Supplementary data
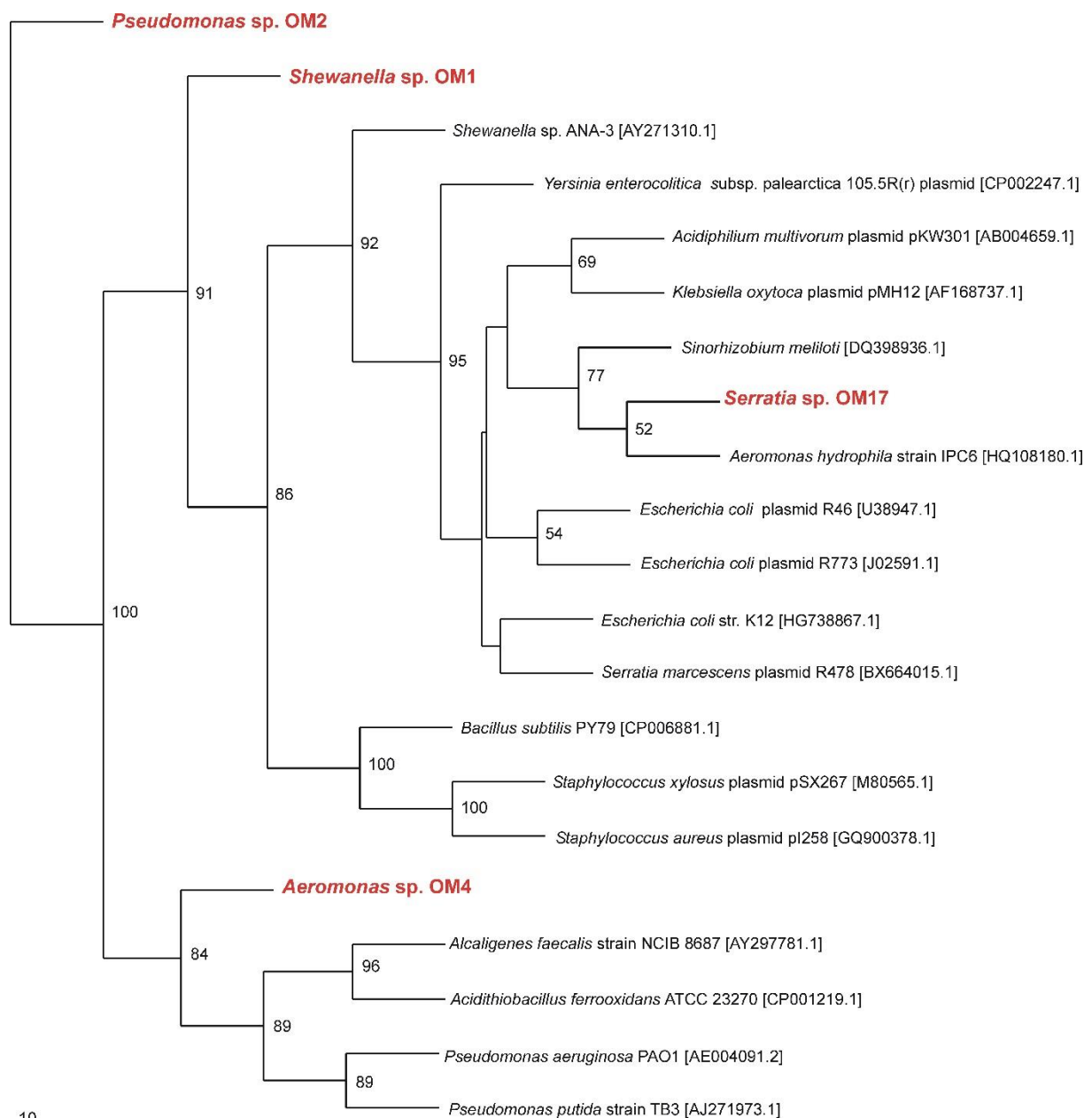
Table S1. Nucleotide sequences of cytoplasmic arsenate reductase (*arsC*) and respiratory arsenate reductase (*arrA*) genes

Strain	Nucleotide sequence 5'→3'
cytoplasmic arsenate reductase (*arsC*) genes	
Shewanella sp. OM1	GTGCTCTTTCTATGTACCCATAATGCCTGTCGCAGCATCCTAGCTGAAGCTATAGGTCGAGATCTCG TCGGTAAGCAAGCTTTGACTACTATTGCTCAATGGCAATTTGCGAGTGCCGGTCGTGAACCTGCCG GGGTCGTTCATCCTCAAACTCTATTGCAACTAGCACACAGAGGCTATGTTACCGAAGGGCTCTCCAG CAAAAGCTGGGTTATGATGGCGGATTTCACTCCTGACTTAGTGATCACTGTTTGTGATAATGCTGCG GGAGAAACCTGTCCTTTGTGGTTAGGTCAAACACTTAAATTACATTGGGGTTTACCCGACCCAACAT CAATCGACGCCCCCGATATAGATGAGCAATTTAGCTATGTTATAGAAACACTT
Pseudomonas sp. OM2	AGATTAGTCCTGTTCATGTGCACGGCCAACAGCTGCCGCAGCATCCTCTCTGAAGCCATGTTCAATC ATCTGGCGCCAGCGGGATTCGAAGCGGTGAGTGCCGGCAGCTTCCCCAAAGGTCAGGTGTTGCCG CGCAGCCTGTCGACGCTGCAACAGGCCGGCATCGCCATTGATGGTTTGCACAGCAAAGGCAACGAC GCTTTTGAAAGCAACCCGCCGGACATCGTCATCACCGTGTGCGACAAAGCCGCTGGCGAGACTTGC CCGGTGTATTTCGGCCCGGCGCTGAAATCCCACTGGGGGCTGGAAGATCCCTCCGAAGTGAAGGG CGACGAAGCCACTGTCGACGCGGCATTCCACGCCAAATCAC
Aeromonas sp. OM4	ATGCACAGGCAACTCTTGCCGTTCCATTCTGGCAGAGGCGACCTTTAACCACCTGGCTCCAGCCGGT TGGCATGCCATGAGTGCCGGTAGTCAGCCAACCGGTGAGGTGCATCCCCGTTCACTGGCGTTATTG ACCCGCGAAGGTATCGATATCAGCGGATTGCACAGCAAATCCTGGCATGAGCTGCCGGTGACGCCC GATGTTGTGATCAGCGTGTGTGGTAACGCGGCCAATGAAACCTGTCCTGTCTATTTGGGGCCTGTAT TGCGAGCCCACTGGGGCGTAGATGATCCCGCCCATGTGACCGGCAGCGAGGAGCAGATAGCGCTC GCCTTTCACTGTGCATACTCGACGCTGAGAAAGCGTATCGAAGCCCTCTTGTCGCAG
Serratia sp. OM17	ACGTACCAGCCGGCTTGCGGCACATCGCGCAATACGTTGGCACTGATCCGCAACAGTGGTGTGGAA CCGACGGTGATTTTGTATCTGGAGACACCGCCCGACCGTCAGCAATTGCTCAAGCTGATTGCCGATA TGGGGATATCTGCGCGAGCCTTATTGCGTAAAAACGTGGAGCCTTATGAATCGTTGGGGCTGGCGG AGGTAGGCTGGAGTGACGAACAGTTGATCGACTTTATGTTGCAACAGCCGATATTGATTAATCGAC CTATTGTGGTGACACCCTTGGGCACCCGTCTGTGTCGACCGTCGGAAGCCGTGCTGGATATCCTGCC GGATCCGCAGCAAGGTCCTTTCACTAAGGAAGACGGTGAAAAAGTA
respiratory arsenate reductase (*arrA*) genes	
Shewanella sp. OM1	GCCCTTAAGGTGTATGGAATAAAGCGTTTGTTGGAGATTTTATTGAGGGTAAAAACCTGTTTAAAGC GGGTAAAACCGTCCGTATCGAGAGCTTTAAAGAAAGCCATACCTACGGTTTAGTGGAGTGGTGGAA CCAAGCTCTTAAAGACTATACCCCGAAGTGGGCACCTGAAATCACAGGAAGGGC
Pseudomonas sp. OM2	GCCCTTAAGGTGTATGGAATAAAGCGTTTGTTGCCGATTTCACTGACCCTGACCAGCGCTTTGTCAC CGGGCAGCCGGTGAGCGCAGAGCTCTTCGCCGAGCGTCATACCCATGCTCTGGTGCAATGGTGGA ATCTAGAACTGAAAGATCGGACACCCAAATGGGCACCTGAAATCACAGGAAGGGC
Aeromonas sp. OM4	GATAAGGTGTATGGAATAAAGCGTTTGTGGGAGACTTCACTGACCCTGAGCAGCGCTTTGTCACCG GGCAGCCGGTGAGCGCAGAGCTCTTCGCCGAGCGTCATACCCATGGTCTGGTGCAATGGTGGAAT CTGGAACTGAAAGATCGGACACGCCGAAATGGGCACCTGAAATCACAGGAATCACTAGT
Serratia sp. OM17	AAGGTGTATGGAATAAAGCGTTTGTGGGCGACTTCACCGACCCTGAGCAGCGCTTTGTGGACCGGC CAGCCGGTGAGCGCAGAGCTCTTCACCGAGCGTCATACCCATGGTCTGGTGCAATGGTGGAATCTG GAACTGAAAGATCGGACCCCCAAATGGG CACCTGAAAT CACAGG

Figure S1. Phylogenetic tree of the cytoplasmic arsenate reductase gene (*arsC*) based on 21 sequences. The unrooted tree was constructed using the Maximum Parsimony algorithm according to Kimura model. The statistical support for the internal nodes was determined by 100 bootstrap replicates. Values of >50% are shown. Accession numbers of the nucleotide sequences used for the phylogenetic analysis are given in parentheses. Sequences derived from arsenate respiratory isolates (OM1, OM2, OM4, OM17) are indicated in large bold red type, sequences derived from others strains are indicated in black type.
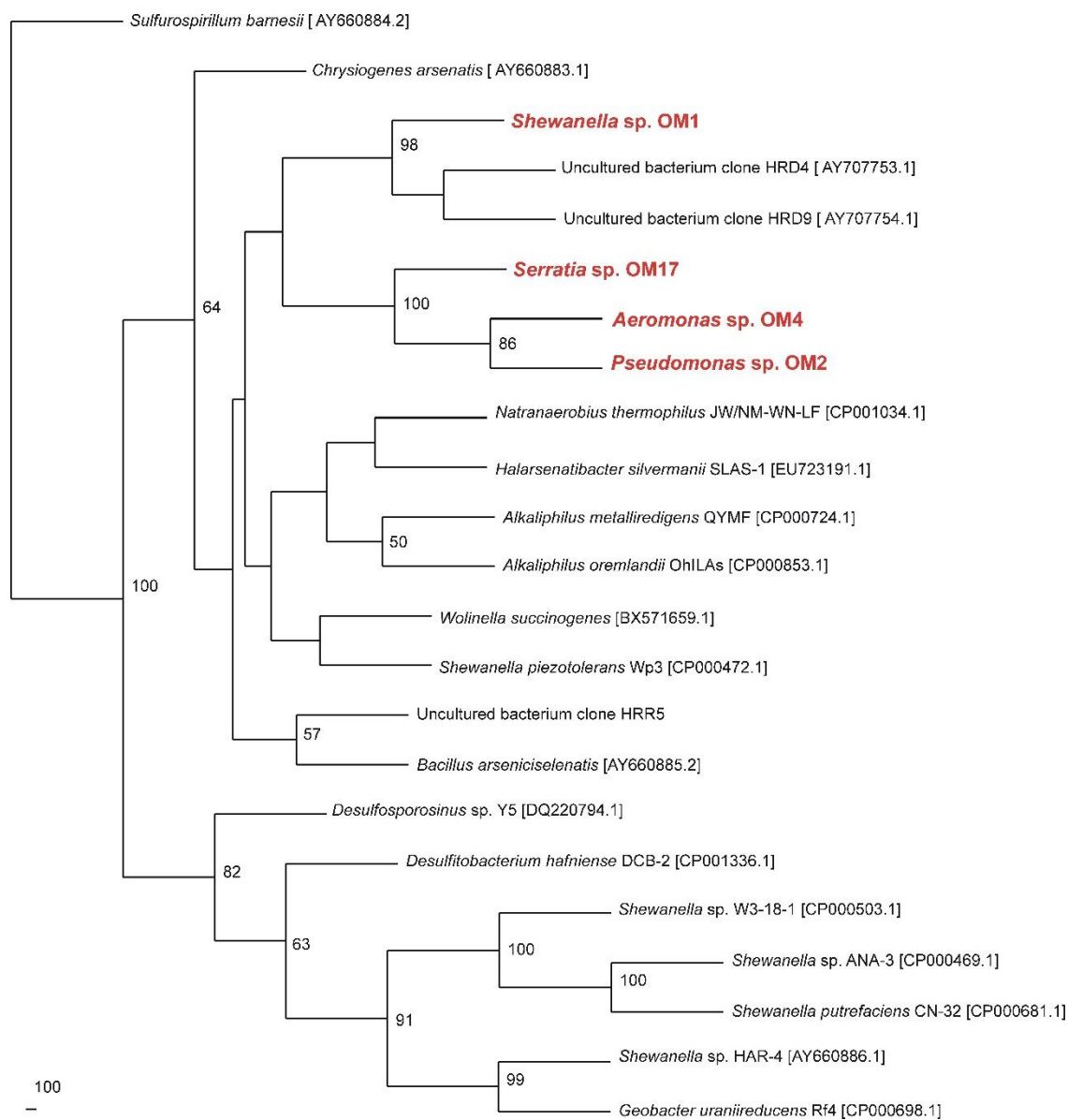
Figure S2. Phylogenetic tree of the respiratory arsenate reductase gene (*arrA*) based on 23 sequences. The unrooted tree was constructed using the Maximum Parsimony algorithm according to Kimura model. The statistical support for the internal nodes was determined by 100 bootstrap replicates. Values of >50% are shown. Accession numbers of the nucleotide sequences used for the phylogenetic analysis are given in parentheses. Sequences derived from arsenate respiratory isolates (OM1, OM2, OM4, OM17) are indicated in large bold red type, sequences derived from others strains are indicated in black type.