SUPPLEMENTS

Taxonomic diversity and functional potential of microbial communities in salt lakes Gudzhirganskoe and Nukhe-Nur (Barguzin depression, Baikal Rift Zone)

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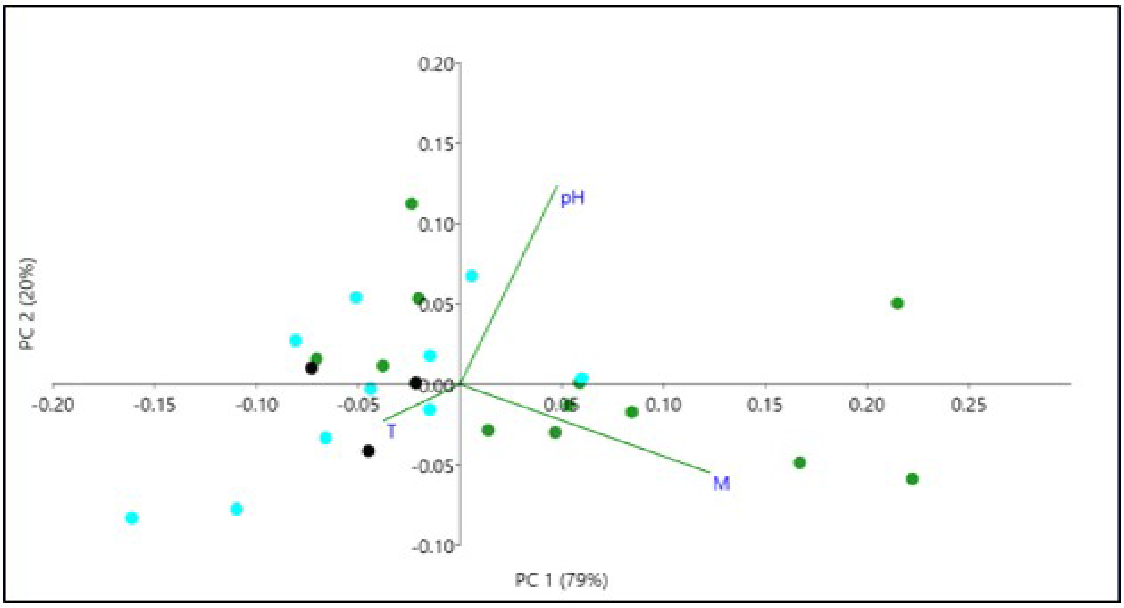

Fig. S1. Principal component analysis (PCA) of physicochemical factors influencing the composition of the dominant phylotypes in summer and winter periods in Lake Gudzhirganskoe. The vectors represent the correlation coefficient between the principal component scores and each physicochemical parameter. Green circles are the dominant genera of the summer period, blue circles are the dominant genera of the winter period, and black circles are in both seasons.

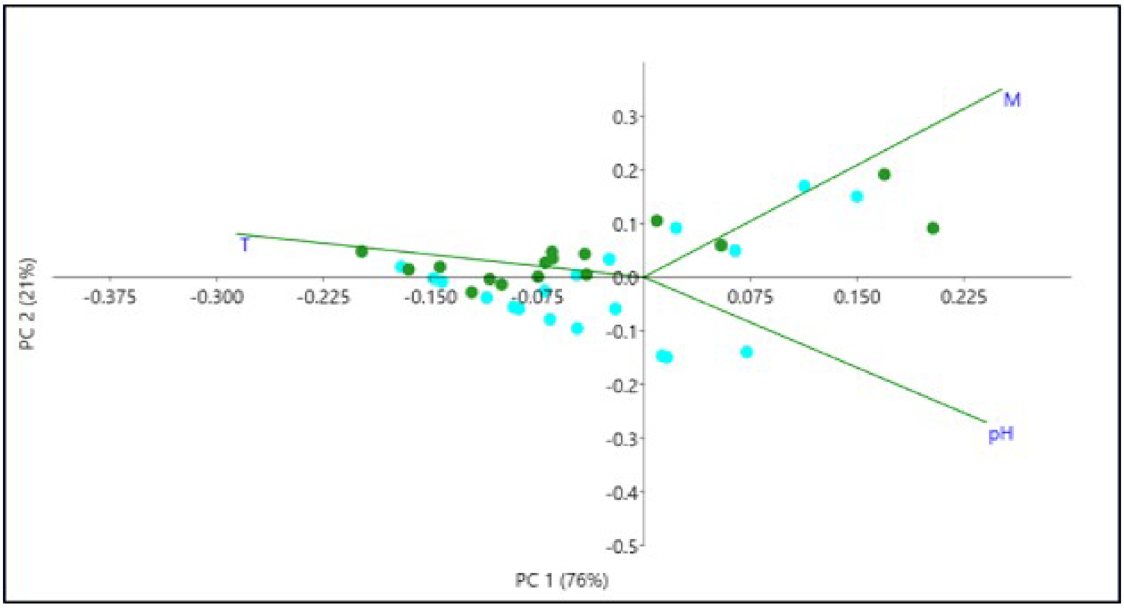

Fig. S2. Principal component analysis (PCA) of physicochemical factors influencing the composition of the dominant phylotypes in summer and winter periods in Lake Nukhe-Nur. The vectors represent the correlation coefficient between the principal component scores and each physicochemical parameter. Green circles are the dominant genera of the summer period, blue circles are the dominant genera of the winter period.

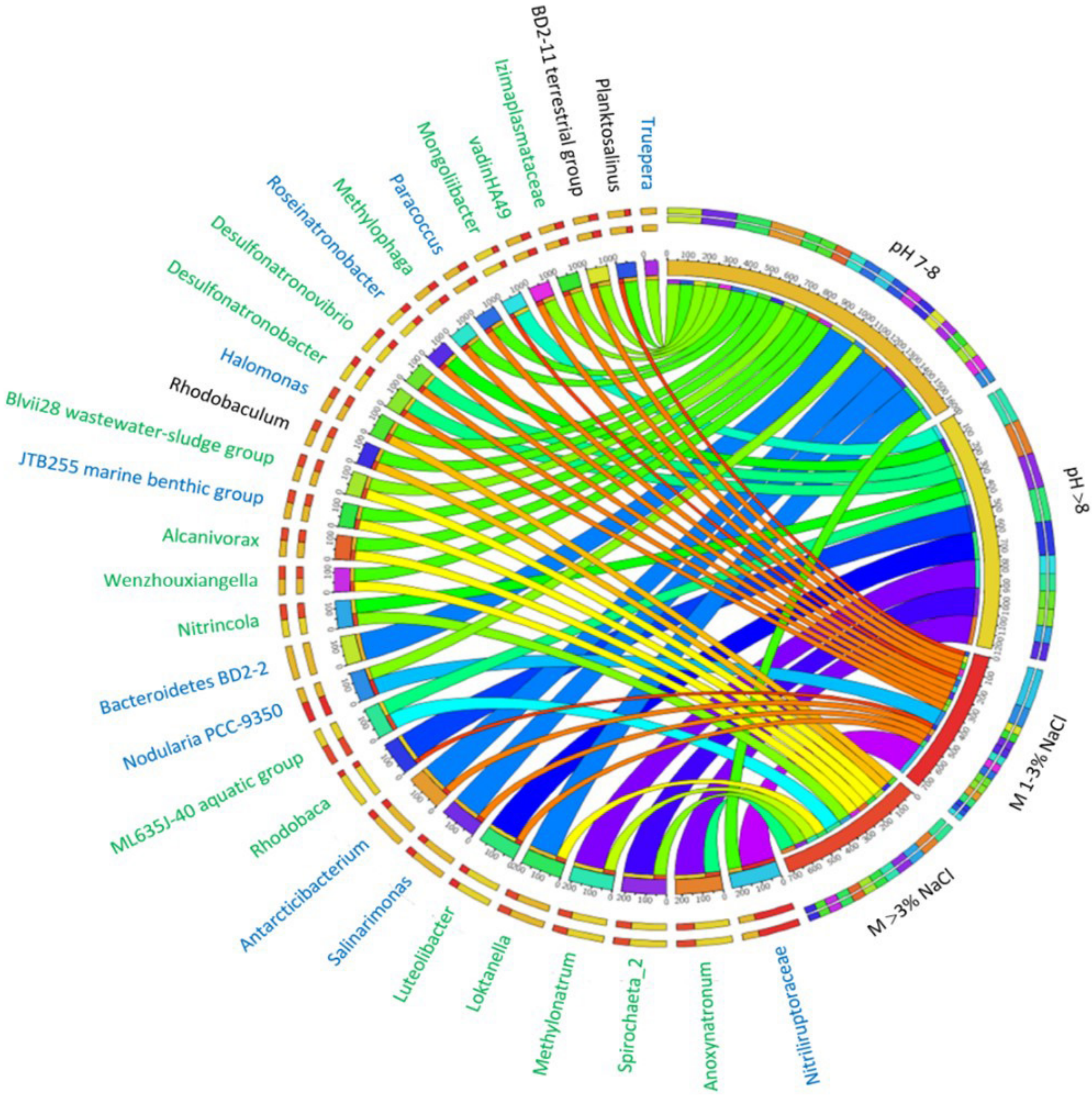

Fig. S3. Distribution of the dominant genera in the summer and winter periods in Lake Gudzhirganskoe according to the values of mineralization and pH. Green signatures are the dominant genera of the summer period, blue signatures are the dominant genera of the winter period, black signatures are in both seasons.

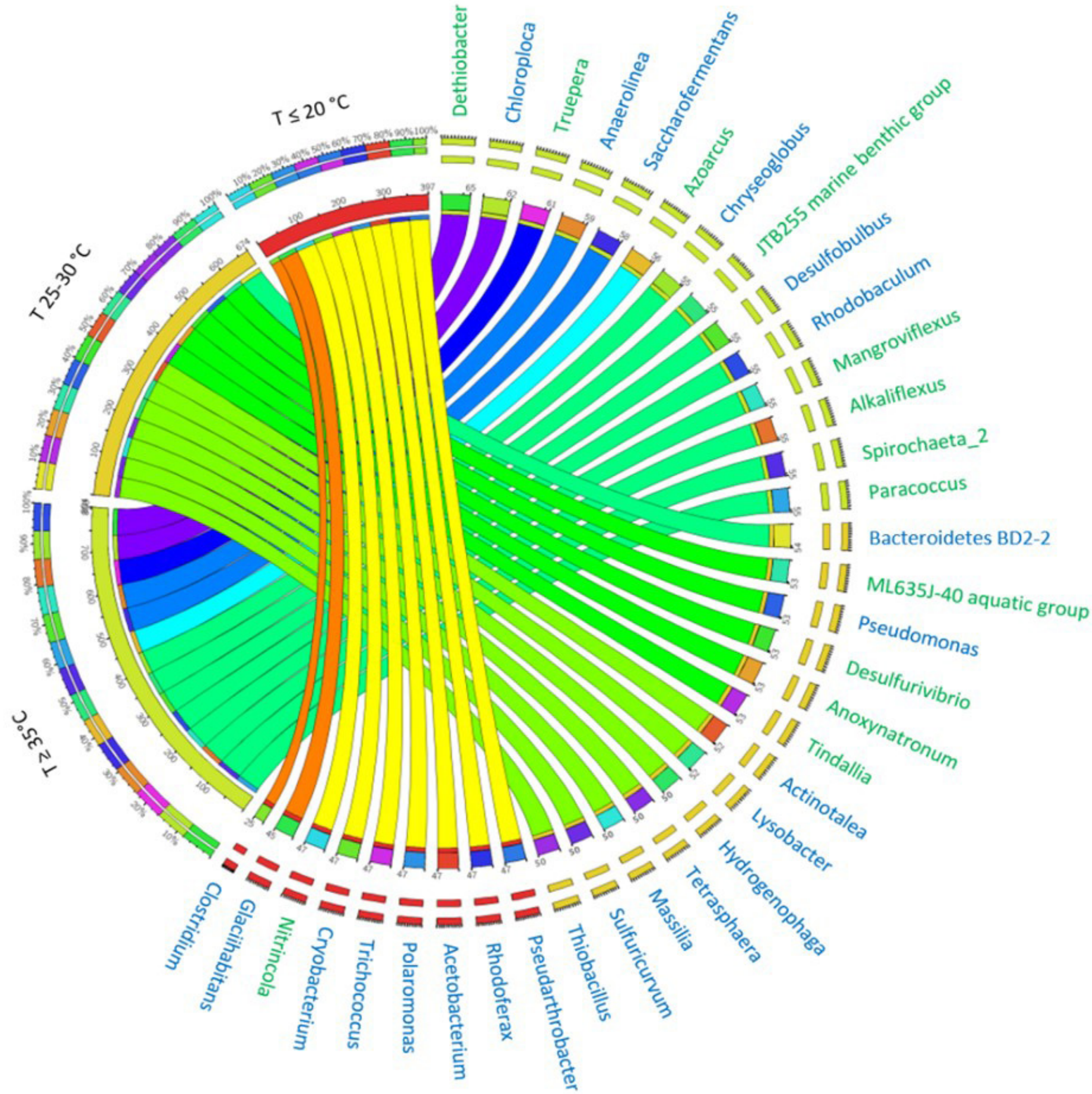

Fig. S4. Distribution of the dominant genera in the summer and winter periods in Lake Nukhe-Nur according to the values of temperature. Green signatures are the dominant genera of the summer period, blue signatures are the dominant genera of the winter period.

Table S1. Relative abundance of marker genes associated with C, N and S cycles as an indicator of metabolic pathway potential

Cycle	Step	KEGG	Gene	Gudzh_W	Gudzh_S	NN_W	NN_S	Taxon
CARBON	**Aerobic C fixation*** (Calvin cycle)	K00855	phosphoribulokinase	54	129	68	39	***Rhodobacterales**: Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Rhizobiales**: Salinarimonas* ***Methanosarcinales*** ***Methanomicrobiales*** ***Methanobacteriales***
		K01602	RuBisCO small chain	56	340	27	59	
	Aerobic CH4 oxidation	K08684	methane monooxygenase	nd	nd	nd	nd	
	Aerobic respiration	K02256	cytochrome c oxidase subunit I (coxI)	nd	nd	nd	nd	***Pseudomonadales**: Pseudomonas;* ***Micrococcales**: Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Rhodobacterales**: Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Rhizobiales**: Salinarimonas;* ***Burkholderiales**: Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Flavobacteriales**: Planktosalinus, Antarcticibacterium;* ***Desulfovibrionales**: Desulfonatronovibrio*
		K02262	cytochrome c oxidase subunit III (coxIII)	nd	nd	nd	nd	
		K02274	cytochrome c oxidase subunit I (coxA)	330	678	827	216	
		K02276	cytochrome c oxidase subunit III (coxC)	174	264	248	69	
	Anaerobic C fixation (Arnon: K00174,K00175,K00244, K01648. Reductive Acetil-CoA: K00194,K00197)	K00174	2-oxoglutarate:ferredoxin oxidoreductase subunit alpha	883	499	1190	393	***Bacteroidales**:* Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Spirochaetales**: Spirochaeta 2;* **Clostridiales**: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Anaerolineales**: Anaerolinea;* ***Rhodobacterales**: Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Lactobacillales**: Trichococcus;* ***Rhizobiales**: Salinarimonas;* ***Desulfobacterales**: Desulfonatronobacter;* ***Micrococcales**: Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Campylobacterales**: Sulfuricurvum*
		K00175	2-oxoglutarate:ferredoxin oxidoreductase subunit beta	545	311	647	240	
		K00244	frdA; fumarate reductase flavoprotein subunit	652	765	270	557	
		K01648	adenosinetriphosphate (ATP) citrate lyase	nd	nd	nd	nd	
		K00194	CO dehydrogenase subunit delta	137	80	1	19	
		K00197	CO dehydrogenase subunit gamma	263	153	4	28	
	CO oxidation	K03518	CO dehydrogenase small subunit (coxS)	150	359	529	152	***Burkholderiales**: Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* **Clostridiales**: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Spirochaetales**: Spirochaeta 2;* ***Anaerolineales**: Anaerolinea;* ***Rhodobacterales**: Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Pseudomonadales**: Pseudomonas*
		K03519	cutM, coxM; carbon-monoxide dehydrogenase medium subunit	74	461	440	145	
		K03520	cutL, coxL; carbon-monoxide dehydrogenase large subunit	75	1344	605	329	

Cycle	Step	KEGG	Gene	Gudzh_W	Gudzh_S	NN_W	NN_S	Taxon
	Fermentation	K00016	L-lactate dehydrogenase	24	31	693	366	***Lactobacillales***: *Trichococcus;* ***Clostridiales***: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Spirochaetales***: *Spirochaeta 2;* ***Acholeplasmatales***: *Acholeplasma*
	Methanogenesis	K00400	coenzyme M methyl reductase beta subunit (mcrB)	nd	1	3	1	
NITROGEN	**Ammonification**	K03385	formate-dependent nitrite reductase periplasmic cytochrome c552 (nrfA)	141	81	292	66	***Bacteroidales***: Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Clostridiales***: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13
		K05904	cytochrome c nitrite reductase (nrfA)	nd	nd	1	nd	
	Anammox (SRAO)	K10535	hydroxylamine oxidoreductase/hydrazine oxidoreductase (hao/hzo)	11	38	1	5	
	Denitrification	K00376	nitrous oxide reductase (nosZ)	188	291	38	49	***Flavobacteriales***: *Planktosalinus, Antarcticibacterium;* ***Rhodobacterales***: *Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Pseudomonadales***: *Pseudomonas;* ***Burkholderiales***: *Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Rhizobiales***: *Salinarimonas;* ***Cytophagales***: *Mongoliibacter;* ***Bacteroidales***: Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Lactobacillales***: *Trichococcus*
		K02305	nitric-oxide reductase (norC)	57	79	11	13	
		K04561	nitric-oxide reductase (norB)	217	269	103	48	
	Nitrate reduction + Nitrite oxidation	K00370	nitrate reductase alpha & nitrite oxidoreductase (narG/nxrA)	565	266	506	49	***Rhodobacterales***: *Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Pseudomonadales***: *Pseudomonas;* ***Micrococcales***: *Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Bacteroidales***: Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Clostridiales***: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Rhizobiales***: *Salinarimonas;* ***Burkholderiales***: *Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus*
		K00371	nitrate reductase beta & nitrite oxidoreductase (narH/nxrB)	288	147	206	21	
	Nitrate reduction	K02567	periplasmic nitrate reductase (napA)	272	313	77	56	***Burkholderiales***: *Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Pseudomonadales***: *Pseudomonas;* ***Campylobacterales***: *Sulfuricurvum*
		K02568	cytochrome c-type protein (napB)	41	42	12	8	

Cycle	Step	KEGG	Gene	Gudzh_W	Gudzh_S	NN_W	NN_S	Taxon
NITROGEN	**Nitrification**	K10944	ammonia monooxygenase subunit A (amoA)	nd	nd	nd	nd	
		K10945	ammonia monooxygenase subunit B (amoB)	nd	nd	nd	nd	
		K10946	ammonia monooxygenase subunit C (amoC)	nd	nd	nd	nd	
	Nitrogen assimilation (K00360+K00367+K01915+K00265+K00284)/3	K00265	glutamate synthase (NADPH/NADH) large chain (gltB)	1657	2088	2001	430	***Pseudomonadales**: Pseudomonas;* ***Campylobacterales**: Sulfuricurvum;* ***Burkholderiales**: Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Rhodobacterales**: Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Micrococcales**: Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Bacteroidales**:* Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Clostridiales**: Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Rhizobiales**: Salinarimonas;* ***Flavobacteriales**: Planktosalinus, Antarcticibacterium;* ***Spirochaetales**: Spirochaeta 2;* ***Oceanospirillales**: Alcanivorax* *Halomonas, Nitrincola;* ***Lactobacillales**: Trichococcus;* ***Desulfobacterales**: Desulfonatronobacter*
		K00284	glutamate synthase (ferredoxin-dependent) (gltS)	43	67	374	133	
		K00360	assimilatory nitrate reductase	nd	nd	1	nd	
		K00367	assimilatory nitrate reductase	nd	nd	nd	nd	
		K01915	glutamine synthetase (glnA)	2076	2600	1359	665	
	Nitrogen Fixation (K00531+K02586+K02588+K02591)/4	K00531	nitrogenase	1	6	nd	1	***Bacteroidales**:* Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Clostridiales**: Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Nostocales**: Geitlerinema PCC-7105, Nodularia PCC-9350;* ***Spirochaetales**: Spirochaeta 2;* ***Campylobacterales**: Sulfuricurvum*
		K02586	nitrogenase molybdenum-iron protein alpha chain (nifD)	177	234	22	65	
		K02588	nitrogenase iron protein (nifH)	148	194	16	71	
		K02591	nitrogenase molybdenum-iron protein beta chain (nifK)	159	251	23	65	

Cycle	Step	KEGG	Gene	Gudzh_W	Gudzh_S	NN_W	NN_S	Taxon
	Nitrogen Mineralization K00260+K00261+K00262	K00260	glutamate dehydrogenase	82	51	143	72	***Pseudomonadales***: *Pseudomonas;* ***Campylobacterales***: *Sulfuricurvum;* ***Burkholderiales***: *Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Rhodobacterales***: *Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Micrococcales***: *Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Bacteroidales***: Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Clostridiales***: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Rhizobiales***: *Salinarimonas;* ***Flavobacteriales***: *Planktosalinus, Antarcticibacterium;* ***Spirochaetales***: *Spirochaeta 2;* ***Oceanospirillales***: *Alcanivorax Halomonas, Nitrincola;* ***Lactobacillales***: *Trichococcus;* ***Anaerolineales***: *Anaerolinea;* ***Verrucomicrobiales***: *Luteolibacter*
		K00261	glutamate dehydrogenase	104	306	554	143	
		K00262	glutamate dehydrogenase	435	256	183	479	
SULFUR	**Assimilatory sulfate reduction** (K00860+K00956+K00957)/3	K00860	adenylylsulfate kinase (cysC)	157	73	90	33	***Pseudomonadales***: *Pseudomonas;* ***Burkholderiales***: *Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Micrococcales***: *Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Bacteroidales***: Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus;* ***Clostridiales***: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Rhizobiales***: *Salinarimonas;* ***Flavobacteriales***: *Planktosalinus, Antarcticibacterium;* ***Lactobacillales***: *Trichococcus*
		K00956	sulfate adenylyltransferase subunit 1 (cysN)	216	68	74	16	
		K00957	sulfate adenylyltransferase subunit 2 (cysD)	287	133	99	43	
	Dissimilatory sulfate reduction and sulfide oxidation** (K00394+K00395+K11180)/3	K00394	adenylylsulfate reductase subunit A (aprA)	355	209	10	39	***Clostridiales***: *Anoxynatronum, Tindallia, Clostridium* sensu stricto 13
		K00395	adenylylsulfate reductase subunit B (aprB)	65	38	2	0	
		K11180	sulfite reductase (dsrA)	237	131	9	2	

Cycle	Step	KEGG	Gene	Gudzh_W	Gudzh_S	NN_W	NN_S	Taxon
SULFUR	**Sulfur Mineralization**	K00456	cysteine dioxygenase	nd	nd	nd	nd	***Pseudomonadales****: Pseudomonas;* ***Burkholderiales****: Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Rhodobacterales****: Rhodobaca, Loktanella, Rhodobaculum, Roseinatronobacter, Paracoccus;* ***Micrococcales****: Tetrasphaera, Pseudarthrobacter, Actinotalea, Chryseoglobus, Glaciihabitans, Cryobacterium;* ***Clostridiales****: Anoxynatronum, Tindallia, Clostridium* sensu stricto 13; ***Rhizobiales****: Salinarimonas;* ***Flavobacteriales****: Planktosalinus, Antarcticibacterium;* ***Lactobacillales****: Trichococcus;* ***Cytophagales****: Mongoliibacter*
		K01011	3-mercaptopyruvate sulfurtransferase	455	546	635	180	
	Polysulfide reduction	K08352	polysulfide reductase chain A (psrA)	198	117	28	9	***Burkholderiales****: Hydrogenophaga, Massilia, Rhodoferax, Polaromonas, Thiobacillus, Azoarcus;* ***Bacteroidales****:* Blvii28 wastewater-sludge group, ML635J-40 aquatic group, *Bacteroidetes* BD2-2, *Mangroviflexus, Alkaliflexus*

nd stands for not determined.

Table S2. Relative abundance of KOs associated with adaptation to high salt conditions

Enzyme No	KEGG No	Type of enzyme	Gudzh_W	Gudzh_S	NN_W	NN_S
1.2.1.8	K00130	Betaine-aldehyde dehydrogenase	497	635	259	117
1.4.1.2	K00260	Glutamate dehydrogenase	82	51	143	72
1.4.1.3	K00261	Glutamate dehydrogenase (NAD(P)+)	104	306	554	143
1.4.1.4	K00262	Glutamate dehydrogenase (NADP+)	435	256	183	479
1.4.1.13/1.4.1.14	K00265	Glutamate synthase (NADPH/NADH) large chain	1657	2088	2001	430
1.4.7.1	K00284	Glutamate synthase (ferredoxin)	43	67	374	133
1.5.1.2	K00286	Pyrroline-5-carboxylate reductase	428	416	581	129
1.5.3.1	K00301	Sarcosine oxidase	26	59	84	39
1.5.3.1	K00302	Sarcosine oxidase, subunit alpha	407	1520	159	259
1.5.3.1	K00303	Sarcosine oxidase, subunit beta	243	695	312	150
1.5.3.1	K00304	Sarcosine oxidase, subunit delta	38	142	8	23
1.5.3.1	K00305	Sarcosine oxidase, subunit gamma	75	206	13	34
1.14.11.	K00674	Ectoine hydroxylase	253	316	138	63
2.7.7.42	K00982	Glutamate-ammonia-ligase adenylyltransferase	840	979	789	174
3.1.3.12	K01087	Trehalose-phosphatase	81	122	43	23
3.1.6.6	K01133	Choline-sulfatase	145	393	22	65
3.2.1.93	K01226	Trehalose-6-phosphate hydrolase	39	13	366	69
6.3.1.2	K01915	Glutamine synthetase	2076	2600	1359	665
3.6.3.32	K02000	Glycine betaine/proline transport system ATP-binding protein	493	690	203	165
2.3.1.178	K06718	L-2,4-Diaminobutyric acid acetyltransferase	92	40	11	3
4.2.1.108	K06720	L-Ectoine synthase	114	60	10	4