



S1(a)

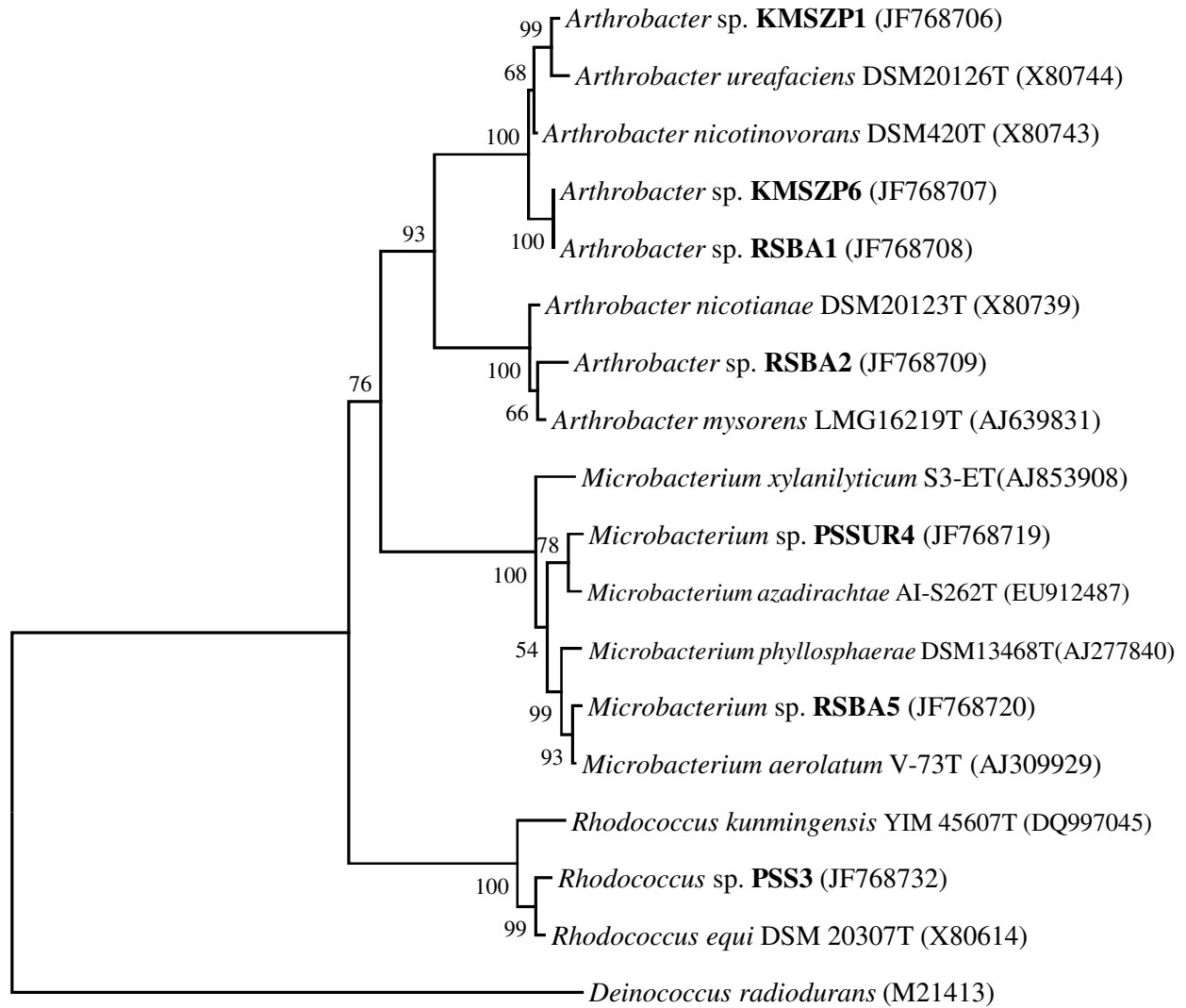


S1(b)

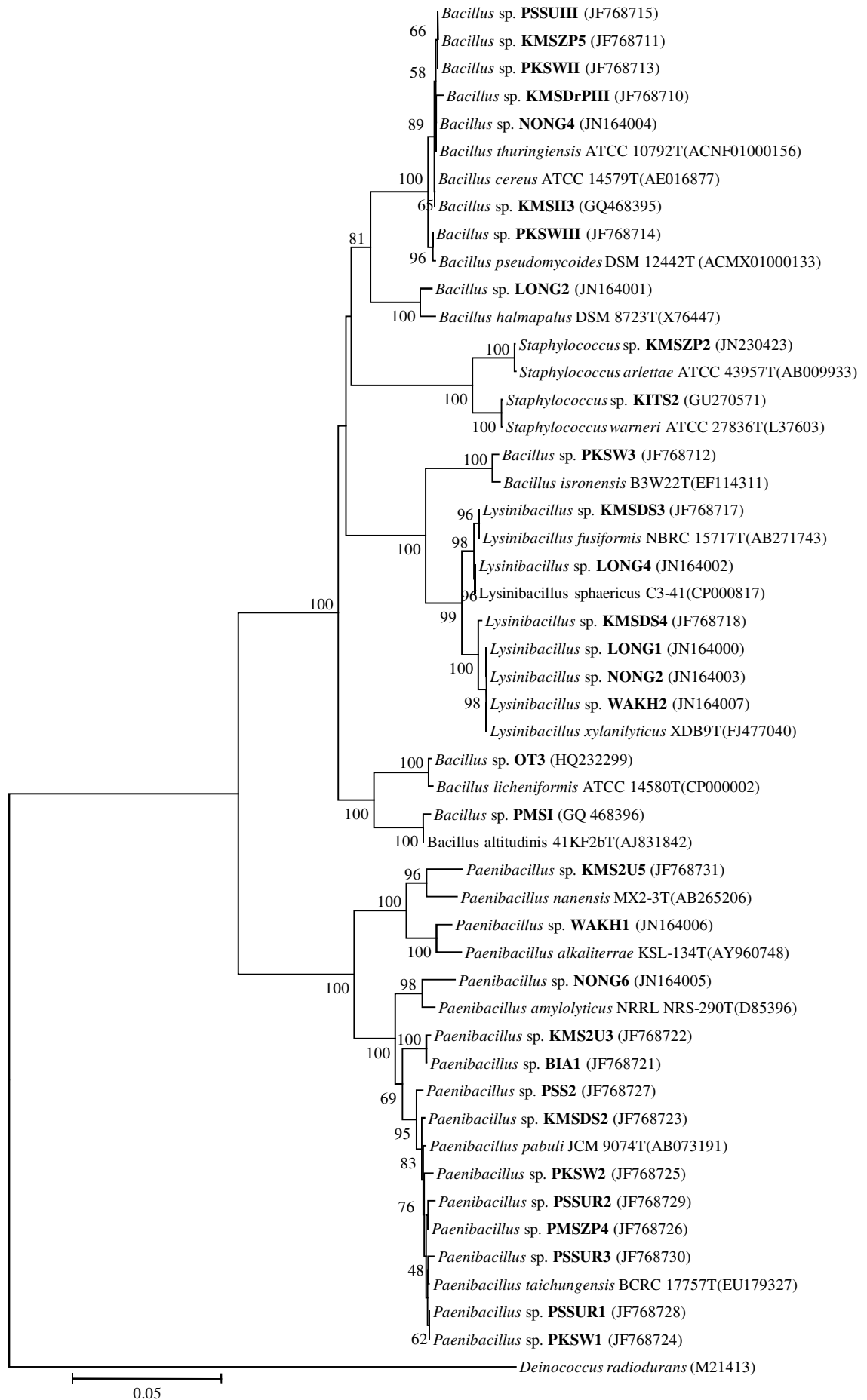


S1(c)

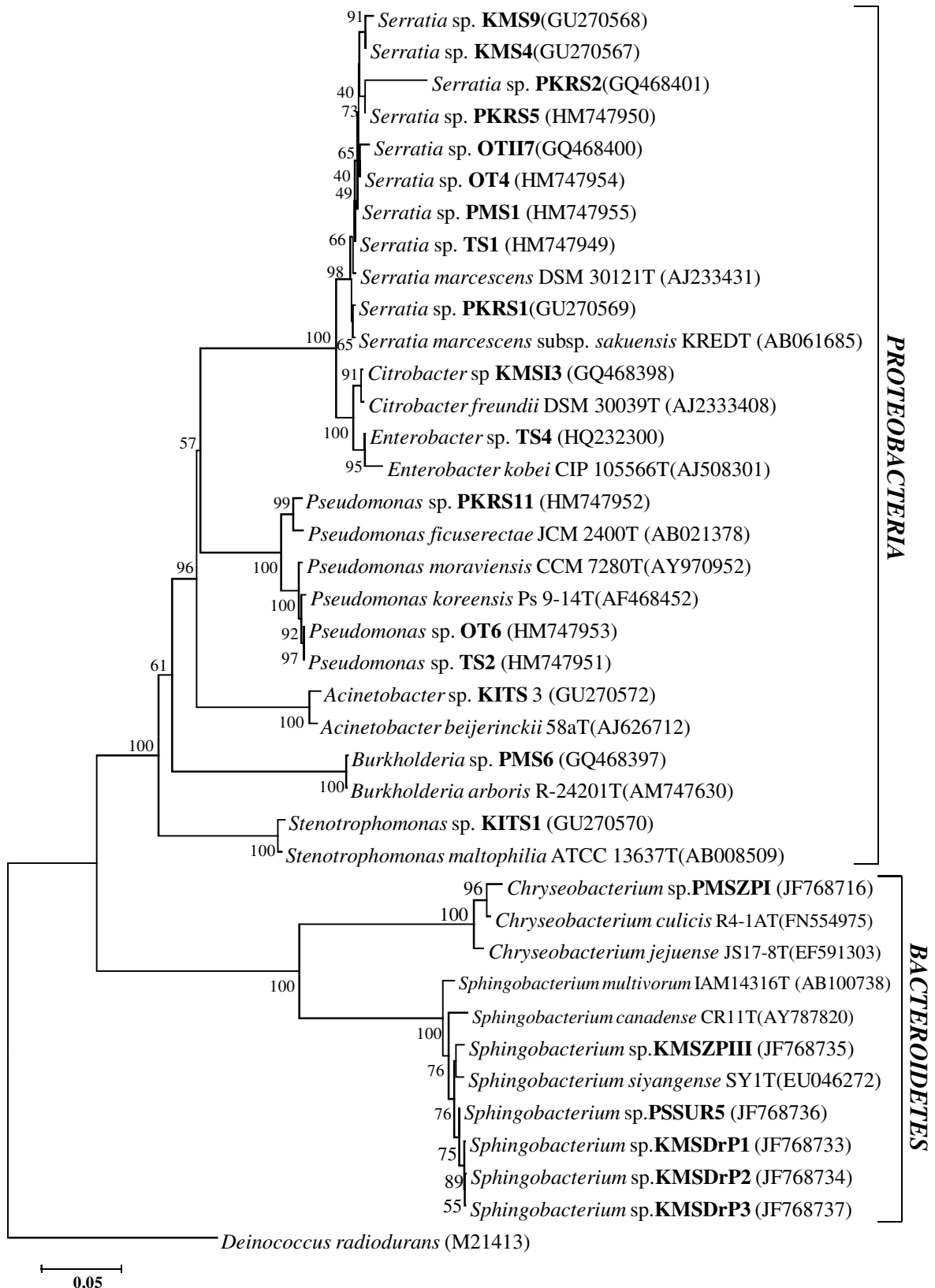
Fig. S1 Sampling site description. (a) Snapshots of sampling Site I showing Kylleng Nala and the greyish-white rocky surface across dissected Nala section, (b) Snapshots of sampling Site II which lies around the designated mining site, (c) Snapshots of sampling Site III which comprises of sample around mining site and from adjoining areas



S2(a)



S2(b)



S2(c)

Fig. S2 Neighbor-joining tree based on 16S rRNA (more than 1300 bases) gene sequences representing the phylogenetic relationships between the representative (a) high GC, gram positive (Firmicutes) ; (b) low GC, gram positive (Actinobacteria) ; (c) proteobacteria and bacteroidetes; and the related species obtained from the database of type strains with validly published prokaryotic names at EzTaxon-e identification service. *Deinococcus radiodurans* (M21413) was taken as the outgroup organism. The scale bar corresponds to the expected number of changes per nucleotide position.

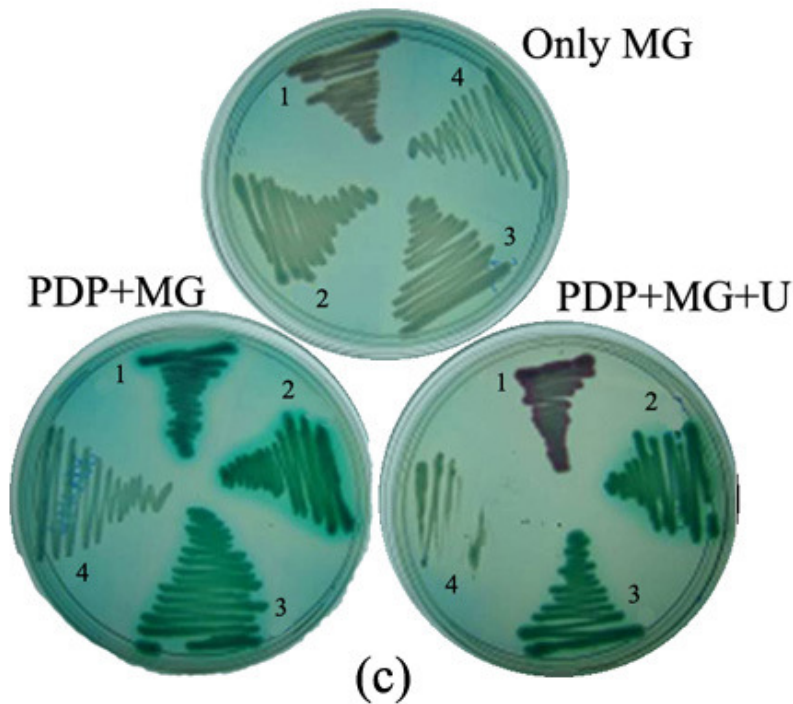
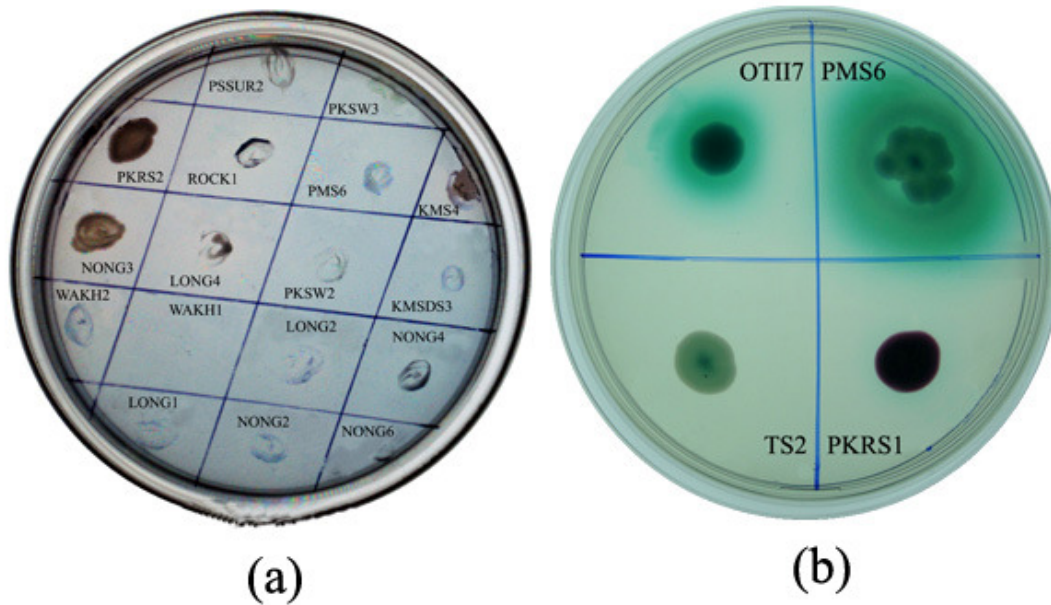


Fig. S3 Analysis of phosphatase activity of identified isolates on histochemical plates. (a) Number of colonies patched on the histochemical plate for random and fast selection of positive isolates. (b) Patching of individual isolate on histochemical plate for detailed study as in this figure it explains as, OTII7 shows intra and extracellular phosphatase(s), PMS6 has extracellular phosphatase(s), PKRS1 portrays intracellular phosphatase and TS2 may not have an active phosphatase or if at all it has, it may have a stationary phase inducible phosphatase (c) Comparative test for positive isolates in various conditions, The plates containing only MG and no phosphate source (PDP) does not show any bluish-green colouration around the colony while when phosphate source is added the three bacteria except TS2 showed bluish green concentration and as these bacteria can tolerate U, they were tested for their phosphatase activity in its presence which has shown similar reading as in PDP-MG plates apart from diminished growth of cultures. The positive screening on PDP-MG plates without U confirms that the phosphatase enzyme is expressed constitutively and is not produced only when there is a stress factor.

Table S1 Presence of P<sub>IB</sub> type ATPase gene in the multi-metal resistant Domiasiat isolates and their closest identified match in the NCBI GenBank database

Isolates (Accession No.) <sup>a</sup>	Closest identified match in NCBI GenBank with similarity percentage <sup>b</sup>
<b><i>cadA</i> gene</b>	
<i>Bacillus halmapalus</i> LONG2 ( JN222559)	Cadmium-transporting ATPase, <i>Geobacillus kaustophilus</i> HTA426, (YP 146205), 64%
<i>Bacillus thuringiensis</i> KMSZP5 ( JN034438)	Cadmium-transporting ATPase, <i>Lysinibacillus sphaericus</i> C3-41, (YP 001699920), 94%
<i>Bacillus isronensis</i> PKS3 ( JN034437)	Cation transport ATPase, <i>Solibacillus silvestris</i> StLB046, (BAK 15053.1), 94 % Cadmium-transporting ATPase, <i>Lysinibacillus sphaericus</i> C3-41, (YP 001696058.1), 67 %
<i>Lysinibacillus xylanilyticus</i> WAKH2 ( JN222556)	Cadmium-transporting ATPase CadA, <i>Lysinibacillus fusiformis</i> ZC1, (ZP 07051554), 81 %
<i>Lysinibacillus xylanilyticus</i> NONG2 (JN222557)	Cadmium-transporting ATPase CadA, <i>Lysinibacillus fusiformis</i> ZC1, (ZP 07051554), 85 %
<i>Lysinibacillus xylanilyticus</i> LONG1 (JN222558)	Cadmium-transporting ATPase CadA, <i>Lysinibacillus fusiformis</i> ZC1, (ZP 07051554), 82 %
<i>Lysinibacillus xylanilyticus</i> KMSDS4 (JN034436)	Cadmium-transporting ATPase, <i>Lysinibacillus sphaericus</i> C3-41, (YP 001699920), 95%
<b><i>copA</i> gene</b>	
<i>Pseudomonas koreensis</i> OT6 (JN034439)	Copper-transporting P-type ATPase, <i>Providencia rettgeri</i> DSM 1131, (ZP 06125459), 92%
<i>Arthrobacter mysorens</i> RSBA2 (JN634869)	Cation-transporting ATPase, <i>Arthrobacter arilaitensis</i> Re117, (YP 003918270), 78% Copper-translocating P-type ATPase, <i>Arthrobacter aureescens</i> TC1, (YP 949762), 55%
<b><i>zntA</i> gene</b>	
<i>Paenibacillus pabuli</i> PSS2 (JN034435)	Zinc-exporting ATPase, <i>Sphingobacterium spiritivorum</i> ATCC 33861, (ZP 07080472), 66%
<i>Chryseobacterium culicis</i> PMSZPI (JN034431)	Zinc-exporting ATPase, <i>Chryseobacterium gleum</i> ATCC 35910, (ZP 07084814), 92%
<i>Sphingobacterium siyangense</i> KMSDrP1 ( JN034432)	Zinc-exporting ATPase, <i>Sphingobacterium spiritivorum</i> ATCC 33861, (ZP 07080472), 66%
<i>Sphingobacterium siyangense</i> KMSDrP2 ( JN034433)	Zinc-exporting ATPase, <i>Sphingobacterium spiritivorum</i> ATCC 33861, (ZP 07080472), 66%
<i>Sphingobacterium siyangense</i> KMSDrP3 ( JN034434)	Zinc-exporting ATPase, <i>Sphingobacterium spiritivorum</i> ATCC 33861, (ZP 07080472), 66%
<i>Sphingobacterium siyangense</i> KMSZPIII ( JN634870)	Zinc-exporting ATPase, <i>Chryseobacterium gleum</i> ATCC 35910, (ZP 07089093), 76%
<i>Bacillus cereus</i> KMSII3 ( JN222560)	Zinc-transporting ATPase, <i>Bacillus thuringiensis</i> serovar <i>israelensis</i> ATCC 35646, (ZP 00741169), 99%

<sup>a</sup> Accession number obtained from NCBI GenBank for identified P<sub>IB</sub>-type ATPase gene are given in parenthesis

<sup>b</sup> Closest identified match (phylogenetic neighbours) of the identified gene in NCBI GenBank database. Numbers in parenthesis indicate their GenBank accession numbers followed by maximum identity percentage