

Supporting information

Additional Supporting Information may be found in the online version of this article:

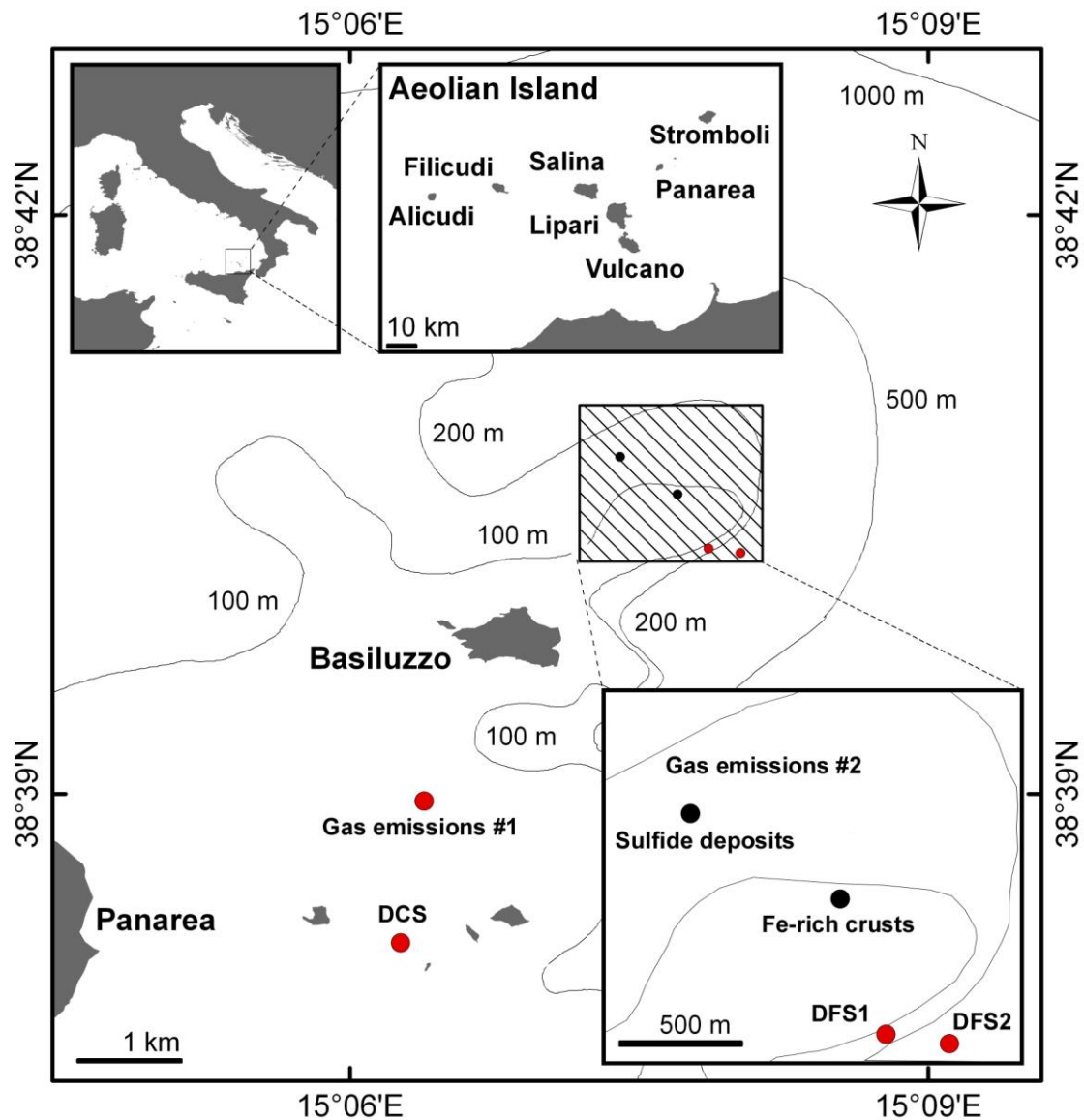


Figure S1. Map of Basiluzzo hydrothermal field located north-east of Panarea Island. Sampling sites, mentioned in the present study, are indicated as red (hydrothermally active sites) and black (inactive cold sites) dots.



Figure S2. Internal texture of DFS structure represented by amorphous ferrihydrite-type Fe-oxyhydroxides occurring as an extensive slime-like material.

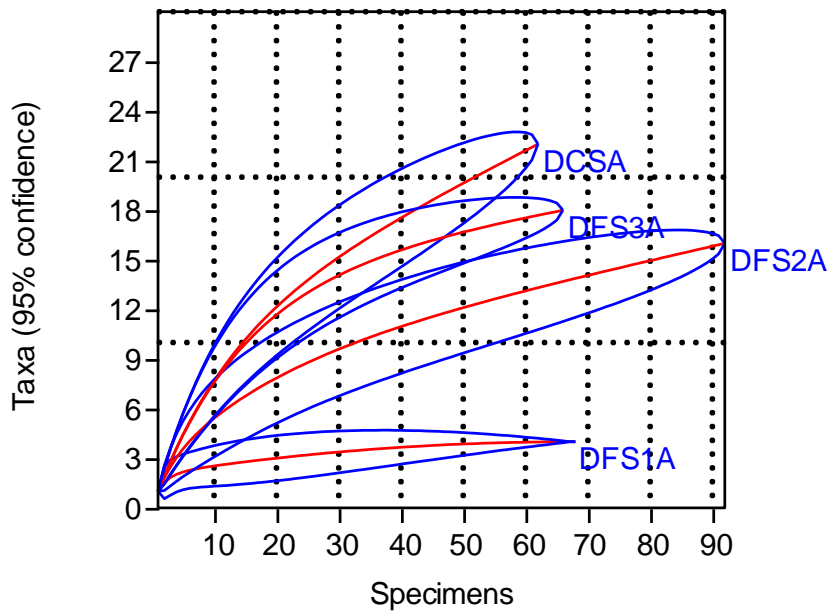
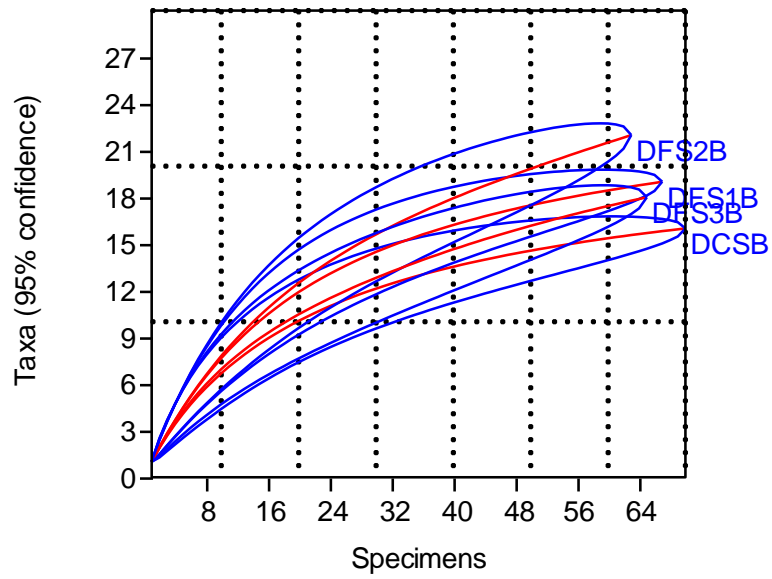


Figure S3. Rarefaction analysis of the eight clone libraries obtained from the 4 different *Basiluzzo* SHS samples (DCS, DFS1, DFS2 and DFS3). Abbreviation endings either with A or B mean archaeal (down) and bacterial (above) libraries, respectively.

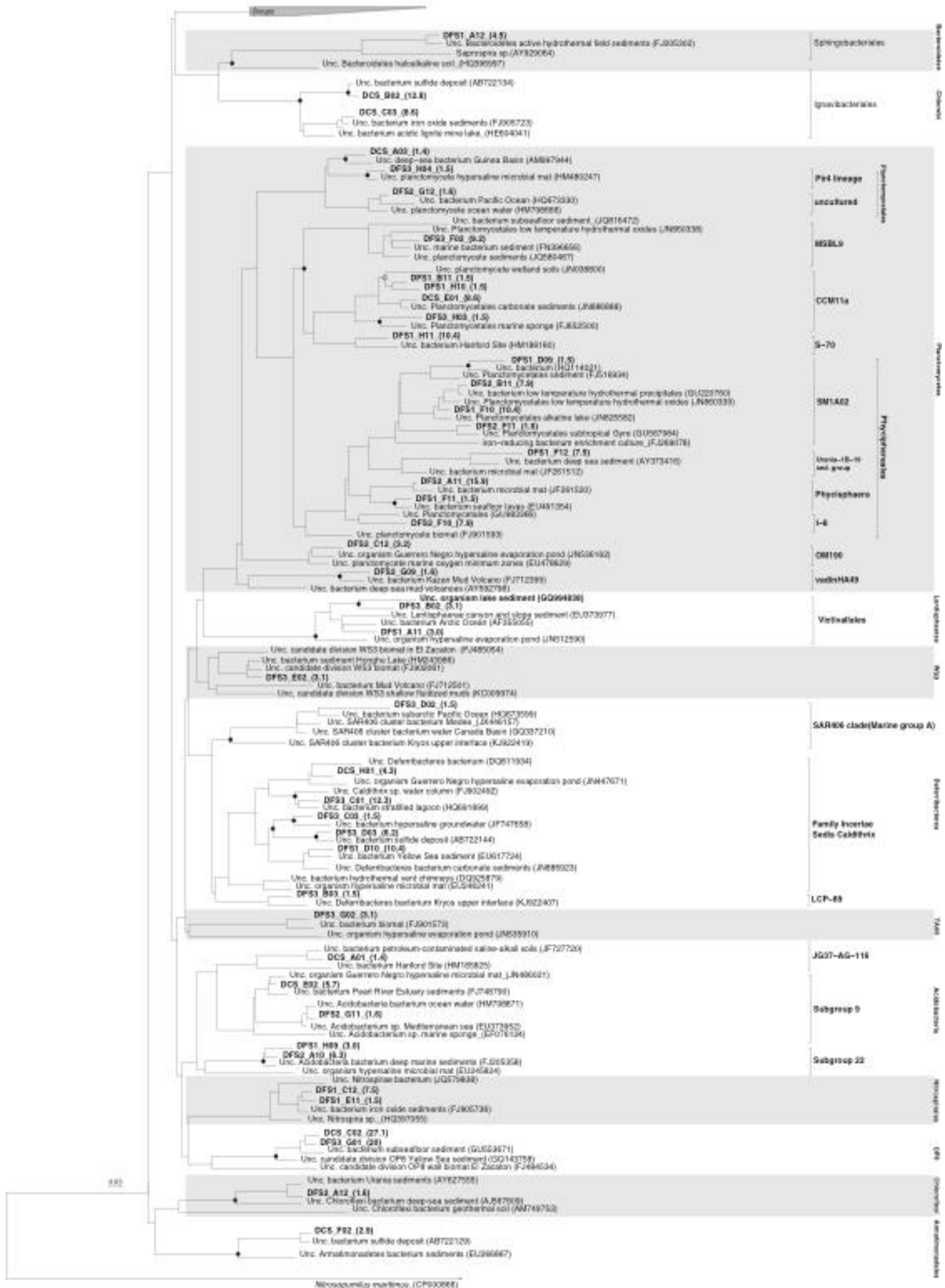


Figure S4. Phylogenetic affiliation and relative abundance (shown in parenthesis as percentage of all clones sequenced in corresponding library) of representative OTUs of bacterial (without proteobacterial) 16S rRNA gene clones. Scale bar corresponds to 3% estimated difference in nucleotide sequence positions. The black and white circles at nodes represent bootstrap support calculated on 1000 re-samplings. Black circles indicate a percentage of bootstrap support of $\geq 75\%$ and the white ones - of $< 75\%$. The ML phylogenetic tree was rooted with *Nitrosopumilus maritimus*_(CP000866) sequence.

Figure S5. Phylogenetic affiliation and relative abundance (shown in parenthesis as percentage of all clones sequenced in corresponding library) of representative OTUs of proteobacterial 16S rRNA gene clones. Scale bar corresponds to 3% estimated difference in nucleotide sequence positions. The black and white circles at nodes represent bootstrap support calculated on 1000 re-samplings. Black circles indicate a percentage of bootstrap support of $\geq 75\%$ and the white ones - of $< 75\%$. The ML phylogenetic tree was rooted with *Nitrosopumilus maritimus*_(CP000866) sequence.



Euryarchaeota

Thaumarchaeota

Figure S6. Phylogenetic affiliation and relative abundance (shown in parenthesis as percentage of all clones sequenced in corresponding library) of representative OTUs of archaeal 16S rRNA gene clones. Scale bar corresponds to 3% estimated difference in nucleotide sequence positions. The black and white circles at nodes represent bootstrap support calculated on 1000 re-samplings. Black circles indicate a percentage of bootstrap support of $\geq 75\%$ and the white ones - of $< 75\%$. The ML phylogenetic tree was rooted with *Alteromonas hispanica* (AY926461) sequence.

Table S1. Diversity indices calculated for 4 bacterial and 4 archaeal clone libraries created from *Basiluzzo* submarine hydrothermal samples (DFS1-3 and DCS).

97%								
similarity	DCSB	DFS1B	DFS2B	DFS3B	DCSA	DFS1A	DFS2A	DFS3A
Taxa_S	16	19	22	18	22	4	16	18
Individuals	70	67	63	65	62	68	92	66
Dominance_D	0.12	0.08	0.07	0.11	0.08	0.47	0.19	0.08
Simpson_1-D	0.88	0.92	0.93	0.89	0.92	0.53	0.81	0.92
Shannon_H	2.40	2.72	2.81	2.51	2.77	0.89	2.04	2.68
Equitability_J	0.87	0.93	0.91	0.87	0.90	0.64	0.74	0.93
Chao-1	17.50	21.50	37.00	22.20	55.00	4.00	44.00	23.00
Singleton	4	5	10	7	12	0	8	5
Coverage	0.94	0.93	0.84	0.89	0.81	1.00	0.91	0.92

Table S2. Quantitative real-time PCR (qPCR) performed with DFS and DCS samples following the protocol of Swan *et al.* (2010).

		Samples			
		DFS1	DFS2	DFS3	DCS
DNA, ng/μl		76.6	476.9	568.3	135.2
Primer	Sequences	16S rRNA gene x 10 ⁶ copy / 50 ng			
Bac331f	TCCTACGGGAGGCAGCAGT	7.70	7.35	4.53	10.02
Bac797r	GGACTACCAGGGTCTAATCCTGTT				
Arch349f	GYGCASCAGKCGMGAAW	1.73	1.83	0.63	0.85
Arch806r	GGACTACVSGGGTATCTAAT				
Bacteria, %		62.4	59.5	73.4	81.2
Archaea, %		37.6	40.5	26.6	18.8

Table S3. Habitat-specific dominant epi-macrofaunal species found at different sites of the Basiluzzo hydrothermal ecosystem.

Site typology	Hydrothermal activity	Latitude	Longitude	Depth	Most frequently found species
	DFS2	38° 40.315' N	15° 07.846' E	211 m	<i>Stenothoe elachista</i> , <i>Phtisica marina</i>
Active	CO ₂ - and sulfide emissions #1	38° 38.971' N	15° 06.393' E	82 m	<i>Holothuria tubulosa</i> , <i>Hacelia attenuata</i>
	CO ₂ - and sulfide emissions #2	38° 40.931' N	15° 07.477' E	123 m	<i>Goodallia triangularis</i> , <i>Apseudes spinosus</i>
Not active	Fe-rich crust	38° 40.685' N	15° 07.606' E	80 m	<i>Ampelisca ledoyeri</i> , <i>Neopycnodonte cochlear</i>
	Sulfide deposits	38° 40.757' N	15° 07.295' E	170 m	<i>Parastichopus regalis</i> , <i>Pseudoleptocheilia</i> sp

Table S4. Abundance of DFS-associated macrobenthic species identified during ROV surveys and microscopically.

Order	Family	Species	Abundance
Leptothecata	Plumulariidae	<i>Nemertesia</i> sp	2
	Lafoeidae	<i>Lafoeidae</i> sp.	2
		<i>Hydrozoa</i> sp.	3
Astrorhizida	Stegnamminidae	<i>Spiculosiphon oceana</i>	3
Amphipoda	Caprellidae	<i>Phtisica marina</i>	4
	Stenothoidae	<i>Stenothoe elachista</i>	7
	Ampithoidae	<i>Ampithoe</i> sp.	3
Isopoda	Aselloidae	<i>Asellota</i> sp.	2
Tanaidacea	Paratanaoidea incertae sedis	<i>Pseudoparatanais batei</i>	1
Trombidiformes	Halacaridae	<i>Halacaridae</i> sp.	1
Polychaeta	Serpulidae	<i>Protula</i> sp.	3
Cheilostomatida	Celleporoidea	<i>Reteporella grimaldii</i>	2
Poecilosclerida	Cladorhizidae	<i>Asbestopluma hypogea</i>	2