

Supplementary material

Table S1. Results of physical chemical parameters not showed in the Piper diagram (**Figure 1**), expressed in the respective unit of measure, for the six mineral bottled water brands examined in the study.

Parameter	Unit of measurement	Sample Code					
		Sparkling			Flat		
		A	D	E	B	C	F
Nitrates	mg/L	2	7.1	3	3.4	1	8
Fluorides	mg/L	1.2	1	1	0.11	< 0.1	1
Total dissolved solids	mg/L	745	1308	1156	262	225	393
Conductivity	μS/cm	1104	1780	1504	460	322	454
pH	-	5.8	6.17	5.9	7.01	7.67	6.66
Free CO ₂	mg/L	1485	1950	2900	18	41.6	108

Table S2. Microorganisms identified with Sanger sequencing in samples B, C, and F from shelf-life evaluation in winter season and isolated both in sample storage at variable temperature (VT) and at constant temperature (CT). [AE: aerobe; AN: anaerobe; FA: facultative aerobe; T: growth temperature; M: mesophilic; P: Proteobacteria]. In the “Main sources of isolation” column, whereas germs were previously isolated from mineral waters, it was evidenced in **bold**.

Sample	Microorganism	Day of isolation/ storage condition	Microorganism characteristics						Main sources of isolation	
			Phylum	Gram	T	O ₂ levels				Spore
						AE	AN	FA		
B Flat	<i>Pseudomonas fluorescens</i>	d0	P	-	M	X			Soil, water [24]	
	<i>Pseudomonas veronii</i>	d0	P	-	M	X			Mineral water [25]	
	<i>Rhodoferax saidenbachensis</i>	d0	P	-	M	X			Sediment [26]	
	<i>Stenotrophomonas maltophilia</i>	d0	P	-	M	X			Bottled water [27]	
	<i>Acidovorax delafieldii</i>	d0-d5-10/CT	P	-	M	X			Soil, water [28]	
	<i>Aquabacterium parvum</i>	d5/VT	P	-	M	X			Water [29]	
	<i>Caulobacter henricii</i>	d5/VT	P	-	M	X			Water [30]	
	<i>Brevundimonas vesicularis</i>	d15/CT	P	-	M	X			Environment [31]	
	<i>Acidovorax facilis</i>	d30/CT d5/VT	P	-	M	X			Soil [32]	
	<i>Rhodoferax saidenbachensis</i>	d30/CT d5/VT	P	-	M	X			Sediment [26]	
	<i>Delftia acidovorans</i>	d0	P	-	M	X			Fresh water, soil [33]	
	<i>Delftia lacustris</i>	d0	P	-	M	X			Water [34]	
	<i>Pantoea agglomerans</i>	d0	P	-	M	X			Plants surface, seeds, man [35]	
	<i>Acidovorax radialis</i>	d0-d10-30/CT d30/VT	P	-	M	X			Wheat root [36]	
	<i>Sphingomonas aquatilis</i>	d15/CT	P	-	M	X			Mineral water [37]	
	<i>Brevundimonas mediterranea</i>	d30/VT	P	-	M	X			Sea water [38]	
F Flat	<i>Pseudomonas extremaustralis</i>	d0	P	-	M	X			Water [39]	
	<i>Pseudomonas veronii</i>	d0	P	-	M	X			Mineral water [25]	
	<i>Acidovorax delafieldii</i>	d0- d5-10-15-30/CT d10-30/VT	P	-	M	X			Water, soil [28]	
	<i>Stenotrophomonas maltophilia</i>	d0	P	-	M	X			Bottled water [27]	

Table S3. Microorganisms identified with Sanger sequencing in samples B, C, and F from shelf-life evaluation in spring season and isolated both in sample storage at variable temperature (VT) and at constant temperature (CT). [AE: aerobe; AN: anaerobe; FA: facultative aerobe; T: growth temperature; M: mesophilic; B: Bacteroidetes; P: Proteobacteria]. In the “Main sources of isolation” column, whereas germs were previously isolated from mineral waters, it was evidenced in **bold**.

Sample	Microorganism	Day of isolation/ storage condition	Microorganism characteristics						Main source of isolation	
			Phylum	Gram	T	O ₂ levels				Spore
						AE	AN	FA		
B Flat	<i>Acidovorax delafieldii</i>	d0	P	-	M	X			Soil, water [28]	
	<i>Pseudomonas fluorescens</i>	d0	P	-	M	X			Soil, water [24]	
	<i>Pseudomonas veronii</i>	d0	P	-	M	X			Mineral water [25]	
	<i>Stenotrophomonas maltophilia</i>	d0	P	-	M	X			Bottled water [27]	
	<i>Rhodoferax saidenbachensis</i>	d0-d15/VT	P	-	M	X			Sediment [26]	
	<i>Ensifer adhaerens</i>	d5-10/CT	P	-	M	X			Soil [40]	
	<i>Flavobacterium succinicans</i>	d30/VT								
		d5-10/VT	B	-	M	X			Marine water [41]	
	<i>Pseudomonas alcaligenes</i>	d5-10/CT	P	-	M	X			Water , soil [42]	
		d15/VT								
	<i>Sphingopyxis ginsengisoli</i>	d5-30/CT	P	-	M	X			Soil [43]	
		d30/VT								
	<i>Aquabacterium commune</i>	d10/CT	P	-	M	X			Water [29]	
	<i>Delftia acidovorans</i>	d10/CT	P	-	M	X			Fresh water , soil [33]	
	C Flat	<i>Blastomonas natatoria</i>	d15/CT	P	-	M	X			Water [44]
<i>Pseudoxanthomonas mexicana</i>		d30/VT								
		d 15/CT	P	-	M	X			Sludge [45]	
<i>Sphingopyxis soli</i>		d15/CT	P	-	M	X			Soil [46]	
		d5/VT								
<i>Delftia acidovorans</i>		d0	P	-	M	X			Fresh water , soil [33]	
<i>Delftia lacustris</i>		d0	P	-	M	X			Water [34]	
<i>Pantoea agglomerans</i>		d0	P	-	M	X			Plants surface, seeds [35]	
<i>Acidovorax radialis</i>		d0-d10-15-30/CT d10-15-30/VT	P	-	M	X			Roots [36]	
<i>Stenotrophomonas maltophilia</i>		d30/VT	P	-	M	X			Bottled water [27]	
F Flat	<i>Acidovorax delafieldii</i>	d0	P	-	M	X			Water , soil [28]	
	<i>Pseudomonas extremaustralis</i>	d0	P	-	M	X			Water [39]	
	<i>Pseudomonas veronii</i>	d0	P	-	M	X			Mineral water [25]	
	<i>Stenotrophomonas maltophilia</i>	d0-d30/CT	P	-	M	X			Bottled water [27]	
	<i>Blastomonas natatoria</i>	d15/CT	P	-	M	X			Water [44]	

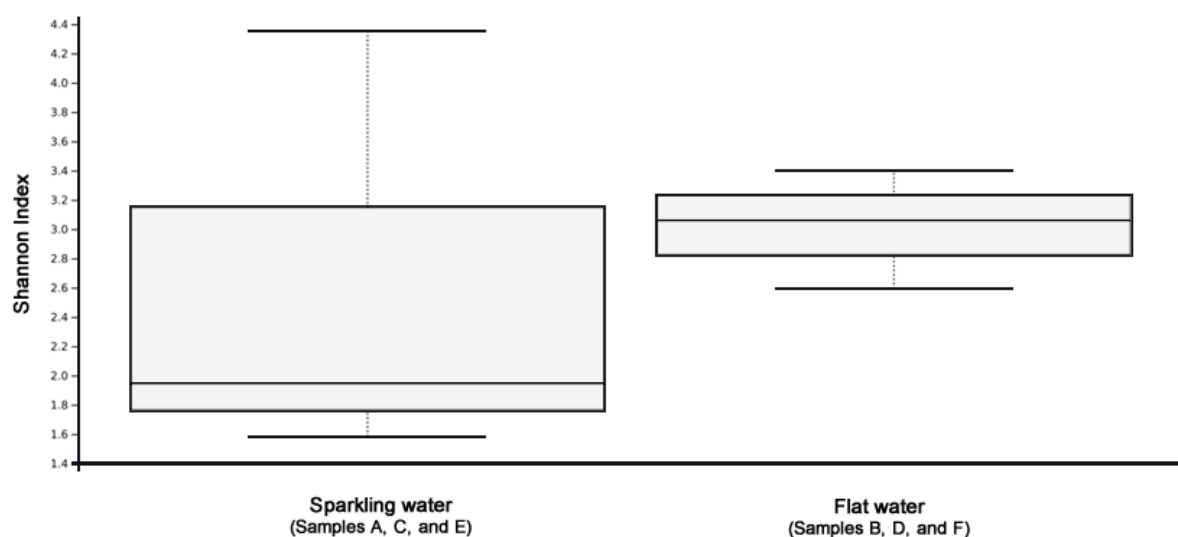


Figure S1. Changes in the Shannon index of diversity based on the number of 16S rRNA Illumina reads.

a) Phylum

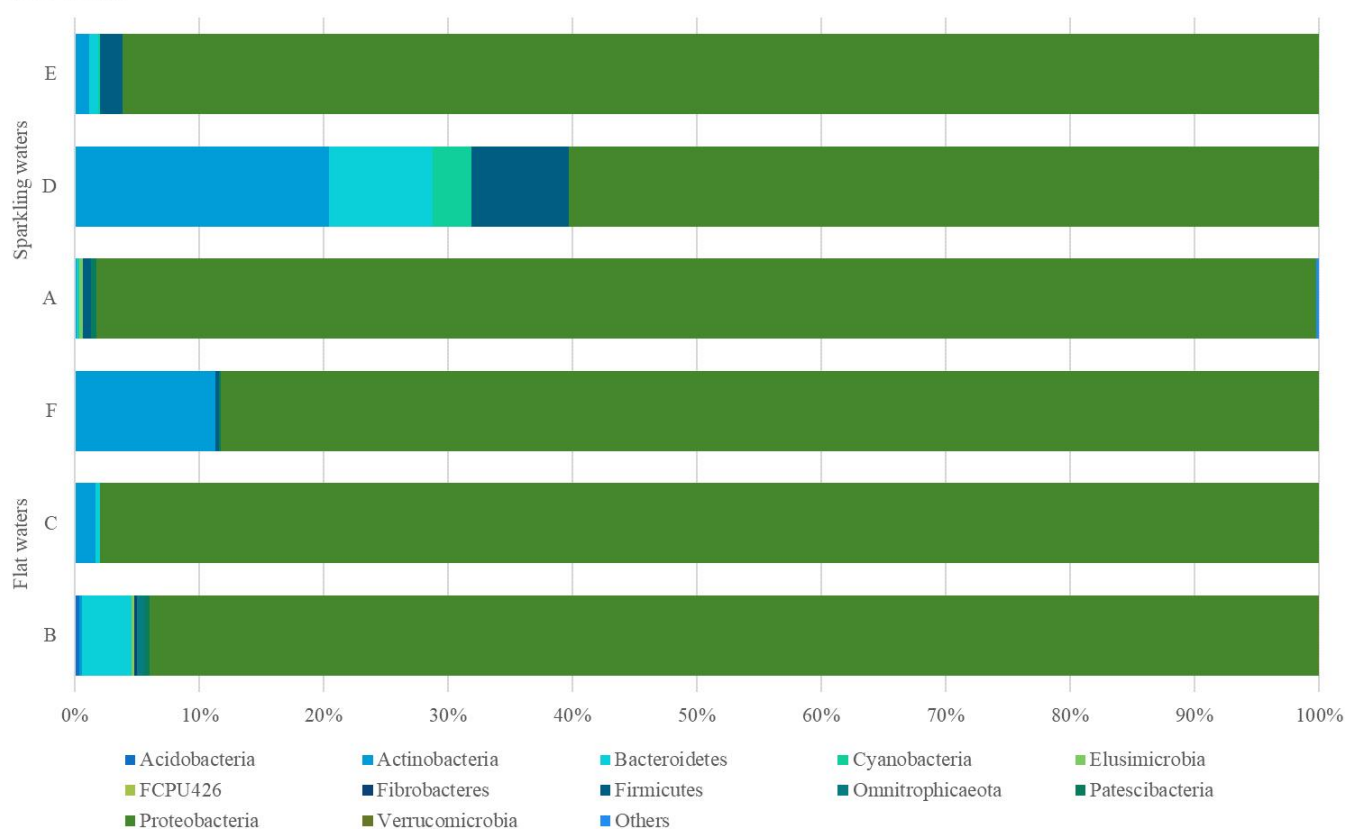


Figure S2. Community structure of the mineral water brands at Phylum level according to 16s rRNA sequencing analysis. Results are expressed as relative abundance of reads.

b) Order

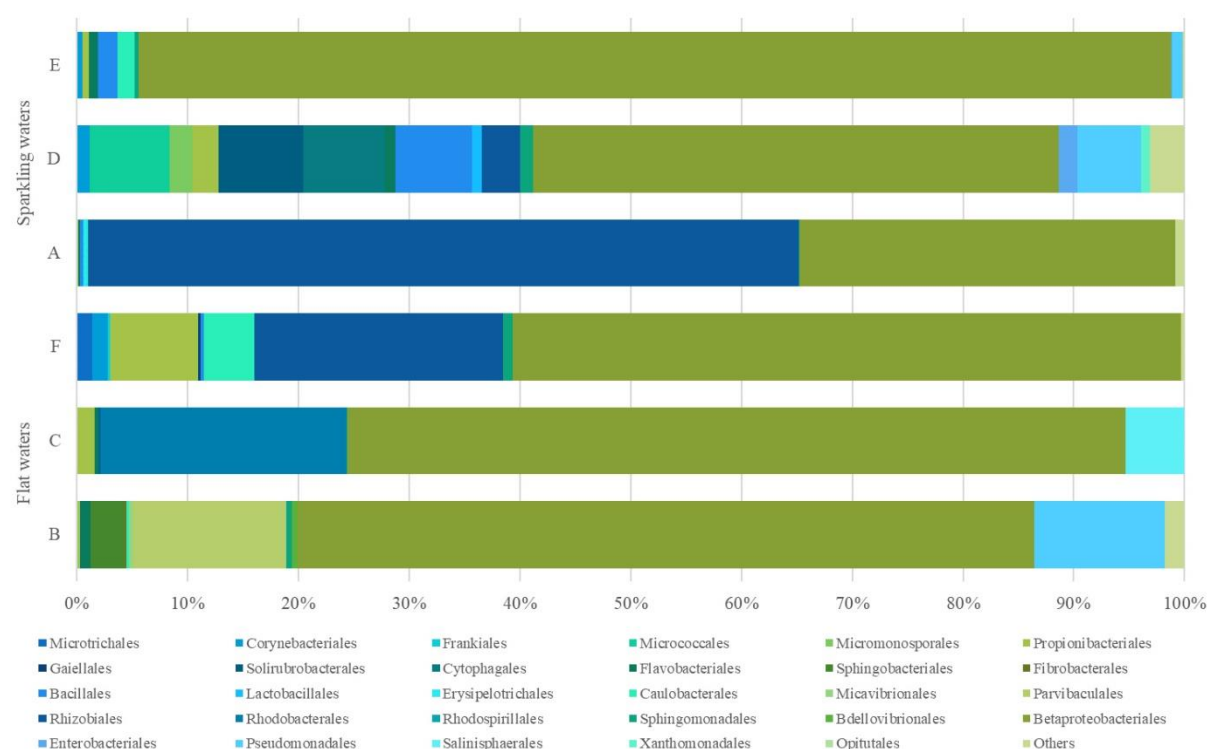


Figure S3. Community structure of the mineral water brands at Order level according to 16s rRNA sequencing analysis. Results are expressed as relative abundance of reads.

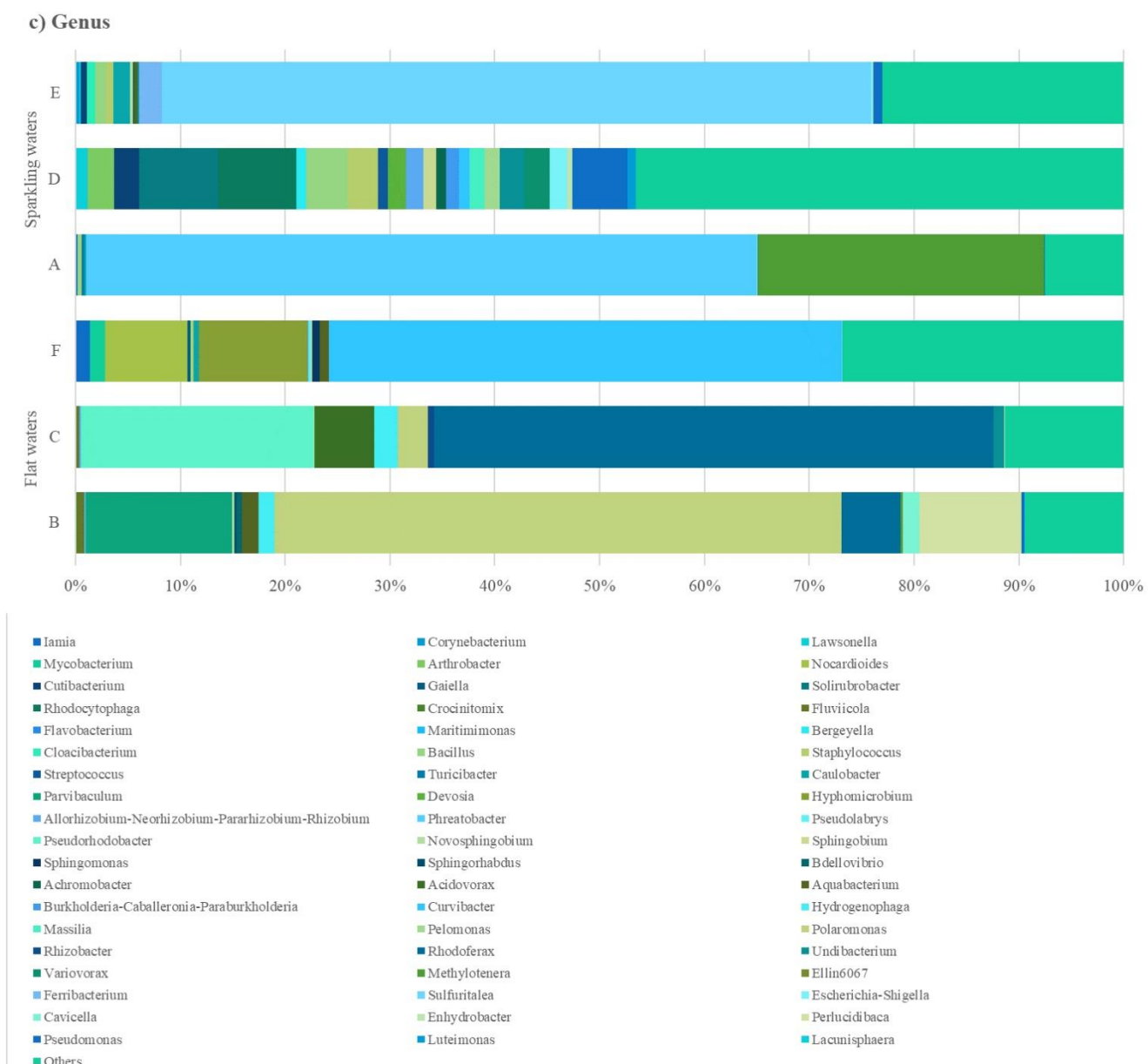


Figure S4. Community structure of the mineral water brands at Genus level according to 16s rRNA sequencing analysis. Results are expressed as relative abundance of reads.

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