

# Supplementary Materials

## **Sulfidogenic microbial communities of the Uzen high-temperature oil field in Kazakhstan**

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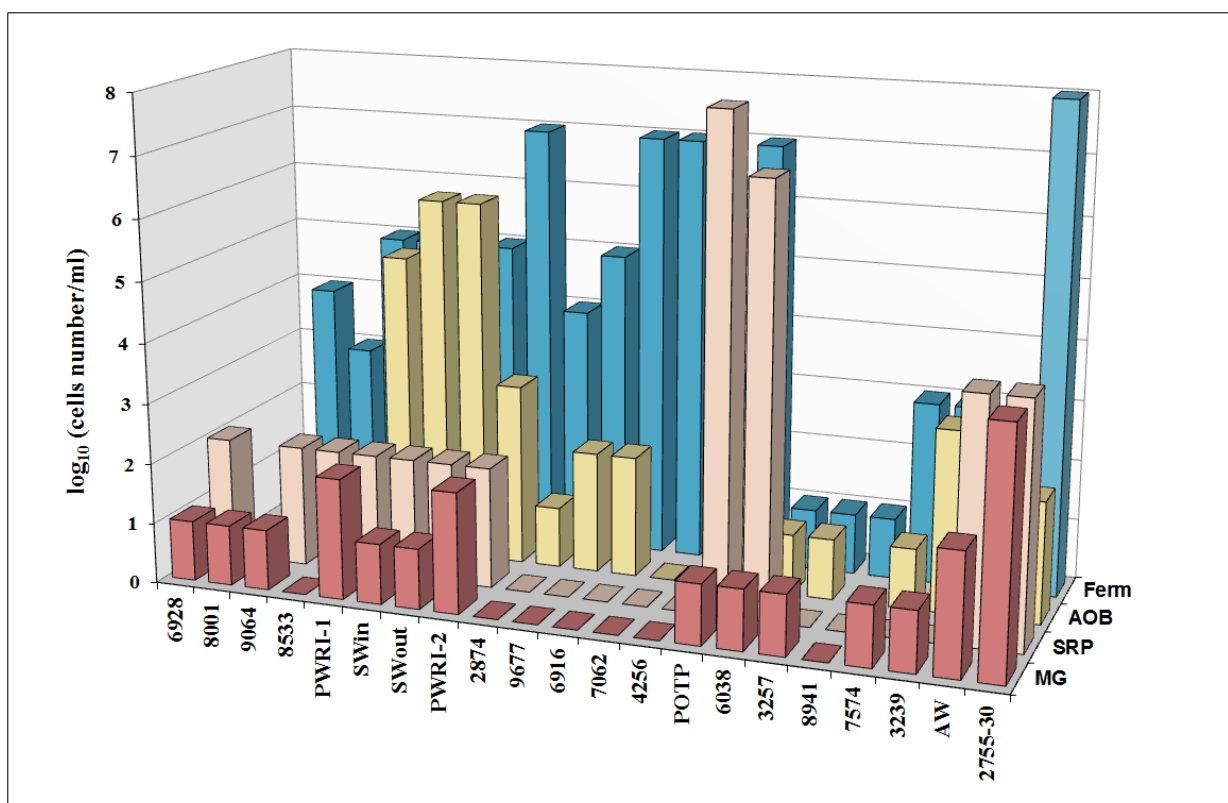
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**Table S1.** Number of sequences and diversity indices in the libraries of the 16S rRNA gene fragments from the microorganisms of injection and production water samples from the Uzen oil field.

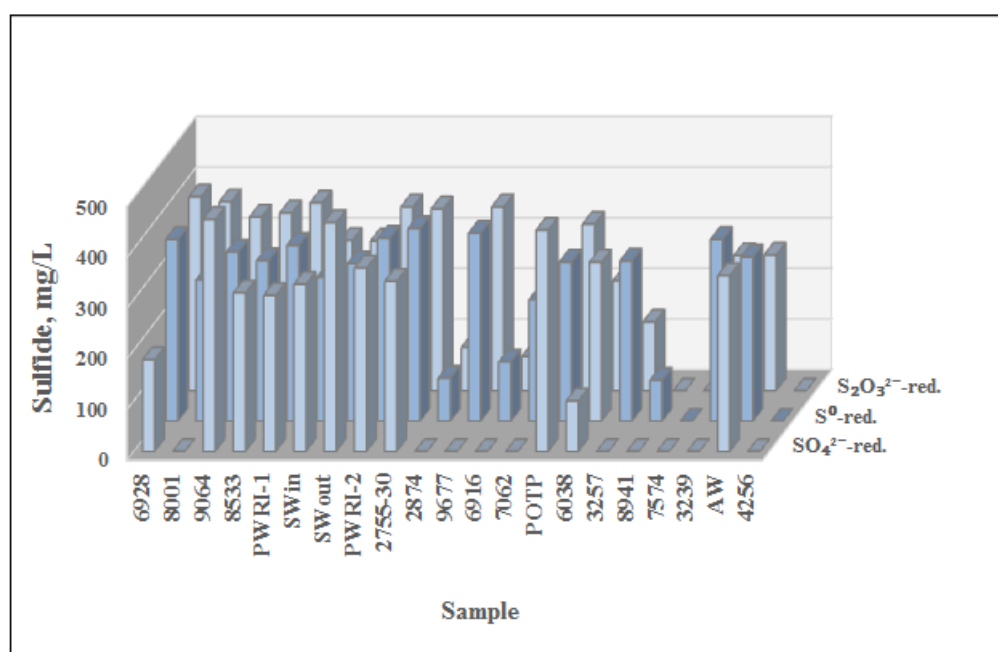
Parameters	6928	8001	9064	8533	PWRI-1	SWin	SWout	PWRI-2	2874	9677	6916
Number of reads	64500	148657	52623	53443	36839	116602	91268	65611	32435	85	76110
OTUs number	245	139	172	655	607	306	119	579	223	34	174
Shannon index (H10)	2.5	1.97	2.37	0.42	0.39	0.33	0.46	0.36	0.69	0.45	1.31
Simpson index (1-D)	0.447	0.507	0.462	0.896	0.908	0.939	0.887	0.925	0.774	0.897	0.648
	7062	POTP	6038	3257	8941	7574	3239	AW	4256	2755-30	
Number of reads	81528	26490	99504	69373	118765	72817	78836	84297	84025	28285	
OTUs number	119	363	142	123	186	230	316	75	240	522	
Shannon index (H10)	2.24	0.56	4.05	3.37	1.23	0.7	0.8	1.34	0.49	0.55	
Simpson index (1-D)	0.455	0.827	0.339	0.367	0.655	0.767	0.736	0.606	0.871	0.84	

**Table S2.** Diversity indices in the libraries of the bacterial 16S rRNA gene fragments from sulfate-reducing (SR), thiosulfate-reducing (TSR), and denitrifying (DNB) enrichments obtained from water samples collected from the near-bottom zone of an injection well 2755 (30 m<sup>3</sup>) and from petroleum oil treatment plant (POTP) of the Uzen oil field.

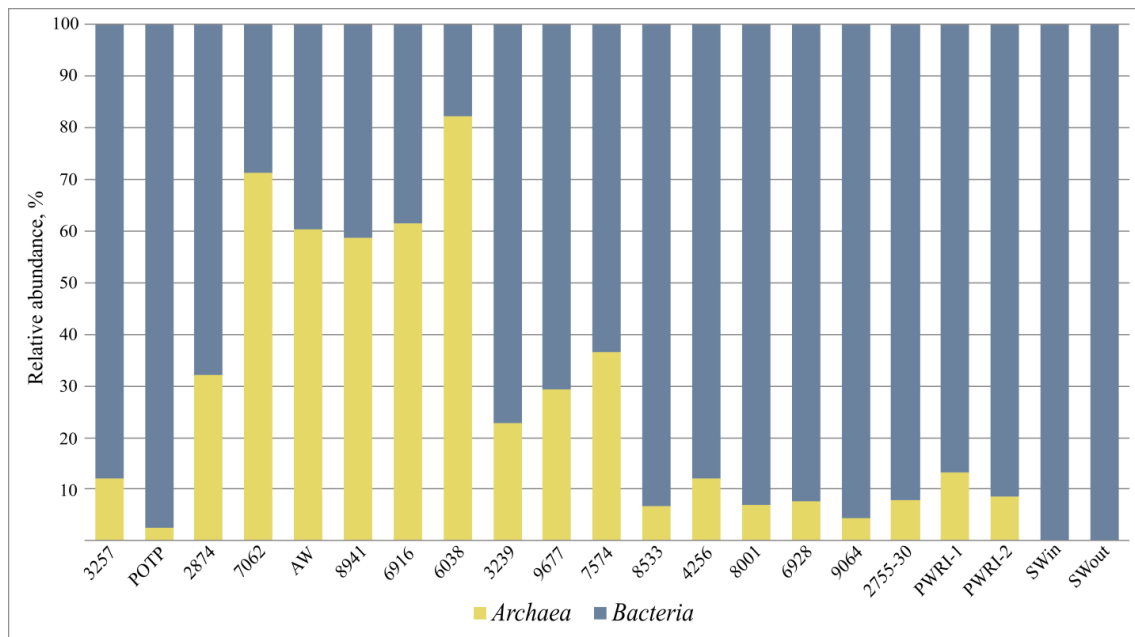
Sample name	Target reads	OTUs	ACE	CHAO	Shannon	Simpson	Phylogenetic diversity	Good's coverage of library (%)
SR-2755-30	88743	97	100.08	97.81	0.95	0.59	125	99.99
TSR-2755-30	83263	322	332.85	325.61	2.24	0.20	299	99.97
DNB-2755-30	82409	244	254.20	246.92	2.65	0.12	264	99.98
SR-POTP	59710	278	285.92	283.00	1.72	0.39	537	99.97
TSR-POTP	73376	216	222.33	217.44	1.40	0.44	209	99.98
DNB-POTP	90139	72	87.34	80.50	1.10	0.55	176	99.98



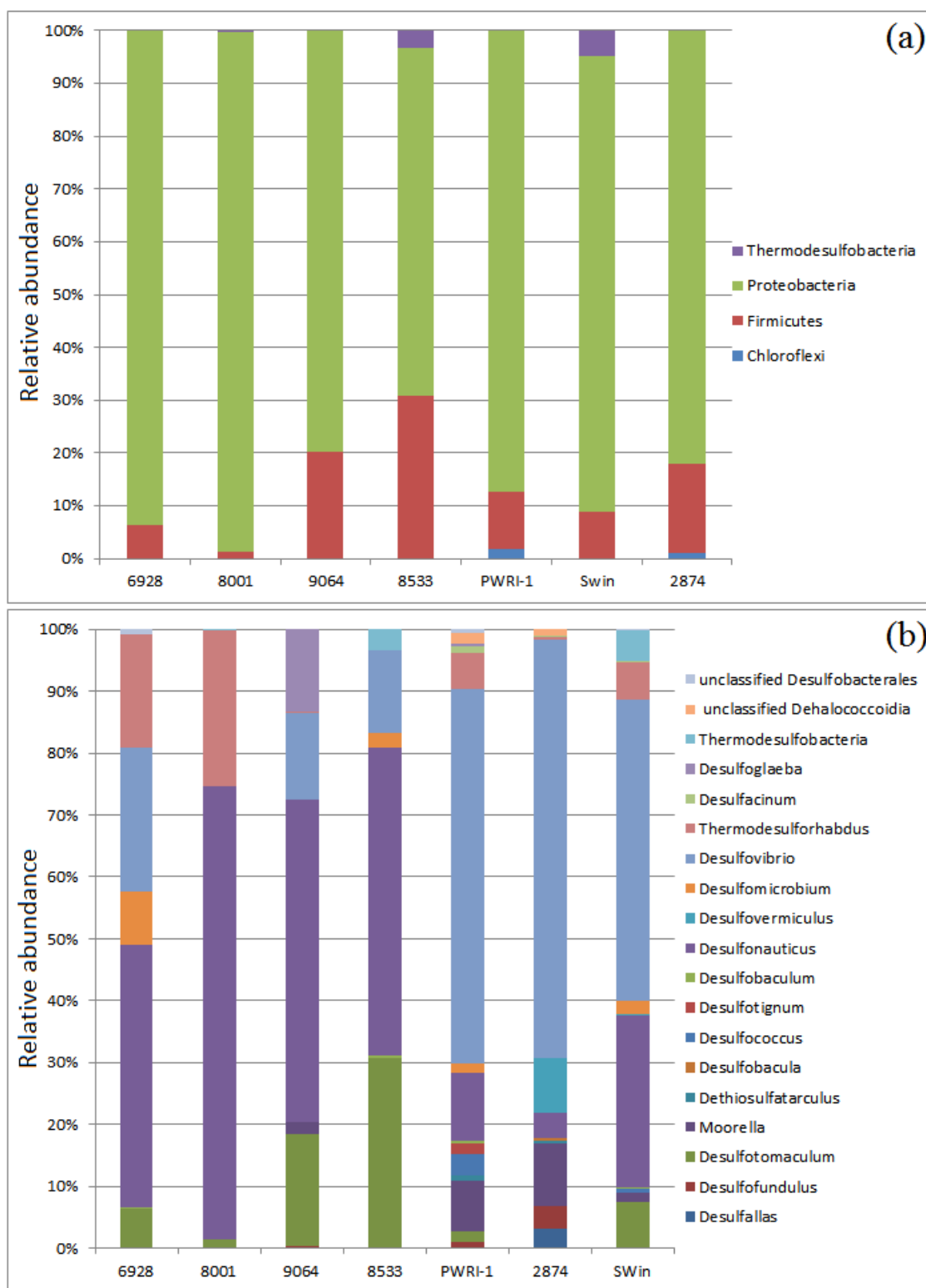
**Figure S1.** Numbers of aerobic organotrophic bacteria (AOB) and anaerobic fermentative (Ferm), sulfate-reducing (SRP) and methanogenic (MG) prokaryotes in injection and production water samples from the Uzen oil field. Microorganisms from Kaspian Sea water (SWin and SWout) were incubated at 25 °C, from PWRI-1, PWRI-2, and POTP – at 42 °C, from production wells and of Alb-Cenomanian water – at 55 °C.



**Figure S2.** Sulfide production in sulfate-reducing (SO<sub>4</sub><sup>2-</sup>-red.), sulfur-reducing (S<sup>0</sup>-red.), and thiosulfate-reducing (S<sub>2</sub>O<sub>3</sub><sup>2-</sup>-red.) enrichments obtained from the Uzen oil field.

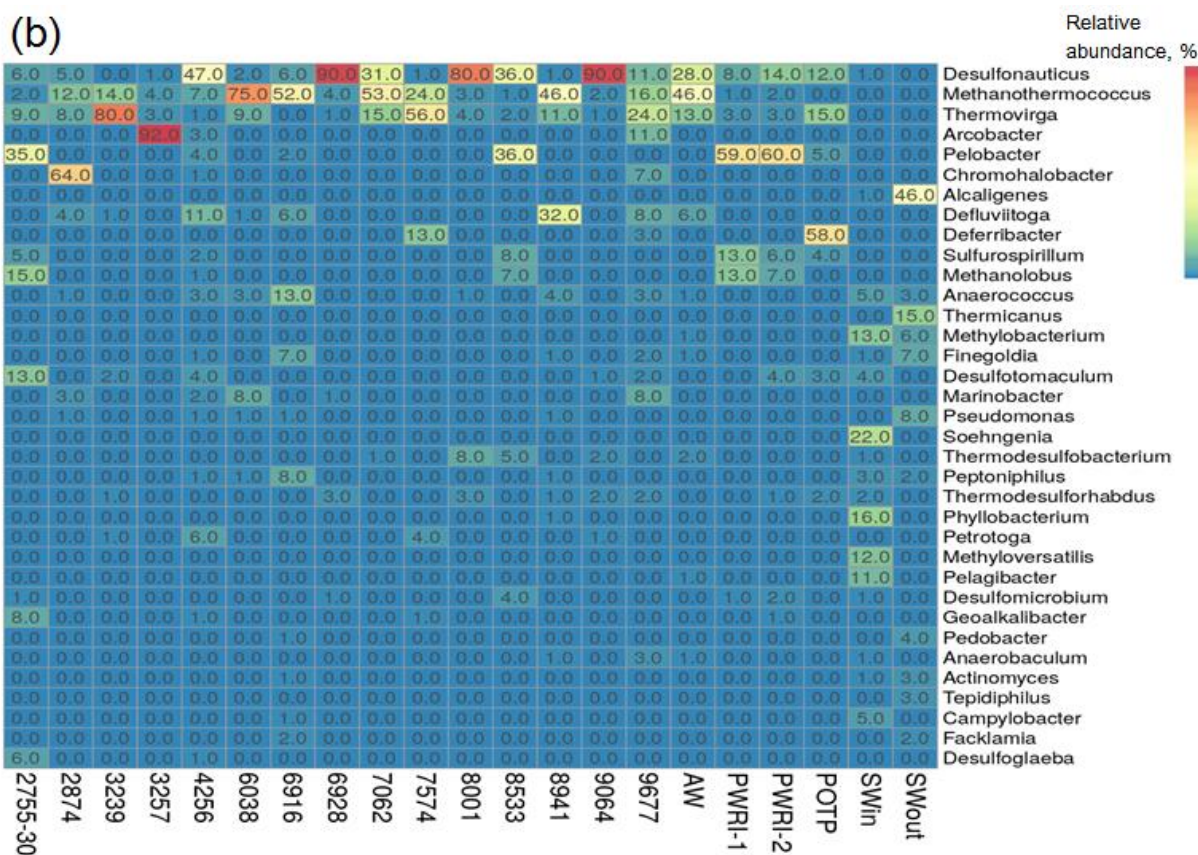
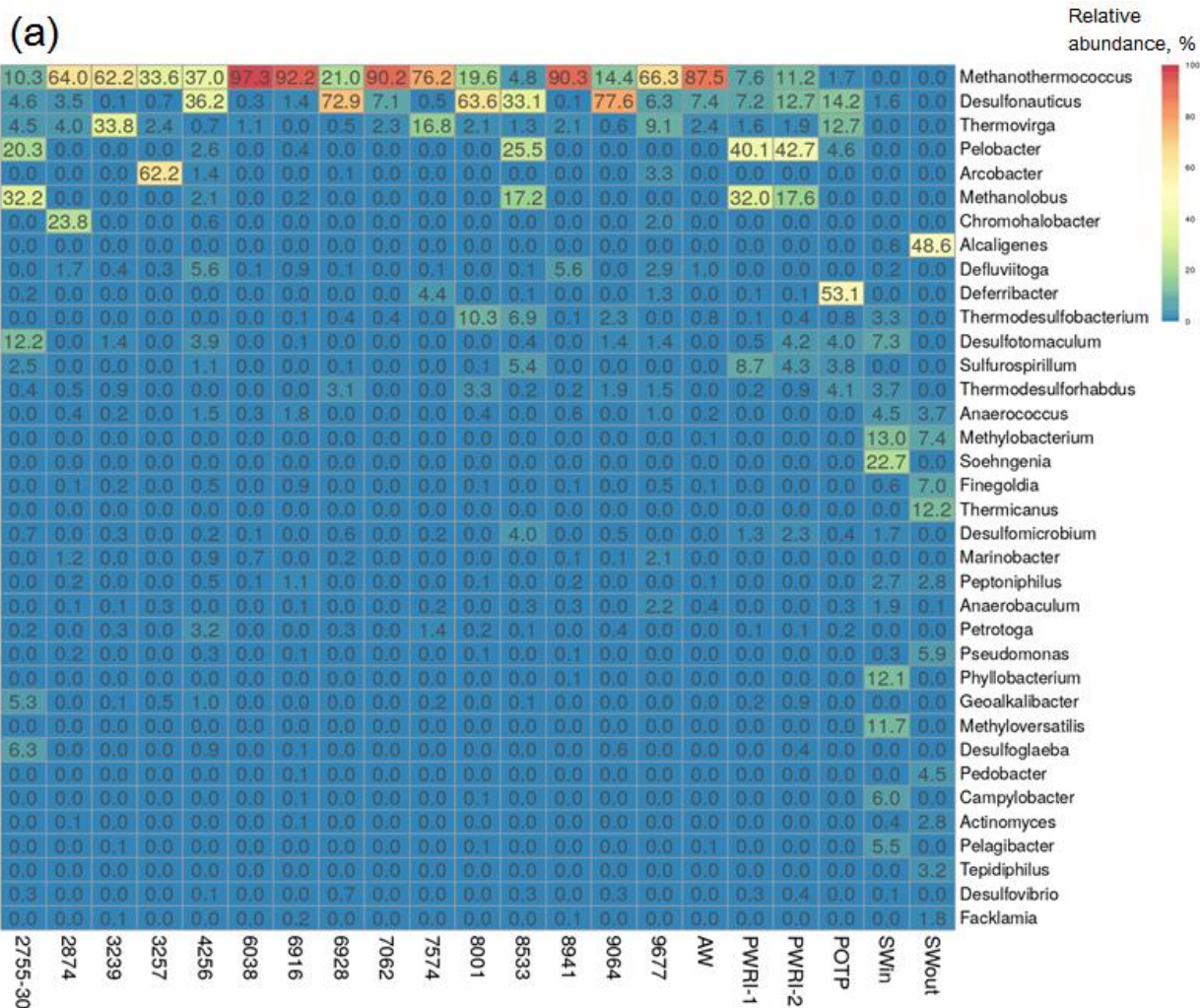


**Figure S3.** Taxonomic classification of 16S rRNA gene fragments in the libraries from water samples from the Uzen oil field at the *Bacteria* and *Archaea* domain level using the RDP classifier.

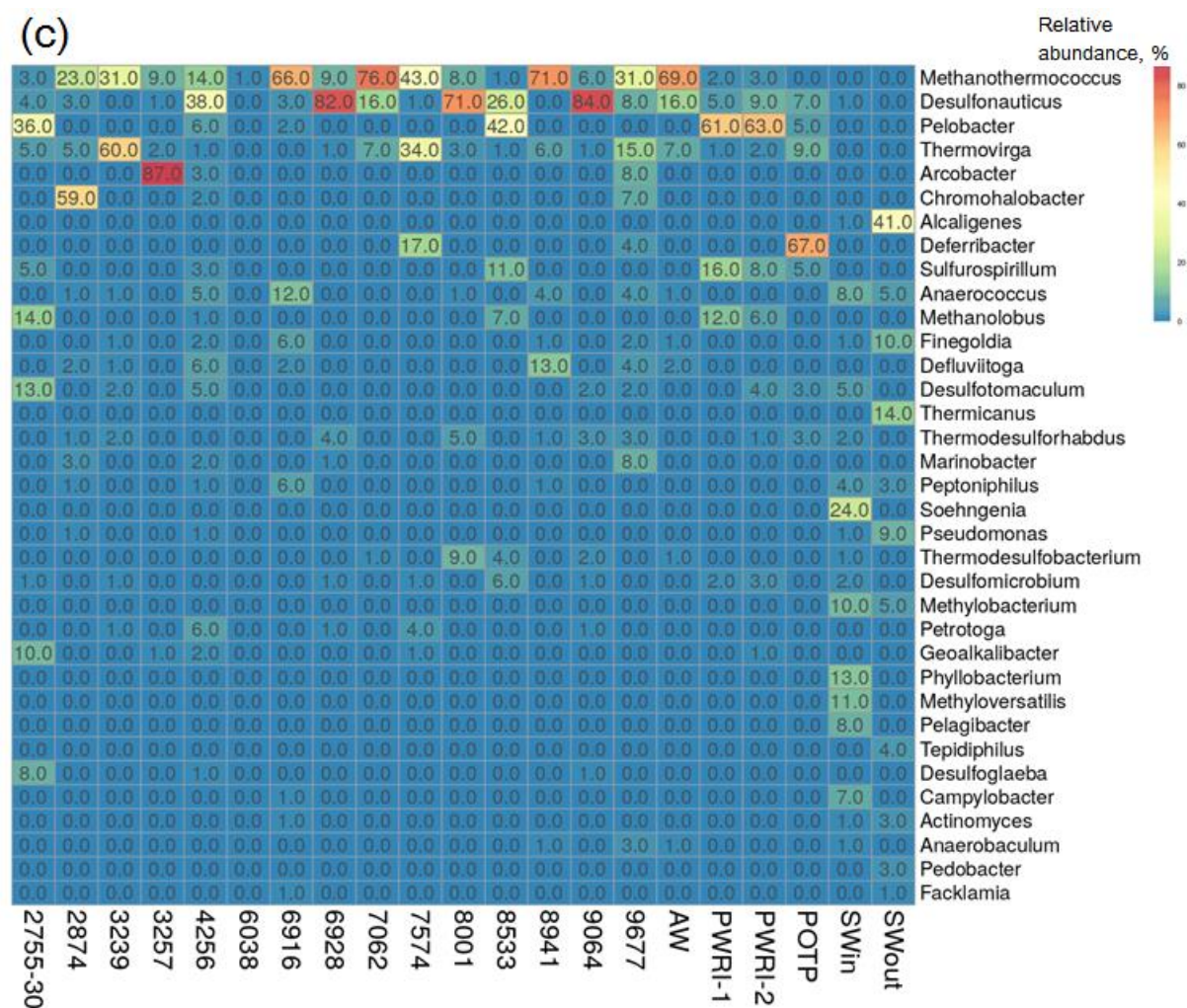


**Figure S4.** Taxonomic classification of *dsrA* gene fragments in the libraries from injection and production water samples at the phylum (a) and genus (b) level using the RDP classifier. The taxa constituting at least >1% in each library are listed.





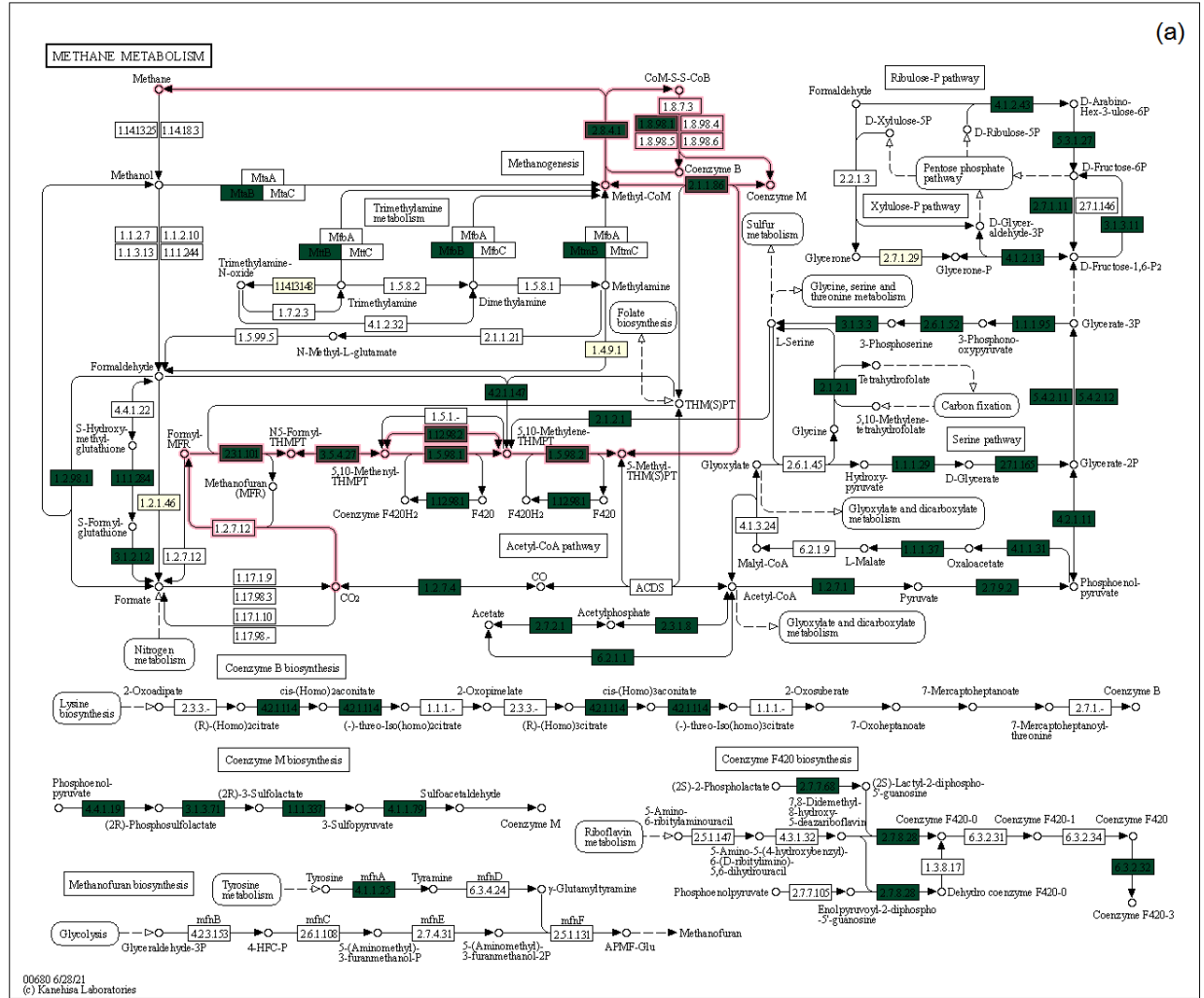




**Figure S5.** Heatmaps highlighting the key contributing microorganisms involved in the “Methane metabolism” (a), “Sulfur metabolism” (b), and “Nitrogen metabolism”(c) pathways in samples of injection and production water from the Uzen oil field.

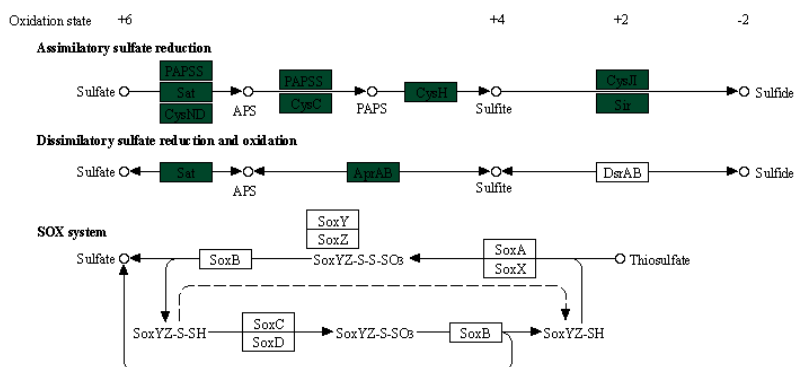
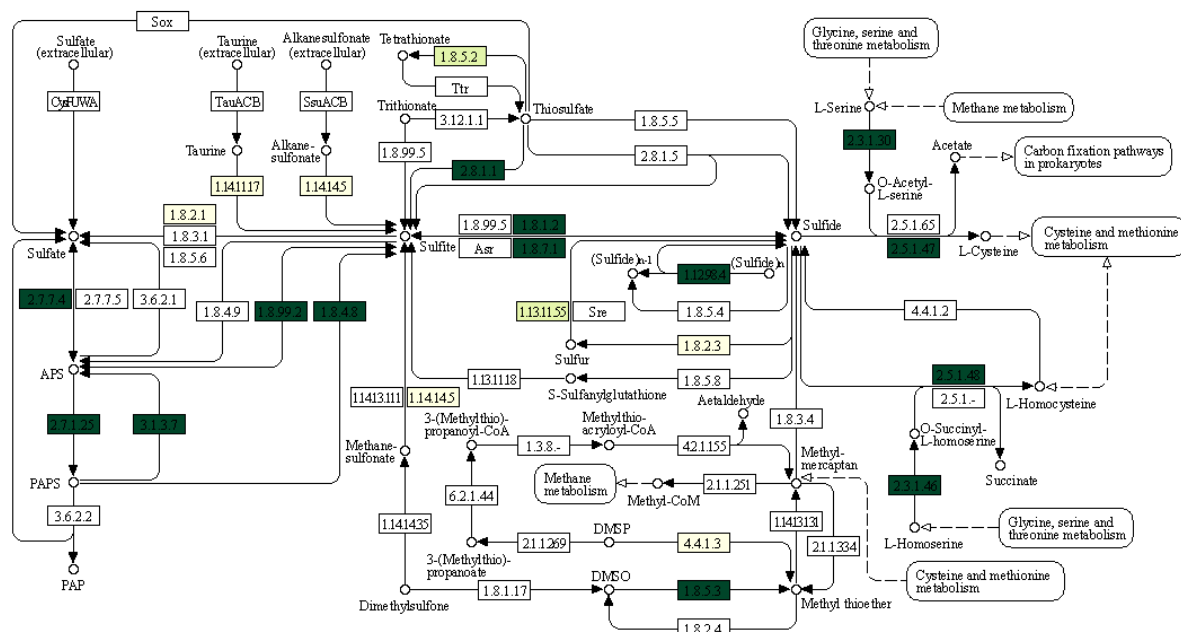


(a)

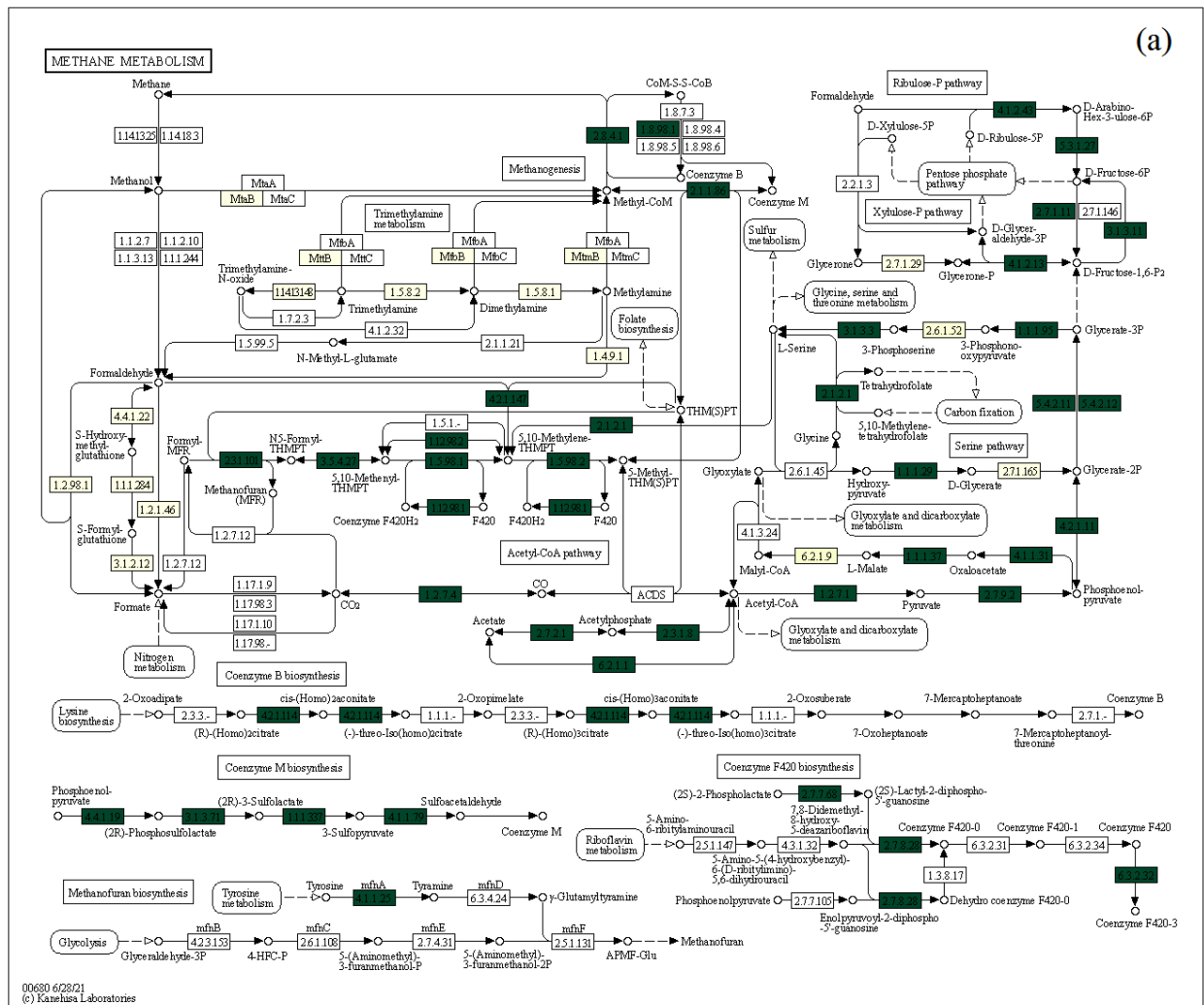


(b)

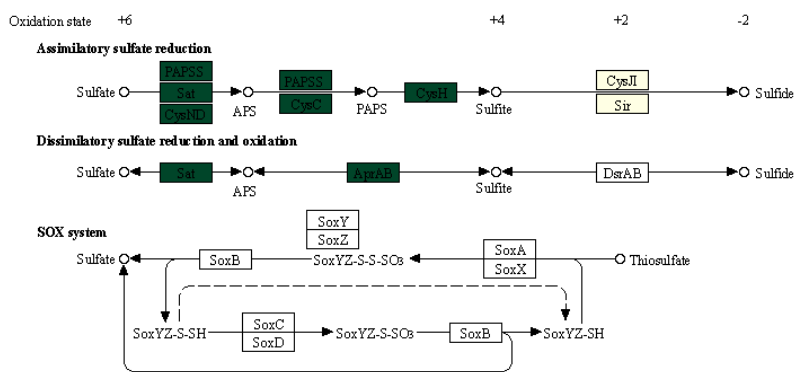
## SULFUR METABOLISM







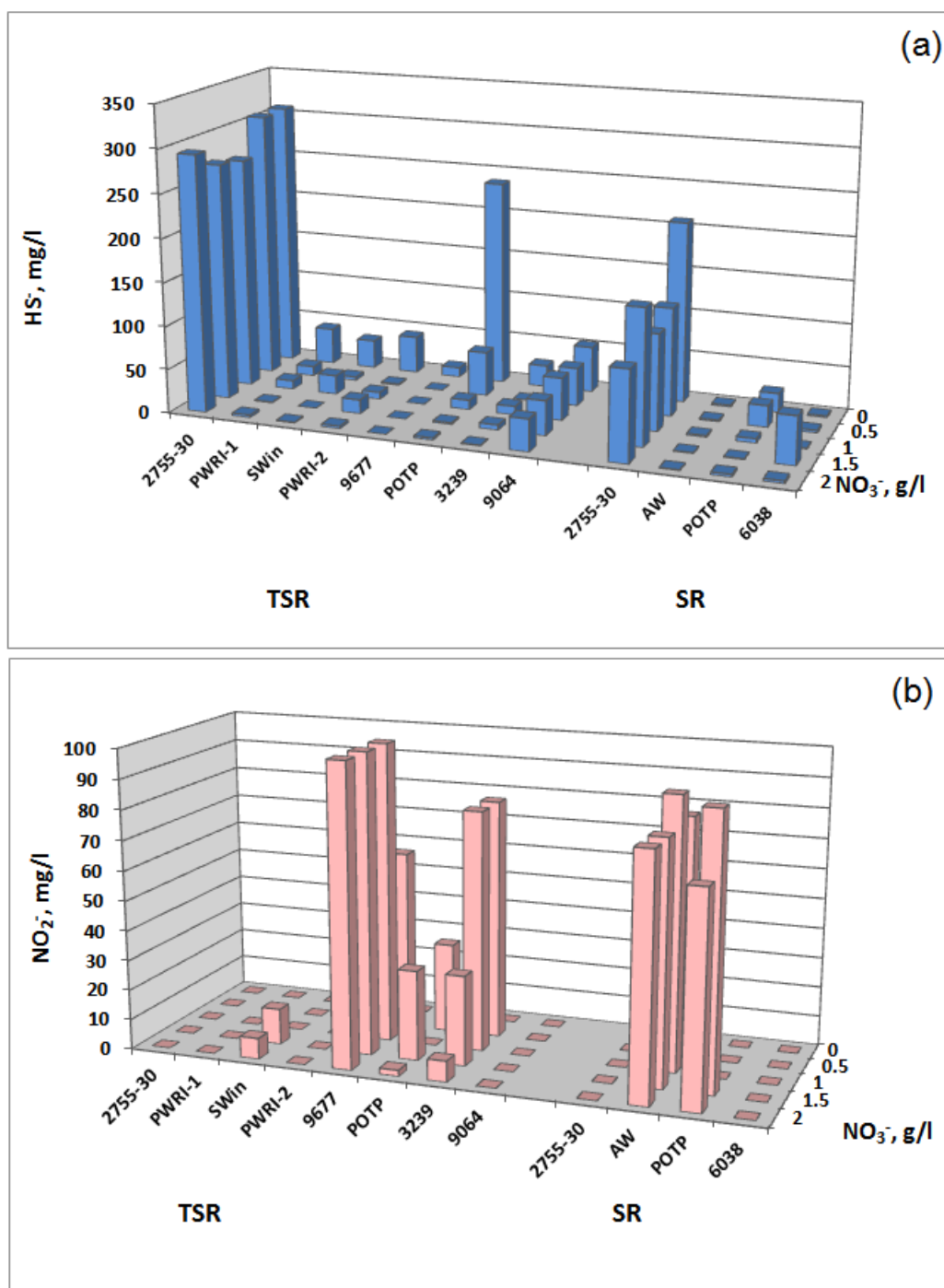
SULFUR METABOLISM



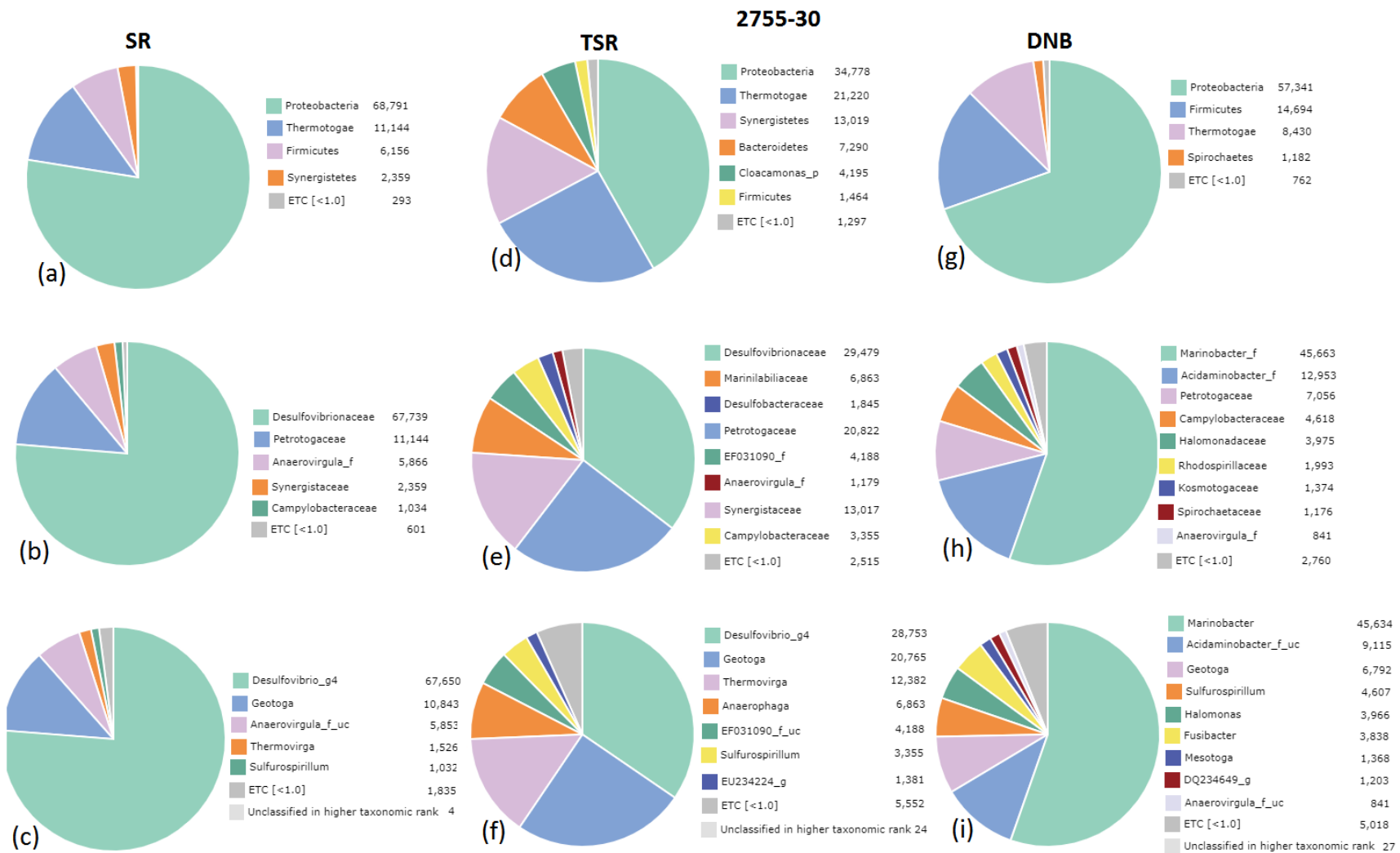
00920 2/4/20  
(c) Kanehisa Laboratories



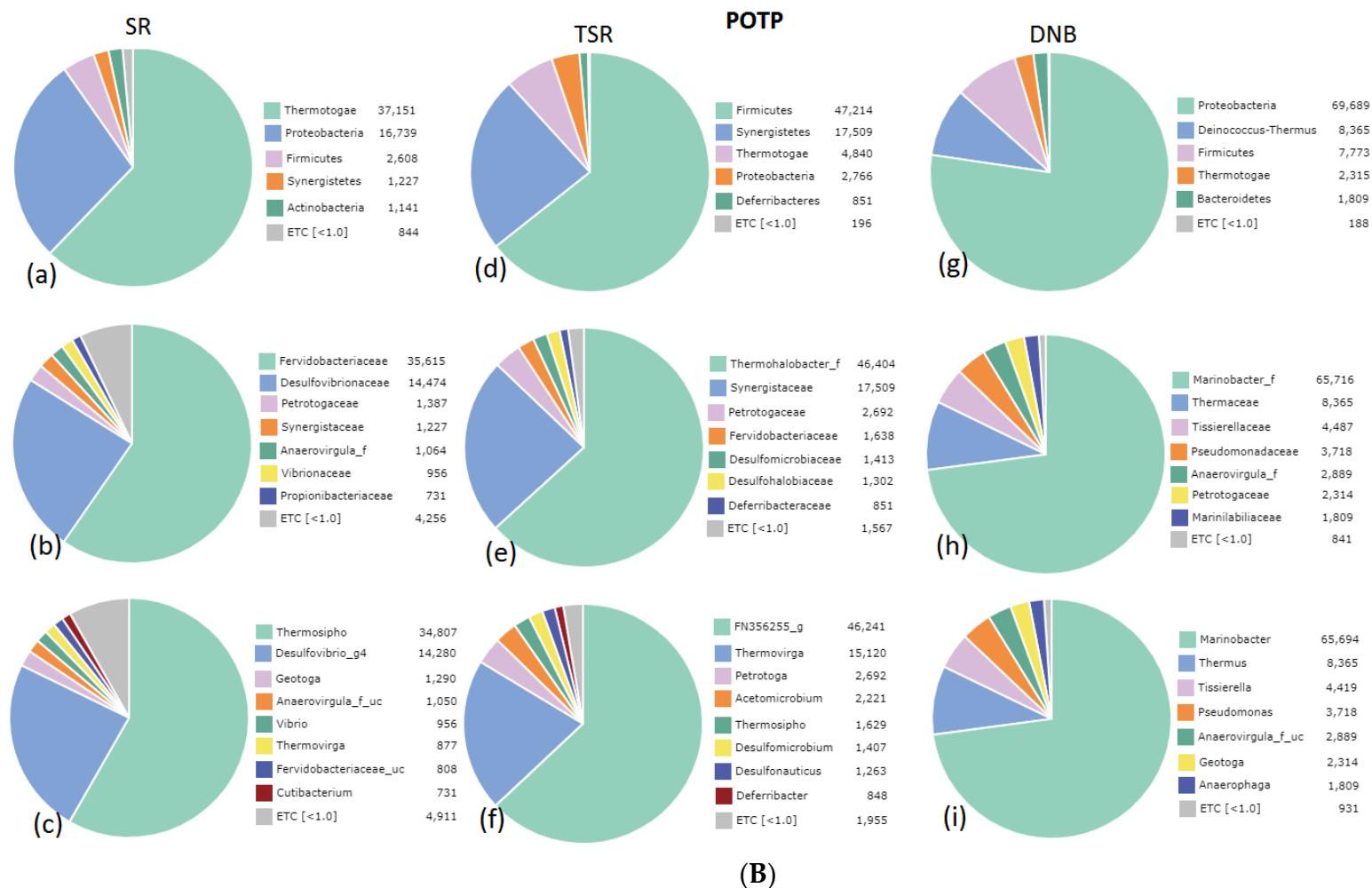




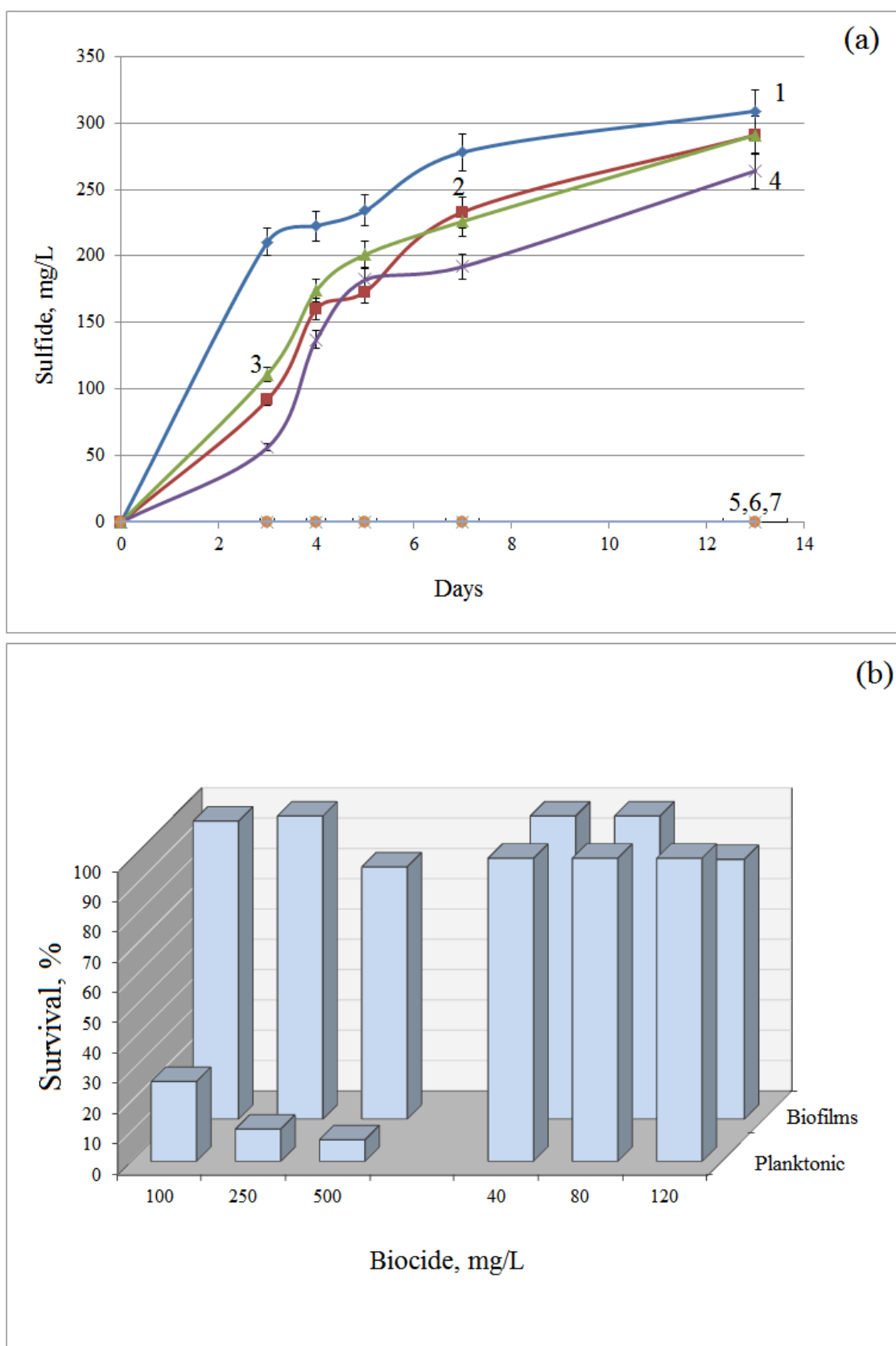
**Figure S8.** Production of sulfide (a) and nitrite (b) by thiosulfate-reducing (TSR) and sulfate-reducing (SR) bacteria of injection and production water samples in the media with different initial nitrate concentrations. Enrichments 2755-30, PWRI-1, PWRI-2, and POTP were incubated at 42 °C; enrichments 9677, 3239, AW, and 6038 were incubated at 55 °C. Cultivation duration was 30 days.



**(A)**



**Figure S9.** The numbers of sequences in the libraries and bacterial diversity in sulfate-reducing (SR), thiosulfate-reducing (TSR), and denitrifying (DNB) enrichments obtained from the near-bottom zone of injection well 2755 (30 m<sup>3</sup>) (A) and from petroleum oil treatment plant (POTP) (B) at the phylum (a, d, g), family (b, e, h), and genus (c, f, i) levels based on the 16S rRNA sequence analysis. The total numbers of sequences in libraries of SR, TSR and DNB enrichments from 2755-30 sample are 88743, 83263, and 82409, and from POTP sample are 59710, 73376, and 90139, respectively.



**Figure S10.** Effect of glutaraldehyde and Rancid on sulfide production (a) and survival (b) of sulfate-reducing bacterium *D. alaskensis* strain Kaz19 in planktonic form and biofilms. Designations in figure (a): Control medium without biocides (Line 1) and with Rancid at concentration 40 (Line 2), 80 (Line 3), and 120 mg·L<sup>-1</sup> (Line 4) and with glutaraldehyde at concentrations 100 (Line 5), 250 (Line 6), and 500 mg·L<sup>-1</sup> (Line 7).