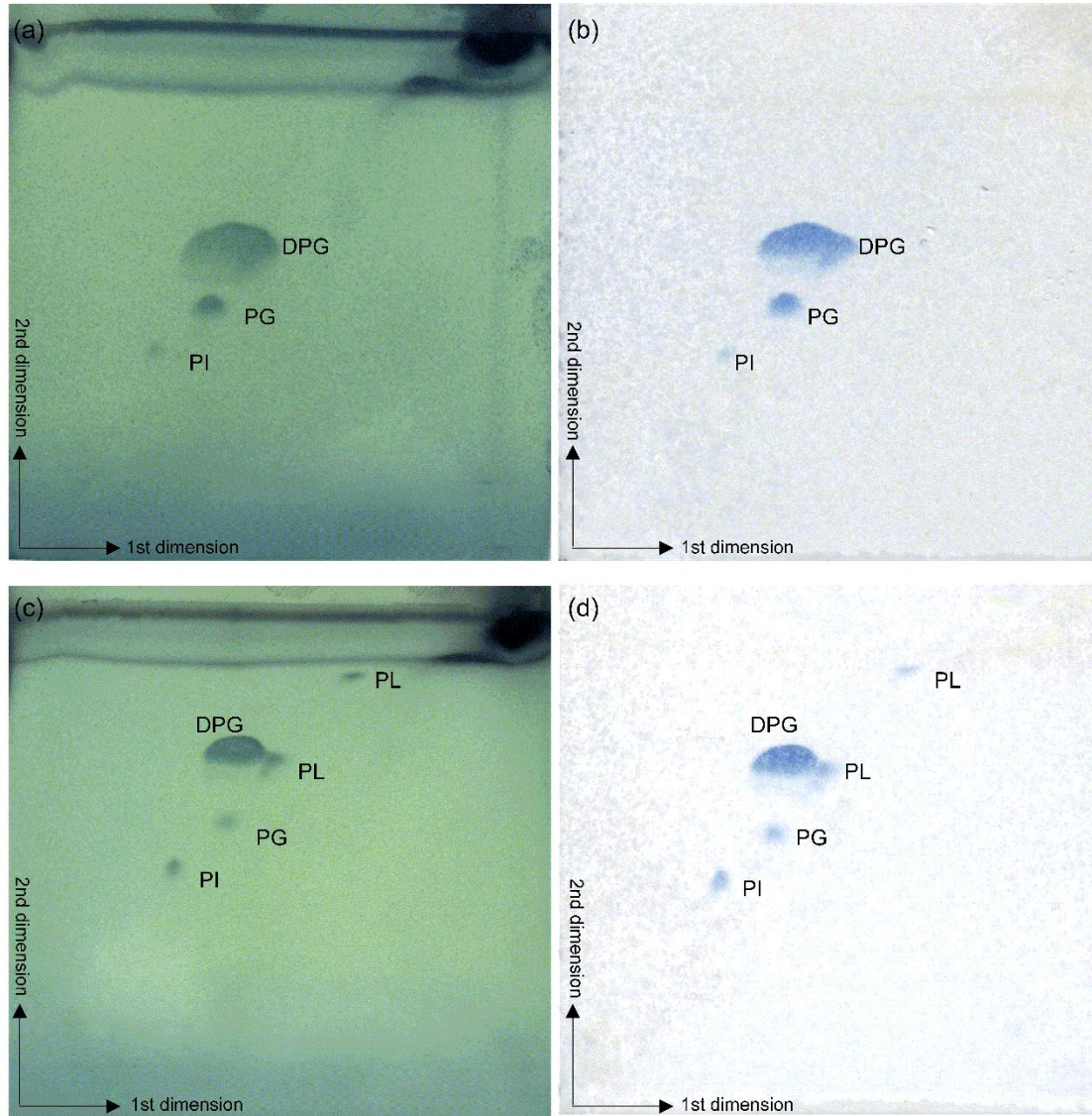
Fig. S5 Two-dimensional TLC patterns of the total polar lipids from strains (a, b) APA_J-2 (6-2)[T] and (c, d) APA_J-5 (13-2), a and c, using molybdophosphoric acid reagent; b and d, using molybdenum blue reagent.

1st dimension: Chloroform: Methanol: Water (65: 25: 4, v/v);

2nd dimension: Chloroform: Acetic acid: Methanol: Water (80: 18: 12: 5, v/v).

Abbreviations: PI, phosphatidylinositol; PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; PL, unidentified phospholipid.

44 **Table S1**. Number of genes associated with metabolism of strains APA_J-2 (6-2)^T,
45 APA_J-5 (13-2) and *O.indicireducens* JCM 17251^T.
46

Metabolism	APA_J-2 (6-2)^T	APA_J-5 (13-2)	*O.indicireducens* JCM 17251^T
Amino acid metabolism	256	252	279
Biosynthesis of other secondary metabolites	33	36	32
Carbohydrate metabolism	406	408	393
Cell growth and death	14	15	15
Cell motility	61	59	57
Energy metabolism	136	139	137
Folding, sorting and degradation	47	47	43
Glycan biosynthesis and metabolism	22	24	23
Lipid metabolism	95	86	98
Membrane transport	178	178	166
Metabolism of cofactors and vitamins	124	118	117
Metabolism of other amino acids	53	51	42
Metabolism of terpenoids and polyketides	32	35	34
Nucleotide metabolism	105	102	109
Overview	289	289	294
Replication and repair	70	69	75
Signal transduction	88	86	91
Transcription	5	5	5
Translation	84	85	86
Transport and catabolism	14	14	14
Xenobiotics biodegradation and metabolism	61	43	27

47