Supporting Information

Role of nanoparticles in controlling arsenic mobilization from sediments near a realgar tailing

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10 pages (including cover page)

2 Tables

10 Figures

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Table S1 Results of some partial 16S rDNA sequences using BLAST in GenBank

Band	Phylogenetic clade	Best match	Similarity (%)
1	*Firmicutes*	uncultured bacterium D24NaBa31(HM438741)	91
2	*Firmicutes*	uncultured bacterium D14R15C102(FM956765)	89
3	*Firmicutes*	uncultured *Clostridia* X3Ba50(AY607140)	94
4	*α-proteobacteria*	uncultured bacterium; PISD-ALB01(AM982632)	82
5	*Firmicutes*	uncultured bacterium EXP.12C-17(AB273851)	86
6	*Firmicutes*	uncultured bacterium; D14R15C33 (FM956741)	94
7	*Nitrospira*	uncultured *Nitrospira* sp. DOK754 (DQ828962)	99
8	*γ-proteobacteria*	*Pseudomonas fulva* BFPB51 (EF600849)	82
9	*Actinobacteria*	actinobacterium ICS20411 (AY456210)	100
10	*Firmicutes*	*Alicyclobacillus* sp. Talven1(EU282873)	100
11	*Gemmatimonadetes*	Iron-reducing bacterium HN122(FJ269078)	91
12	*Firmicutes*	*Alicyclobacillus* sp. NBFF123(AY389833)	92
13	*Firmicutes*	*Alicyclobacillus* sp. WB128(JX133663)	100
14	*Firmicutes*	*Alicyclobacillus* sp. A3608(FJ869170)	94

Table S2. Results of partial 16S rDNA sequences using BLAST in GenBank

Band	Phylogenetic clade	Best match	Similarity (%)
1	*δ-proteobacteria*	uncultured *Geobacter* sp. ZJ-20d-30 (JN091616)	96
2	*δ-proteobacteria*	uncultured *delta proteobacterium* FTL101(AF529129)	93
3	*δ-proteobacteria*	uncultured *Geobacter* sp. L6-A7 (EU595792)	100
4	*δ-proteobacteria*	uncultured *Geobacter* sp. FH-1 (AB293247)	87
5	*δ-proteobacteria*	uncultured *delta proteobacterium* 032T7(DQ110030)	91
6	*Firmicutes*	uncultured bacterium TSNSR003_C15 (AB487756)	91
7	*δ-proteobacteria*	uncultured bacterium Lac302-6A (AY524547)	96
8	*δ-proteobacteria*	uncultured *Geobacter* sp. GS11 (JF736631)	83
9	*δ-proteobacteria*	uncultured *Geobacter* sp. GG-11 (JF736641)	83
10	*Firmicutes*	uncultured bacterium DGS2-42 (GU056116)	93
11	*δ-proteobacteria*	uncultured *Geobacter* sp. CFC1(JF736650)	81
12	*δ-proteobacteria*	uncultured bacterium AR162 (GQ860181)	91
13	*β-proteobacteria*	uncultured bacterium 81(FJ535025)	93
14	*Chloroflexi*	uncultured *Chloroflexi* bacterium g16(EU979025)	100

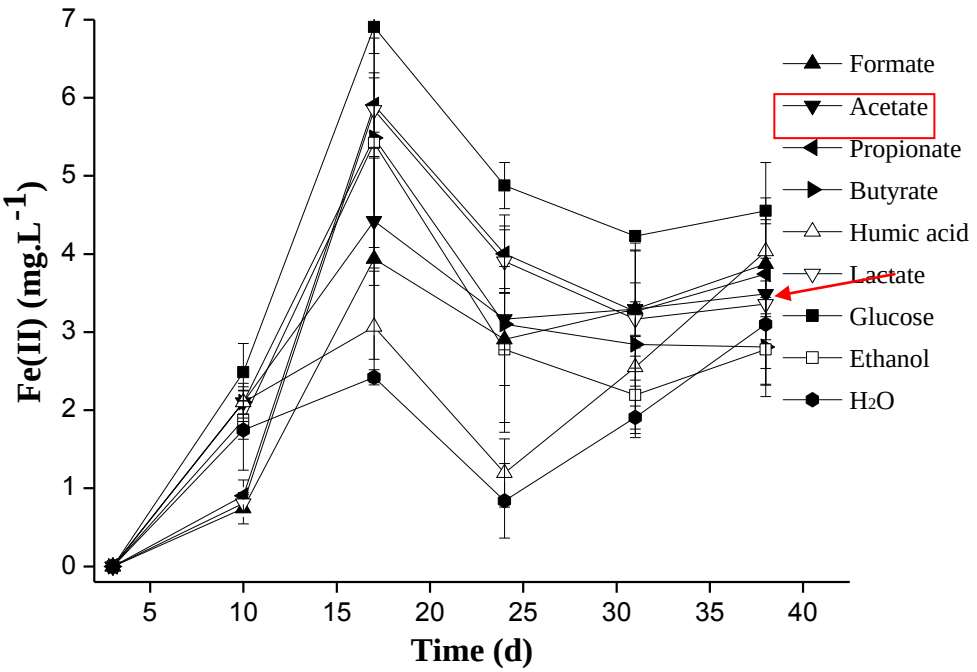


Fig. S1 Microbial impact on Fe(II) release from sediments amended with different organic carbon in microcosms under anaerobic conditions.

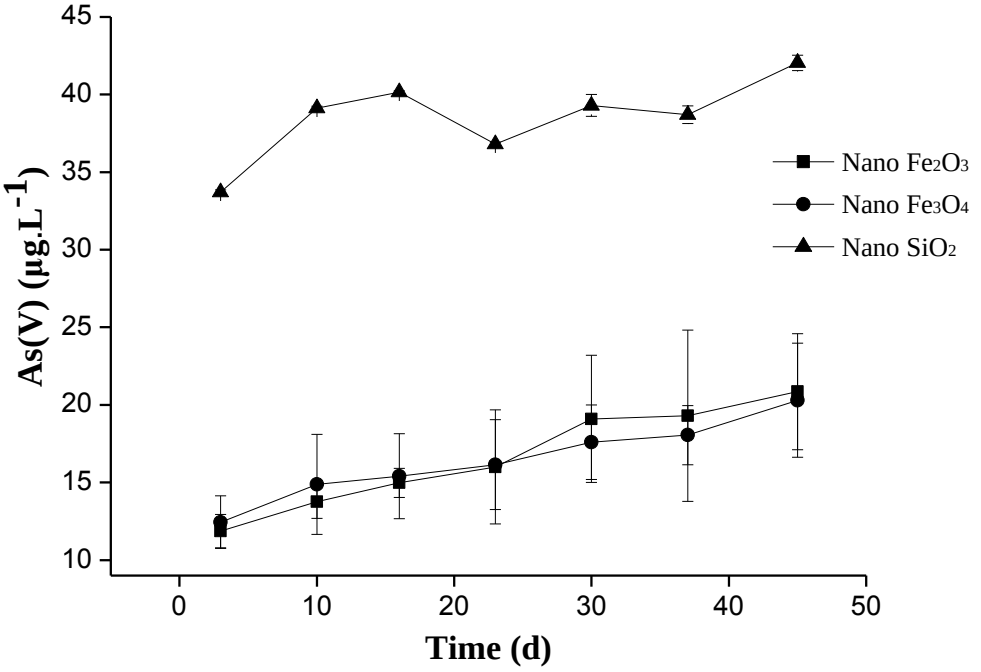


Fig. S2 As(V) release from sediment amended with different NPs(abiotic controls).

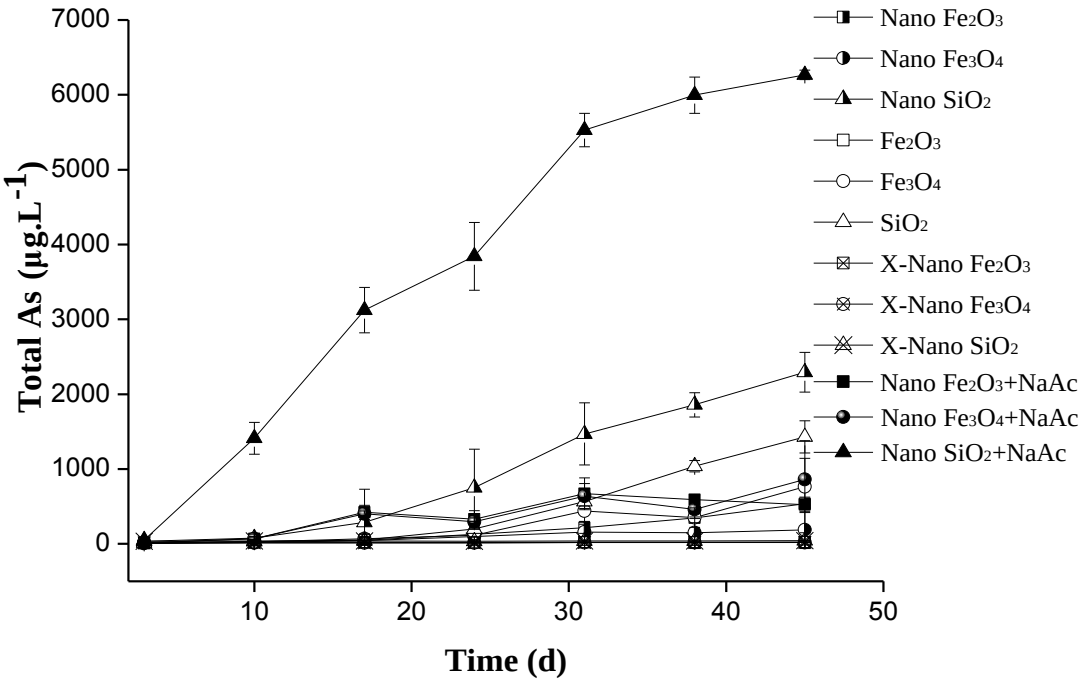


Fig. S3 Microbial mediated As release from sediment amended with different NPs.

X: abiotic controls

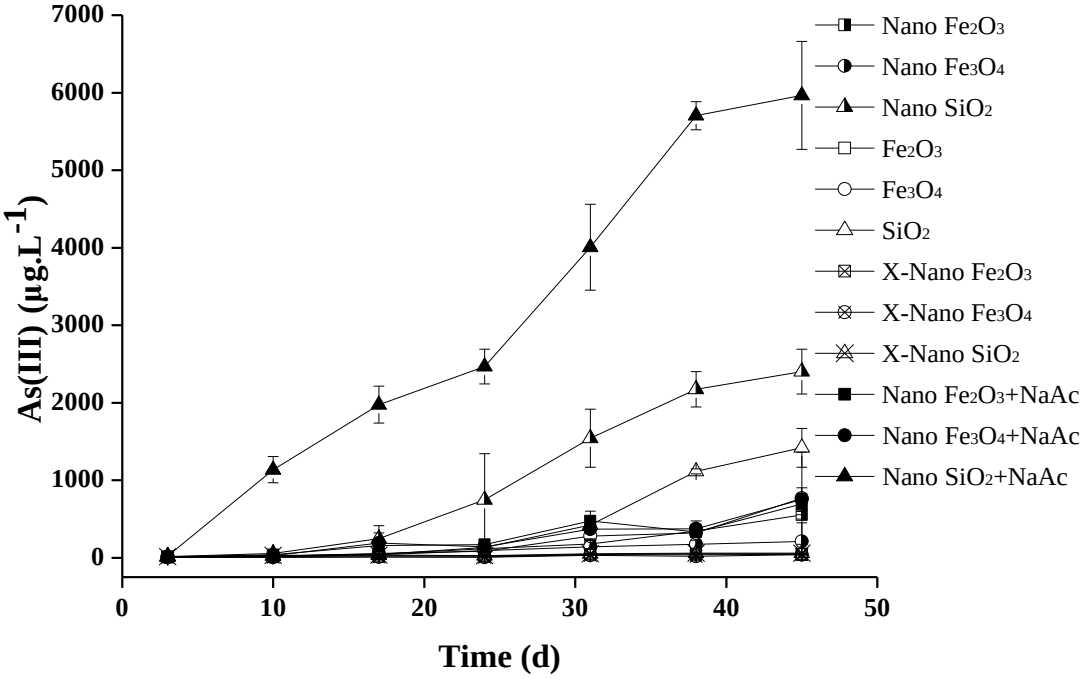


Fig. S4 Microbially mediated As(III) release from sediment amended with different NPs.

X: abiotic controls

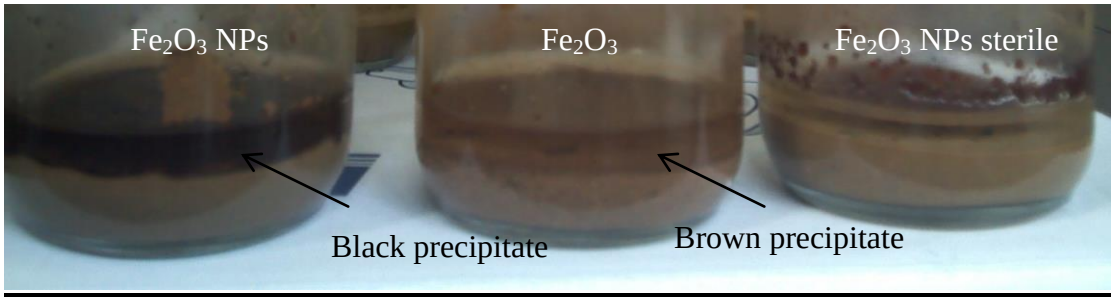


Fig. S5 Sediments amended with Nano Fe_2O_3 or Fe_2O_3 particles.

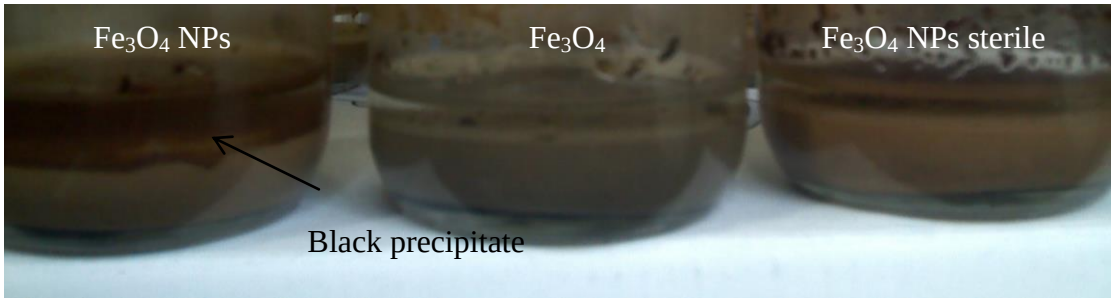


Fig. S6 Sediments amended with Nano Fe_3O_4 or Fe_3O_4 particles.

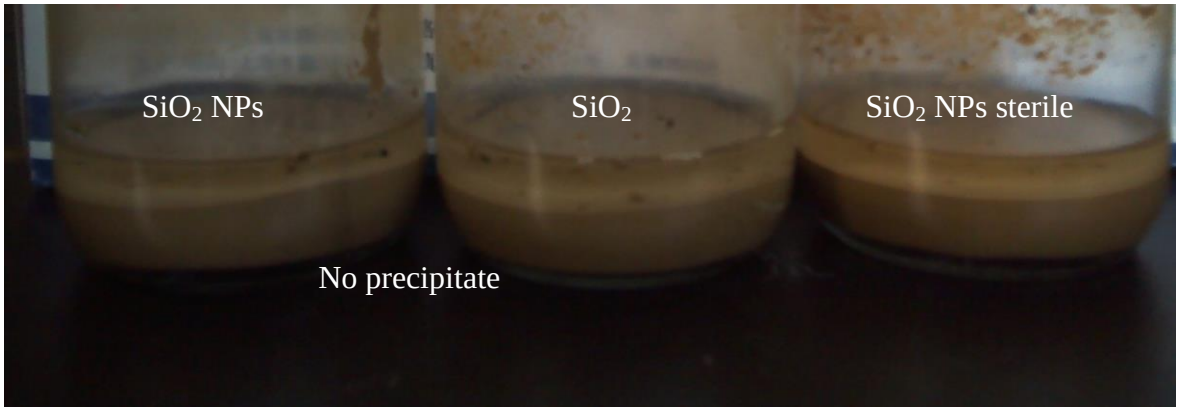


Fig. S7 Sediments amended with Nano SiO_2 or SiO_2 particles.

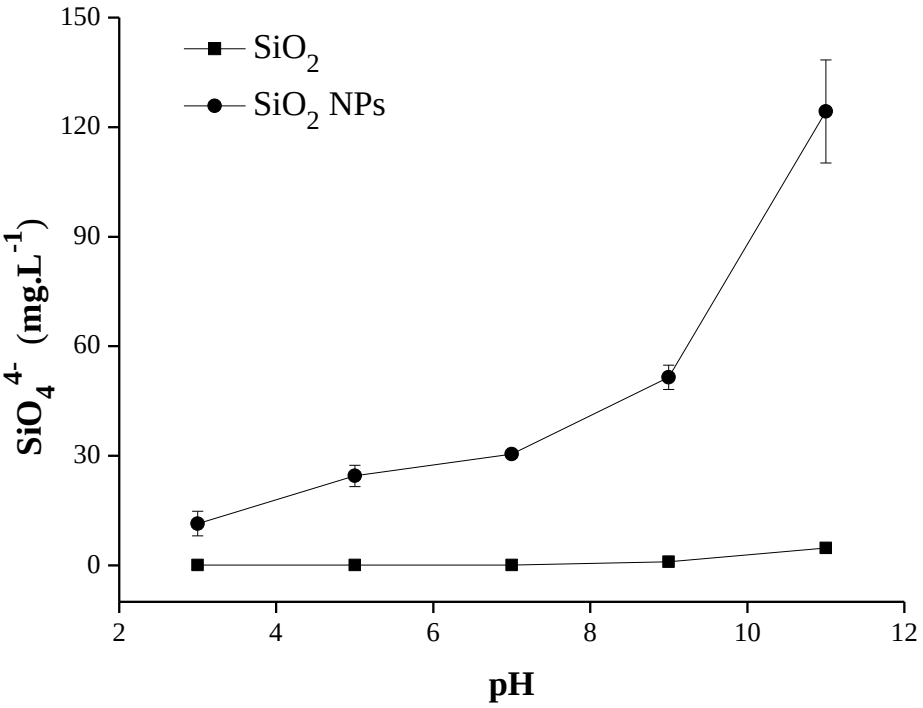
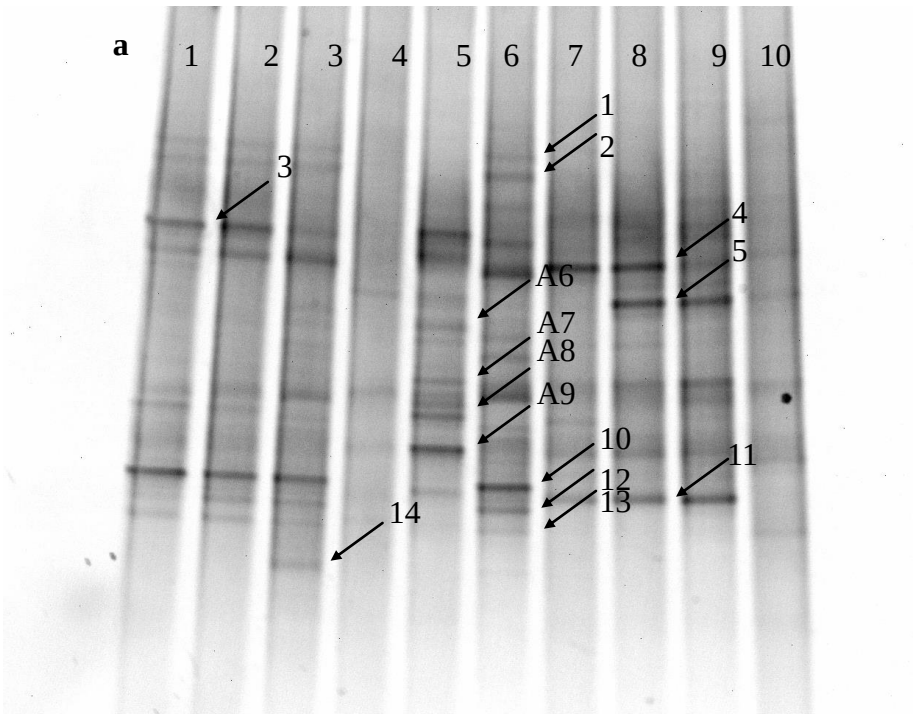


Fig. S8 Influence of pH on dissolution of SiO_2 NPs and SiO_2 Non-NPs with shaking at 150 rpm within 24 h.



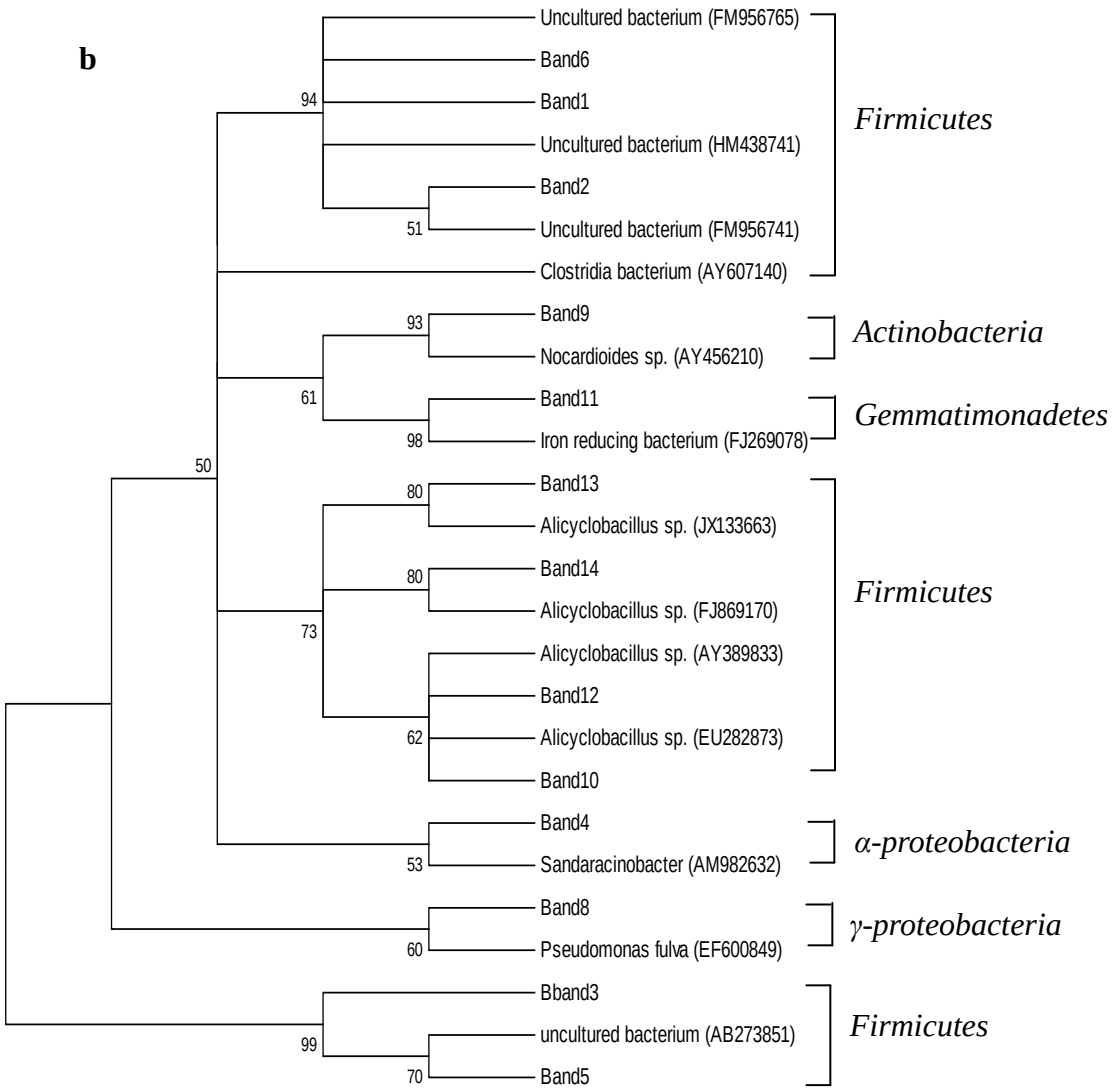
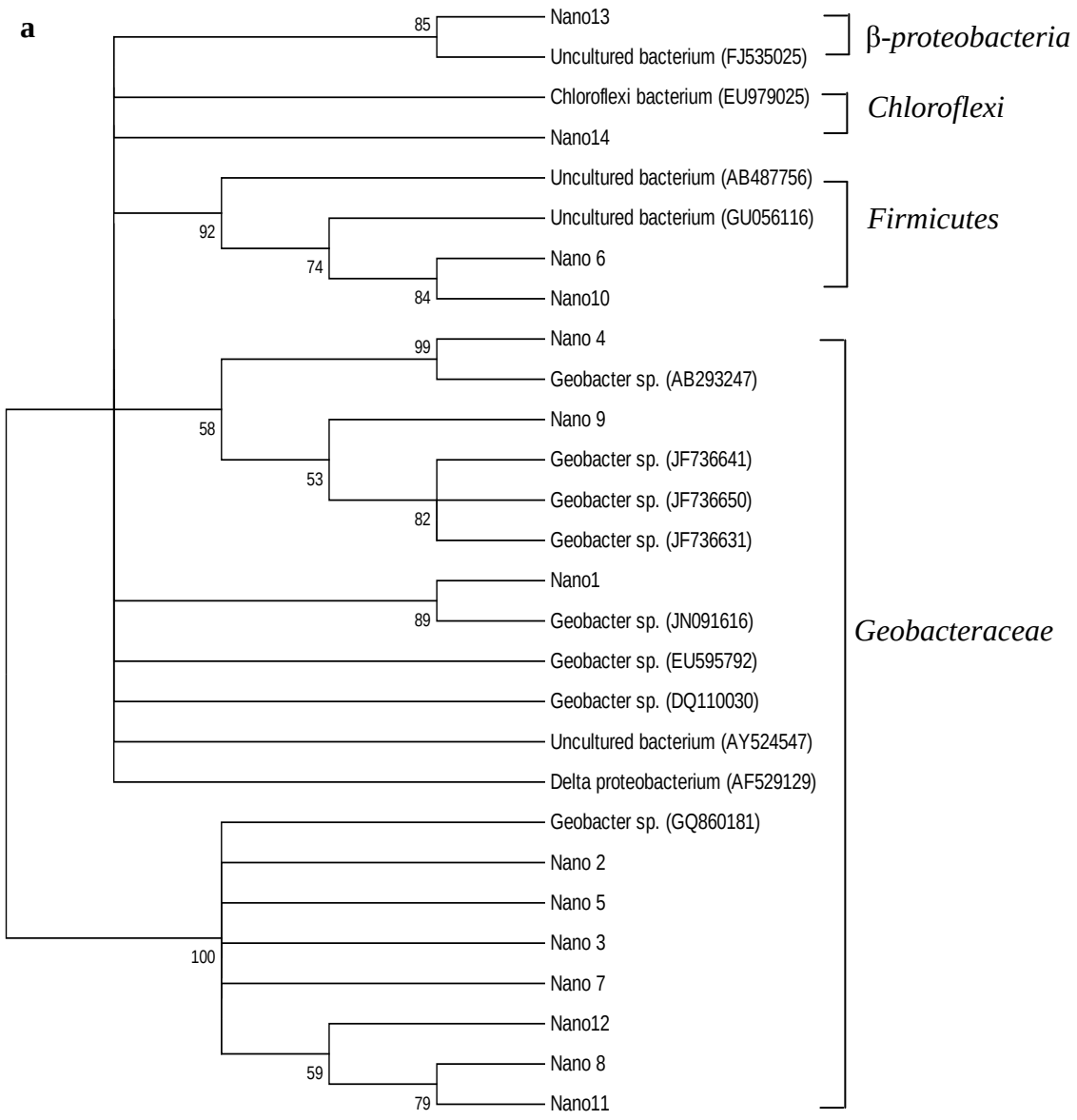


Fig. S9 DGGE profiles of 16S rRNA fragments amplified from DNA extracted from sediments amended with NPs (a); Phylogenetic tree of 16S rRNA gene clones from the sediments amended with NPs (b) (1:SiO_2 NPs; 2: Fe_2O_3 NPs; 3: Fe_3O_4 NPs; 4: SiO_2; 5: Fe_2O_3; 6: Fe_3O_4; 7: NaAc+SiO_2 NPs; 8: NaAc+Fe_2O_3 NPs; 9: NaAc+Fe_3O_4 NPs; 10: Control).


a
Nano13
Uncultured bacterium (FJ535025)
Chloroflexi bacterium (EU979025)
Nano14
Uncultured bacterium (AB487756)
Uncultured bacterium (GU056116)
Nano 6
Nano10
Nano 4
Geobacter sp. (AB293247)
Nano 9
Geobacter sp. (JF736641)
Geobacter sp. (JF736650)
Geobacter sp. (JF736631)
Nano1
Geobacter sp. (JN091616)
Geobacter sp. (EU595792)
Geobacter sp. (DQ110030)
Uncultured bacterium (AY524547)
Delta proteobacterium (AF529129)
Geobacter sp. (GQ860181)
Nano 2
Nano 5
Nano 3
Nano 7
Nano12
Nano 8
Nano11
85
92
74
84
99
58
53
82
89
100
59
79
β-proteobacteria
Chloroflexi
Firmicutes
Geobacteraceae

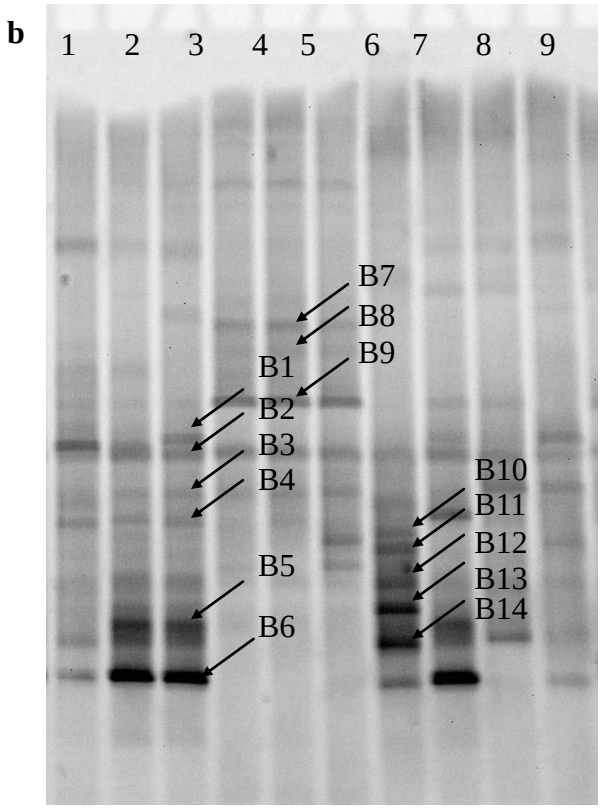


Fig. S10. *Geobacteraceae* community composition in sediments amended with NPs (a) Phylogenetic tree of *Geobacteraceae* clones from sediments amended with NPs (b). (1:SiO_2 NPs; 2: Fe_2O_3 NPs; 3: Fe_3O_4 NPs; 4: SiO_2; 5: Fe_2O_3; 6: Fe_3O_4; 7: NaAc+SiO_2 NPs; 8: NaAc+Fe_2O_3 NPs; 9: NaAc+Fe_3O_4 NPs; 10: Control).