

Table S1. Trace metal and non-metal elemental concentrations for well waters sampled in 2017.

∑ indicates the value is the sum of all species of an element.

	NSHQ14		WAB71	NSHQ04	WAB55	WAB188	Rain	LOQ
Pump depth (m)	50	85	70	5.8	30	78		
∑ As (μM)	0.17	0.14	0.17	0.21	BLOQ	0.13	9.1x10 ⁻²	4x10 ⁻⁴
∑ B (μM)	5.48	6.39	BLOQ	BLOQ	11.70	18.33	5.21	4.25
∑ Ba (μM)	0.11	0.11	4.6x10 ⁻²	0.81	2.85x10 ⁻²	0.05	5.6x10 ⁻²	1x10 ⁻³
∑ Cd (μM)	BLOQ	BLOQ	1.9x10 ⁻³	BLOQ	BLOQ	BLOQ	BLOQ	1x10 ⁻⁴
∑ Cr (μM)	BLOQ	0.01	BLOQ	BLOQ	0.10	2.4x10 ⁻²	4.7x10 ⁻²	9x10 ⁻⁴
∑ Cu (μM)	1.8x10 ⁻²	1.8x10 ⁻²	BLOQ	BLOQ	BLOQ	BLOQ	4.3x10 ⁻²	2x10 ⁻⁴
∑ Li (mM)	BLOQ	BLOQ	4.59E-04	6.85E-04	7.49x10 ⁻⁴	3.39x10 ⁻⁴	BLOQ	1.99x10 ⁻⁴
∑ Mo (μM)	BLOQ	BLOQ	BLOQ	BLOQ	BLOQ	2.9x10 ⁻²	BLOQ	1.1x10 ⁻²
∑ Ni (μM)	9x10 ⁻³	7.5x10 ⁻²	1.76x10 ⁻²	3.7x10 ⁻²	BLOQ	7.23x10 ⁻²	4.5x10 ⁻²	2x10 ⁻⁴
∑ P (μM)	0.63	BLOQ	0.53	0.72	0.52	0.89	3.63	3.41x10 ⁻¹
∑ S (mM)	0.23	0.12	0.16	0.90	0.88	1.16	0.19	8.6x10 ⁻⁴
∑ Sr (μM)	14.19	16.21	7.91	24.84	3.09	4.22	1.97	1x10 ⁻³
∑ V (μM)	BLOQ	BLOQ	BLOQ	BLOQ	BLOQ	0.09	2.4x10 ⁻²	1.6x10 ⁻²
∑ Zn (μM)	0.26	0.37	0.14	0.27	0.87	0.49	0.11	5x10 ⁻³

Table S2. Sequencing information for SSU rRNA, metagenomes, and metatranscriptomes of communities sampled from fracture waters collected from five wells. PF indicates reads that passed the sequencing center quality control filter.

	NSHQ14B (50m)	NSHQ14C (85m)	WAB71 (50m)	NSHQ04	WAB55	WAB188	Neg. PCR control	No RT control
SSU rRNA (DNA)								
No. reads	93,243	29,262	46,409	14,280	30,208	14,811	42	-
SSU rRNA (cDNA)								
No. reads	23,556	14,206	7,330	7,078	18,965	5,896	-	0
Metagenomes								
Total Gbp, PF	18.24	17.46	8.62	16.53	5.90	14.35	-	-
Total paired reads, PF (millions)	72.69	69.56	34.36	65.86	23.51	57.16	-	-
Q 30%	83.89	85.58	85.08	84.07	84.22	86.31	-	-
Avg. quality score	34.64	35.05	34.98	34.69	34.76	35.29	-	-
Metatranscriptomes:								
Total Gbp, PF	3.50	4.31	0.29	5.49	0.18	0.63	-	0.18
Total paired reads, PF (millions)	13.93	17.16	1.16	21.89	0.72	2.51	-	0.72
Q 30%	85.66	83.44	65.23	84.93	84.12	80.18	-	79.79
Avg. quality score	35.14	34.59	30.43	34.98	34.77	33.84	-	33.77

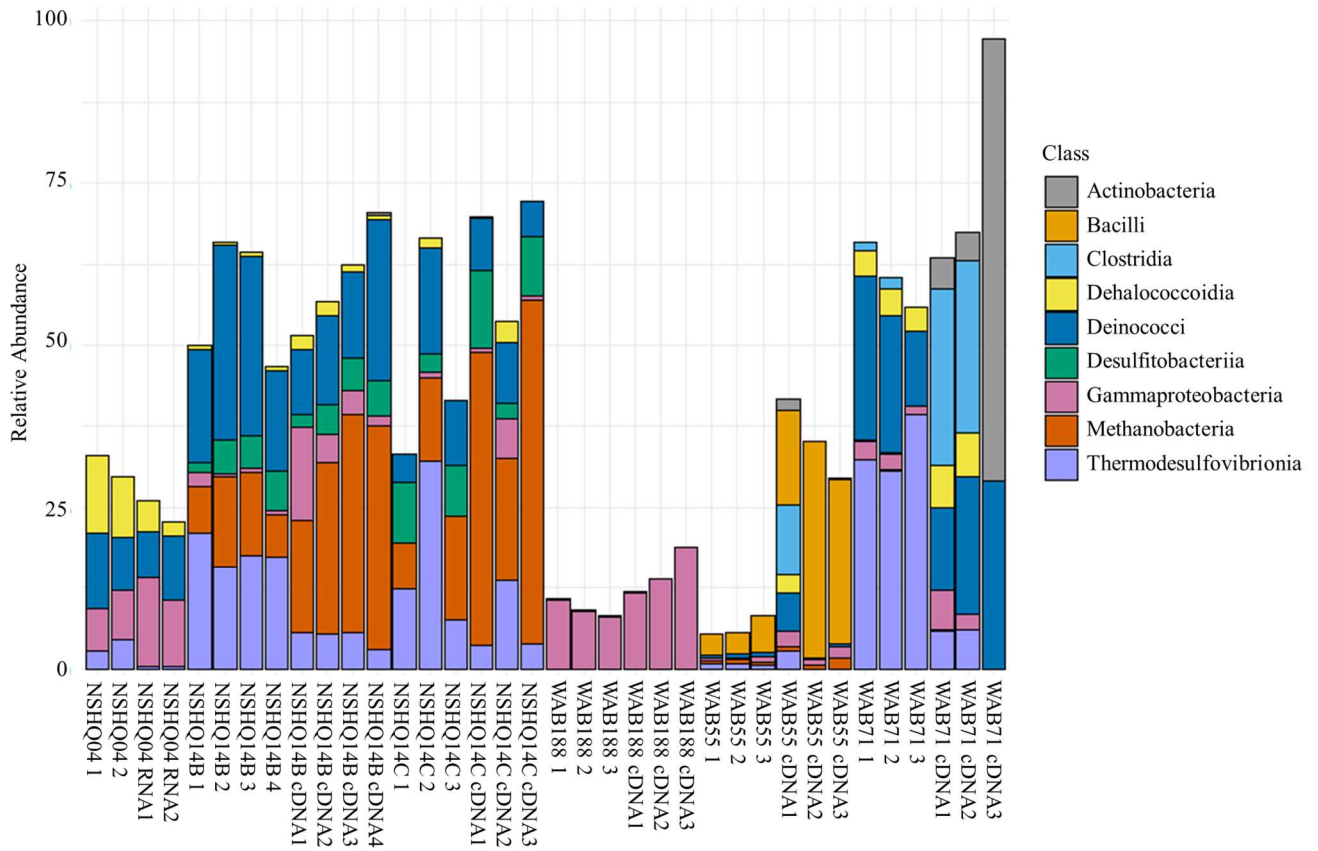


Figure S1: Relative abundance of the top 10 ASVs from DNA and cDNA amplicon sequencing of well samples. Bars are colored by Class. Numbers following well samples on x axis denote biological replicates.

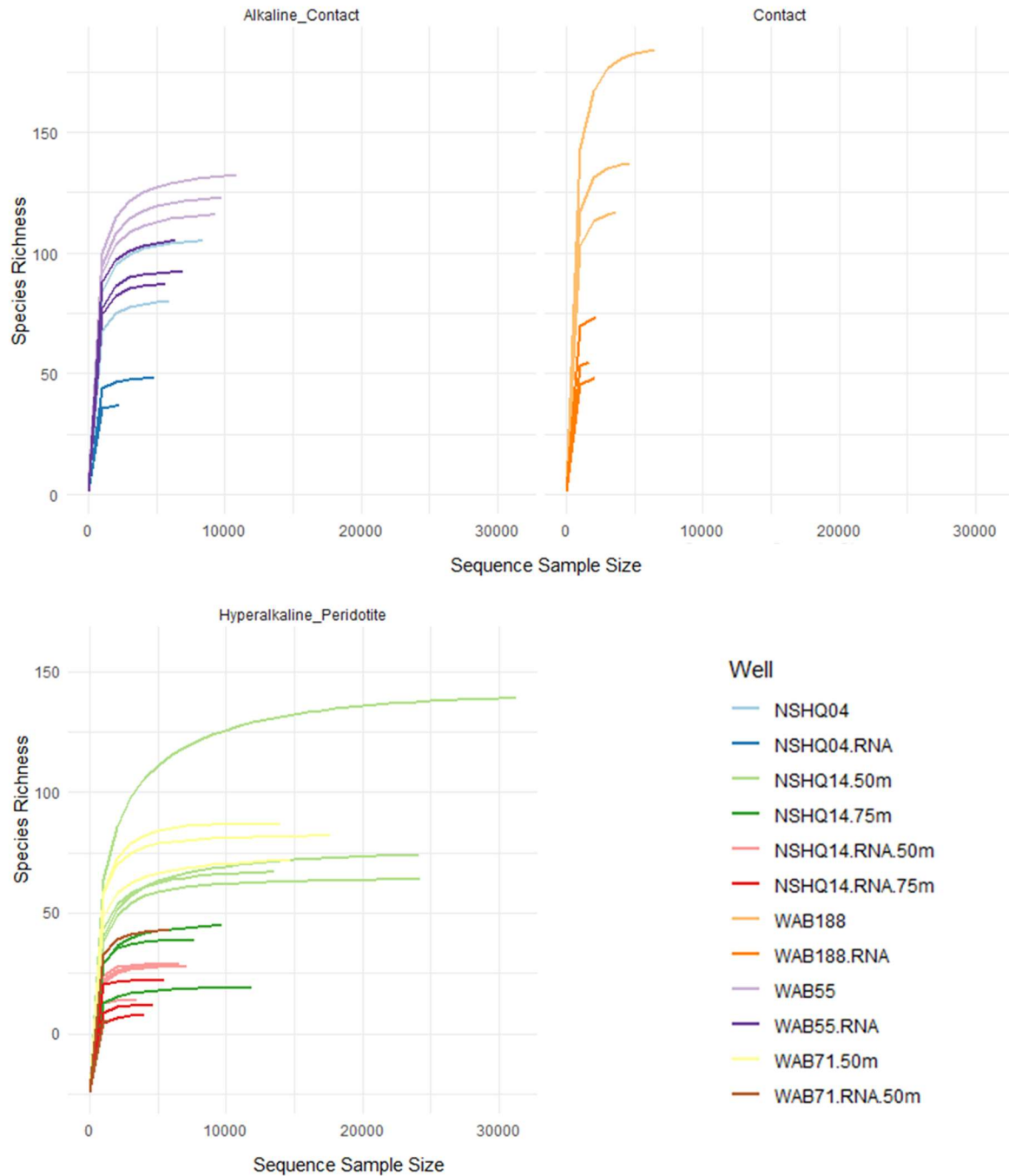


Figure S2: Rarefaction curves of observed species richness (observed ASV counts) against sequence library size plateau indicating SSU rRNA libraries were sufficiently large to capture the majority of ASVs within each well water type.

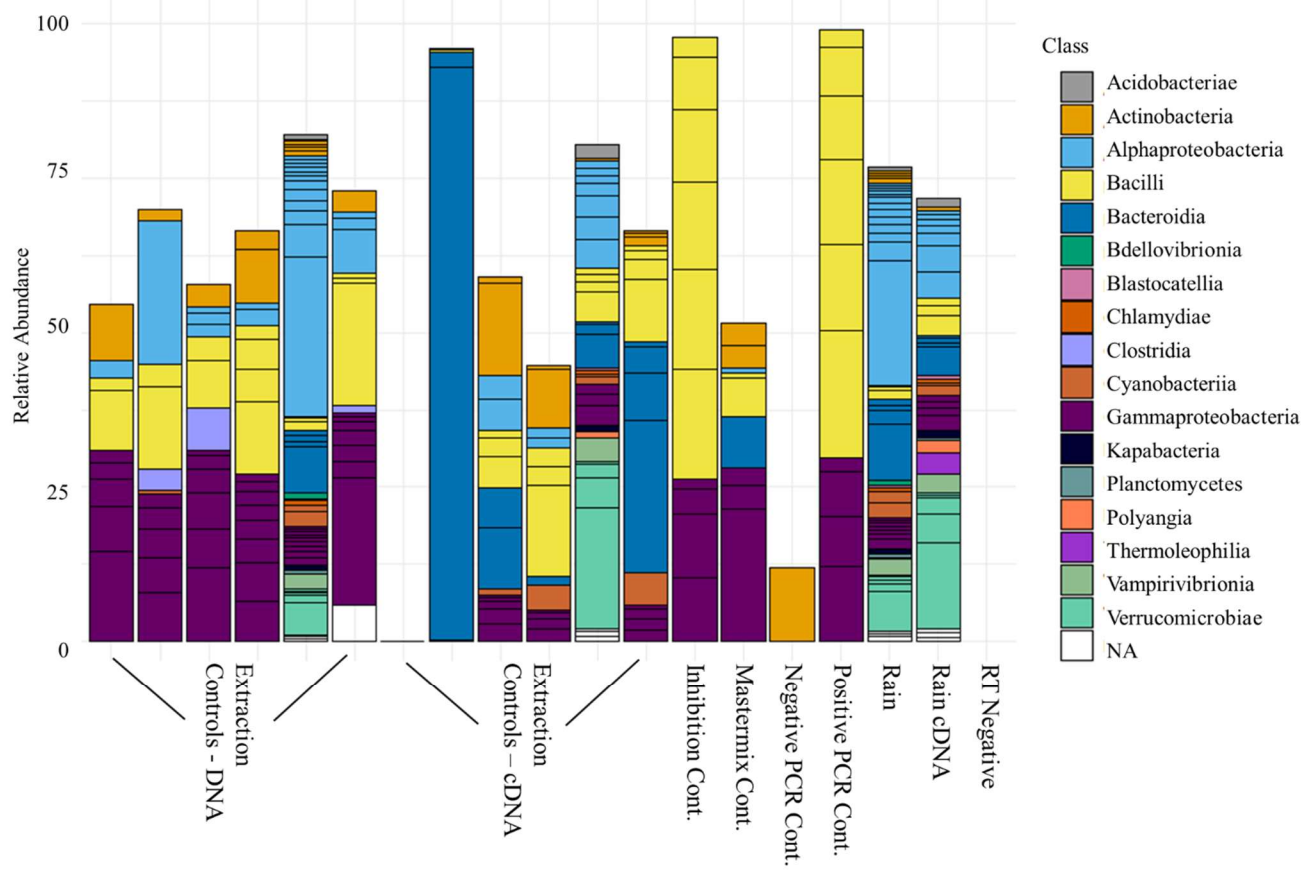


Figure S3: Relative abundance of the top 100 ASVs identified in extraction, PCR amplification, and negative reverse-transcription (RT) controls.