



Figure S1: Location of sampling points in treatment peatland (TP) A and B. Boundaries of the TPs are indicated in white. The wastewater inlet and outlet points are marked with white ovals. Water samples were collected from all sampling points, soil samples were collected from sampling points TP A1, A5 and B2. The aerial photograph was provided by the National Land Survey of Finland (March 2015).

Table S1: Total As concentrations and As speciation in surface waters of TP A and TP B. Sampling was conducted in June 2017. Samples were stabilized on-site with HCl to prevent changes in As speciation.

Sampling point	Distance from inlet (m)	As _{tot} (µg L ⁻¹)	Arsenate (µg L ⁻¹)	Arsenite (µg L ⁻¹)	Recovery (%)
TP A1	52	20.7	17.4	2.1	94
TP A2	168	28.2	25.5	<0.1	92
TP A3	384	0.3	n.a. ^a	n.a.	
TP A4	523	0.1	n.a.	n.a.	
TP A5	629	0.6	n.a.	n.a.	
TP A6	752	1.4	n.a.	n.a.	
TP A7	1083	< 0.1	n.a.	n.a.	
TP B1	203	33.1	28.9	<0.1	87
TP B2	324	30.9	26.2	1.6	90
TP B3	539	28.2	22.7	4.3	96

^a not analyzed: As speciation could not be analyzed due to too low total As concentrations.

Table S2: Arsenic concentrations in peat and porewater at the point where samples were taken for incubations and molecular studies. Samples were taken in June 2017. Porewater samples were flash frozen on-site to prevent changes in As speciation.

Sampling point	Depth (cm)	Peat		Porewater							Recovery (%)
		As _{tot} (mg kg ⁻¹)	As _{tot} (µg L ⁻¹)	Arsenate (µg L ⁻¹)	Arsenite (µg L ⁻¹)	methylated species (µg L ⁻¹)	thiolated species (µg L ⁻¹)	methylthiolated species (µg L ⁻¹)	unidentified As species (µg L ⁻¹)		
TP A1	10	196	24.5	20.8	2.2	0.2	0.0	0.3	0.8	112	
	50 ^a		132	2.0	37.7	6.9	3.6	8.0	1.0	47	
	60	5.1	69.8	1.3	10.0	4.7	<0.1	1.5	0.8	28	
TP A5	10	9.37	15.7	<0.1	0.9	10.6	<0.1	0.1	2.5	90	
	60	3.77	6.14	<0.1	0.5	5.2	<0.1	<0.1	1.4	116	

^a Porewater data from 50 cm are provided additionally due to the very low recovery in the 60 cm As speciation data (the reason for the large As loss in this sample is currently unclear)

Table S3: Additional primer sets tested. The primer sets were tested with PCR cycling programs varying in annealing temperature, annealing and elongation times as well as cycle numbers, variations in primer concentrations and different PCR master mixes.

Gene	Primer set	Forward primer	Reverse primer	Expected PCR product length (bp)	References	Problem
<i>aioA</i>	aoxFM1-2f/ aoxBM2-1R	CCA CTT CTG CAT CGT GGG NTG YGG NTA	GGA GTT GTA GGC GGG CCK RTT RTG DAT	550	Quemeneur et al., 2010 ^a	PCR product unspecific (obtained sequences not <i>aioA</i>)
	arrAf/ arrAr	AAG GTG TAT GGA ATA AAG CGT TTG TBG GHG AYT T	CCT GTG ATT TCA GGT GCC CAY TYV GGN GT	160-200	Malasarn et al., 2004	PCR product unspecific (obtained sequences not <i>arrA</i>)
	HAArrA-D1f/ HAArrA-G2-r	CCG CTA CTA CAC CGA GGG CWW YTG GGR NTA	CGT GCG GTC CTT GAG CTC NWD RTT CCA CC	500	Kulp et al., 2006	No PCR product
	TOArraF/ TOArraR	GGA TAA AAA CAC CGA TGA AGM GNA CNA AYC	CGT TGG CTC TTT CCC ASW YTC NGG RT	1446	Osborne et al., 2015 ^b	No PCR product
	ArrAUF1/ ArrAUR3	TGT CAA GGH TGT ACB DCH TGG	GCW GCC CAY TCV GGN GT	825	Fisher et al., 2008 ^c	No PCR product
<i>arsC</i>	arsCGP-Fw/ arsCGP-Rv	TGC TG ATTT AGT TGT TAC GC	TTC CTT CAA CCT ATT CCC TA	353	Villegas-Torres et al., 2011	Multiple bands, sequences from band of correct not <i>arsC</i>
	arsC6F/ arsC6R1	CAC VTG CMG RAA DGC RAR RVV DTG GCTCG	YKY CRY CBR YVA DRA TCG G	300-400	Escudero et al., 2013	No PCR product
	arsC6F/ arsC6R2	CAC VTG CMG RAA DGC RAR RVV DTG GCTCG	TTR WAS CCN ACG WTA ACA KKH YYK YC	300-400	Escudero et al., 2013	No PCR product
	arsC6F/ arsC6R3	CAC VTG CMG RAA DGC RAR RVV DTG GCTCG	YYV HWY TSK TST TCR YKR AAS CC	300-400	Escudero et al., 2013	No PCR product

^a Quemeneur M, Cebron A, Billard P, Battaglia-Brunet F, Garrido F, Leyval C et al. Population structure and abundance of arsenite-oxidizing bacteria along an arsenic pollution gradient in waters of the Upper Isle River Basin, France. *Appl Environ Microbiol* 2010; **76**: 4566-4570.

^b Osborne TH, McArthur JM, Sikdar PK, Santini JM. Isolation of an arsenate-respiring bacterium from a redox front in an arsenic-polluted aquifer in West Bengal, Bengal Basin. *Environ Sci Technol* 2015; **49**: 4193-4199.

^c Fisher E, Dawson AM, Polshyna G, Lisak J, Crable B, Perera E et al. Transformation of inorganic and organic arsenic by *Alkaliphilus oremlandii* sp. nov. strain OhILAs. *Ann N Y Acad Sci* 2008; **1125**: 230-241.

Table S4

Table S4: Next-related sequences of the groups for each gene (as defined from the phylogenetic trees) as identified by BLAST. Translated amino acid sequences were used for the BLAST search (BlastX).

	OTU	No of ASVs	No of sequences	Next relative			Next cultured relative		
				Accession number	Name	Identity (%)	Accession number	Name	Identity (%)
<i>aioA</i>	Group 1	30	14786	ALE71852, AKS29925	uncultured bacterium	93-99	TIQ91915	<i>Mesorhizobium</i> sp.	76-83
	Group 2	20	9936	AIZ47505, ADE33048	uncultured bacterium	86-99	RBL67125, AGD80889	<i>Pseudomonas</i> sp., <i>Bacillus</i> sp.	67-75
	Group 3	18	3565	AKS30090, AIZ47582	uncultured bacterium	81-99	WP_128627613, AIL29043	<i>Mesorhizobium delmotii</i> , <i>Ochrobactrum cytisi</i>	72-96
	Group 4	9	1594	AIZ47582, AKS30090	uncultured bacterium	88-92	AIL29043, APH81304	<i>Ochrobactrum cytisi</i> , <i>Agrobacterium tumefaciens</i>	81-82
	Group 5	3	488	ALE71852	uncultured bacterium	98-100	TIQ91915	<i>Mesorhizobium</i> sp.	97-99
<i>arrA</i>	Group 1	39	22506	AIZ48352, AIZ48406	uncultured bacterium	78-99	AEK98623, WP_041096744	<i>Geobacter uraniireducens</i> , <i>Sulfuritalea hydrogenivorans</i>	71-88
	Group 2	25	10639	AFG33222, AGT99106	uncultured bacterium	92-99	AEK98608, WP_091938667	<i>Geobacter uraniireducens</i> , <i>Propriovibrio dicarboxylicus</i>	81-92
	Group 3	16	7512	AIZ48282, CAZ04936	uncultured bacterium	86-96	AEK98608, BAM71999	<i>Geobacter uraniireducens</i> , <i>Geobacter</i> sp. OR-1	82-96
	Group 4	10	4971	TRZ93289	uncultured bacterium	80-94	WP_041096744, ASB34198	<i>Sulfuritalea hydrogenivorans</i> , <i>Citrobacter</i> sp.	80-92
	Group 5	5	3957	BAM71903, AGE47838	uncultured bacterium	85-100	BAM71999, AUB45117	<i>Geobacter</i> sp. OR-1, <i>Citrobacter</i> sp.	82-86
	Group 6	11	2621	AIZ48419, AIZ48396	uncultured bacterium	89-99	AEK98606, ASB34198	<i>Geobacter uraniireducens</i> , <i>Citrobacter</i> sp.	79-88
	Group 7	5	762	AGT99107	uncultured bacterium	89-94	AEK98606	<i>Geobacter uraniireducens</i>	81-85
<i>arsC</i>	Group 1	21	26281	OPG54167, PKN69701	uncultured bacterium	66-76	OPY19142, OPY86753	<i>Syntrophus</i> sp., <i>Smithella</i> sp.	65-71
	Group 2	17	14868	RME96185, OGG04701	uncultured bacterium	72-82	WP_077541149, WP_094759900	<i>Sedimentisphaera cyanobacteriorum</i> , <i>Sedimentisphaera salicampi</i>	68-80
	Group 3	7	12901	WP_107743932	uncultured bacterium	51-83	WP_012376477, XP_024744453	<i>Opitutus terrae</i> , <i>Melinomyces bicolor</i>	51-81
	Group 4	10	7164	RME43594, WP_145370046	uncultured bacterium	62-67	WP_072150859, WP_105497273	<i>Cand. Kryptobacter tengchongensis</i> , <i>Cand. Sulfolpaludibacter</i> sp.	59-66
	Group 5	5	4756	OPG54167	uncultured bacterium	82-83	WP_106821703	<i>Syntrophobacter</i> sp.	64-66
	Group 6	2	4728	WP_057292299, EFS15381	<i>Noviherbspirillum</i> sp., <i>Shigella flexneri</i>	74-76	WP_057292299, EFS15381	<i>Noviherbspirillum</i> sp., <i>Shigella flexneri</i>	74-76
	Group 7	4	4624	WP_076269977, WP_115994965	<i>Paenibacillus</i> sp., <i>Cohnella lupini</i>	84-98	WP_076269977, WP_115994965	<i>Paenibacillus</i> sp., <i>Cohnella lupini</i>	84-98
	Group 8	2	3045	WP_012468680	<i>Geobacter lovleyi</i>	63	WP_012468680	<i>Geobacter lovleyi</i>	63
	Group 9	2	2715	OGX19154	uncultured bacterium	86-91	WP_128700398	<i>Vampirococcus</i> sp.	82-87
	Group 10	2	2558	TJ07364, GBD09074	uncultured bacterium	51-67	CUS80610, WP_073093409	<i>Cand. Kryptobacter tengchongensis</i> , <i>Thermosynrotrpha lipolytica</i>	55-66
	Group 11	3	2328	OGV43810	uncultured bacterium	76-77	RUM36967	<i>Desulfovulus</i> sp.	65-66