

Title: New insights into hydrothermal vent processes in the unique shallow-submarine arc-volcano, Kolumbo (Santorini), Greece

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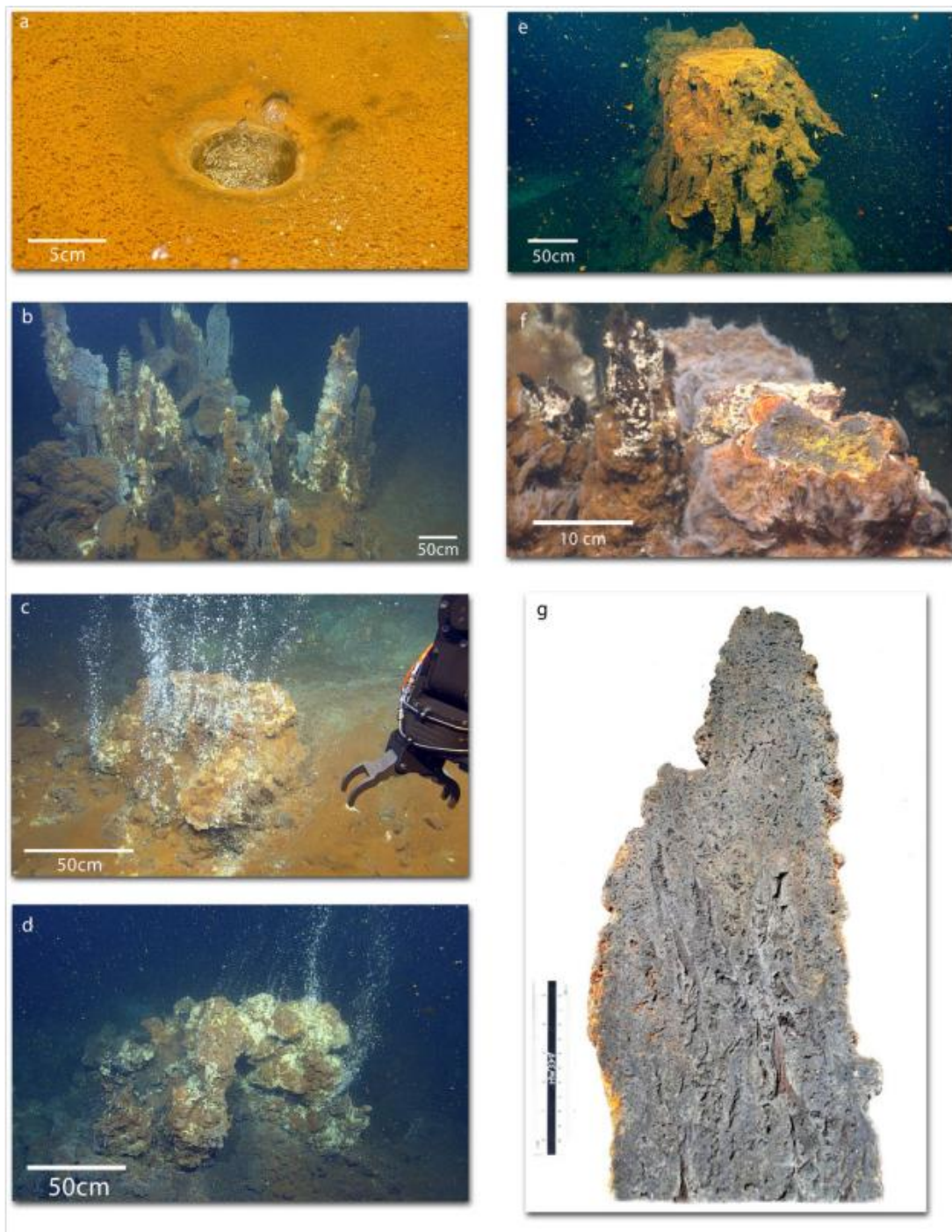
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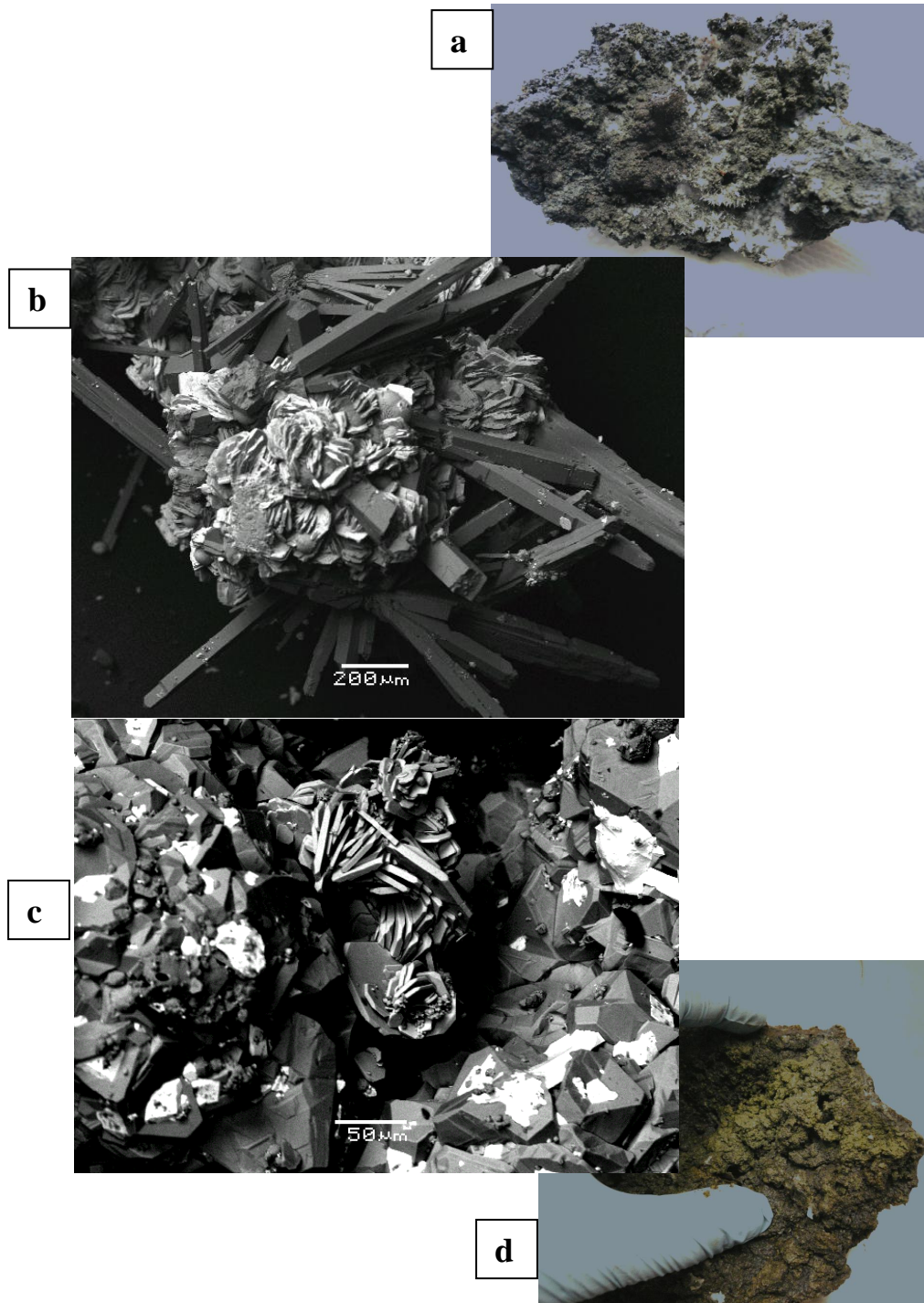
This supplement contains:

- 1. Supplementary Figures (7)**
- 2. Supplementary Tables (4)**
- 3. Supplementary References**

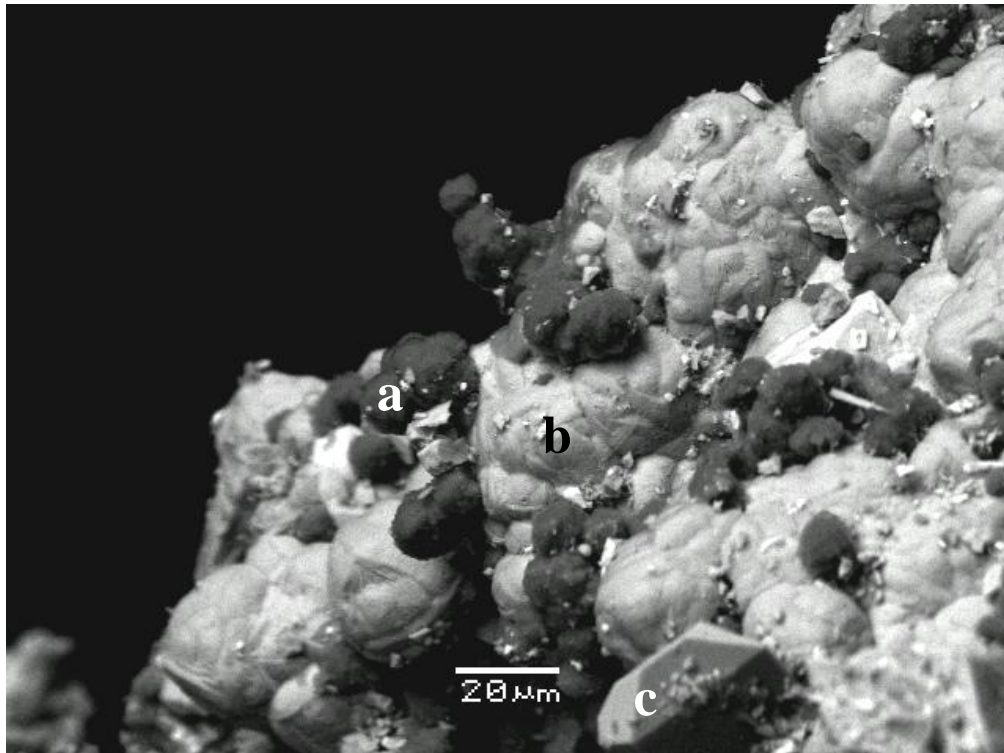


Supplementary Figure 1| Bottom photographs from ROV Hercules submersible and single intact recovered chimney (Submarine photographs taken by co-Chief Scientists Steven Carey, Katherine Croff Bell, Paraskevi Nomikou onboard E/V Nautilus during oceanographic cruises NA007-NA014). **a**, Small pockmark-like crater discharging low-temperature (70°C) fluids. **b**, Politeia Vent Complex (“Politeia”): Field of multiple inactive and active sulphide/sulphate , spires

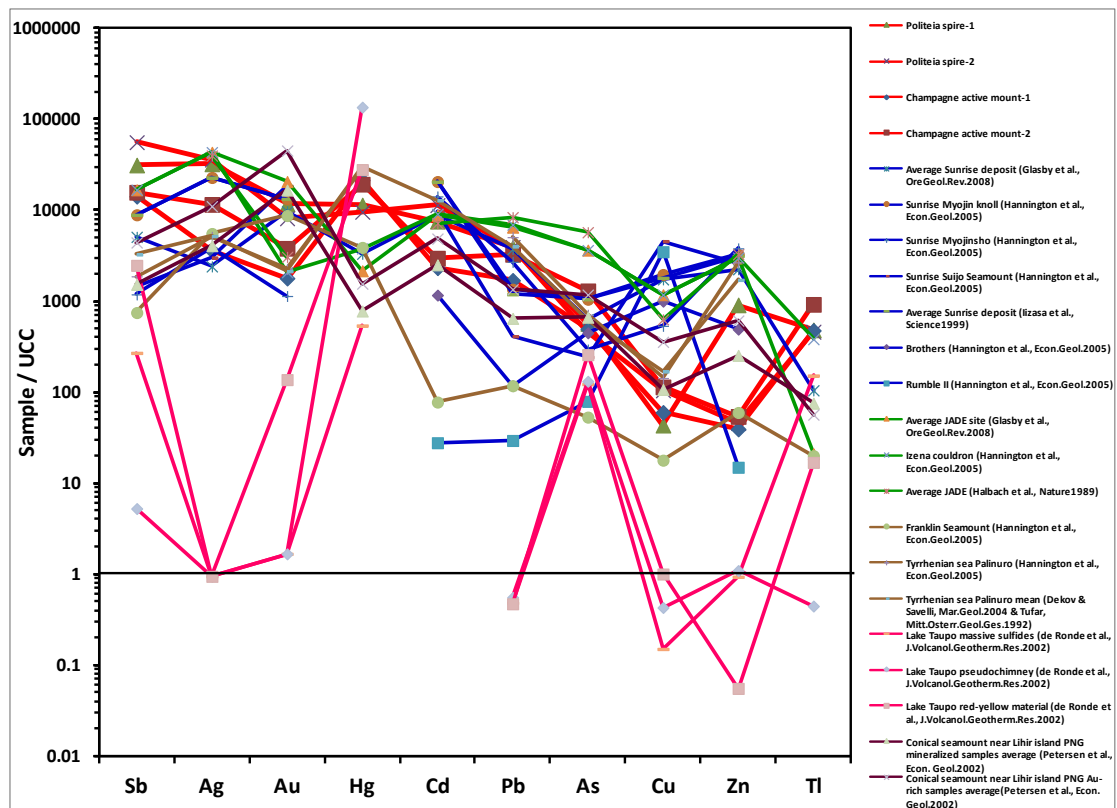
up to 2 m high on top of a hydrothermal mound with spire fragments draped by Fe-bearing bacterial mats. Clear fluids vent from active spires (not visible). **c**, The base of the knocked over vent spire sample NA014-003, revealing textural zones (see Figure 5a). The exterior of the spire is covered by grayish active suspended filamentous microbial biofilms (streamers). Note the “flame-like” jets of hydrothermal steam on far back spire (left corner). **d**, Champagne Vent Complex (“Champagne”): Active high-temperature (220°C) vent discharging both gases (>99 % CO₂) and fluids. **e**, Diffuser II Vent Complex (“Diffuser II”): Vent with bacterial covering and gas bubbling. **f**, Poet’s Candle: The largest observed (height ~ 4 m) inactive vent with bacterial covering. **g**, Section of the NA014-003 single intact spire. Bar is 10 cm long.



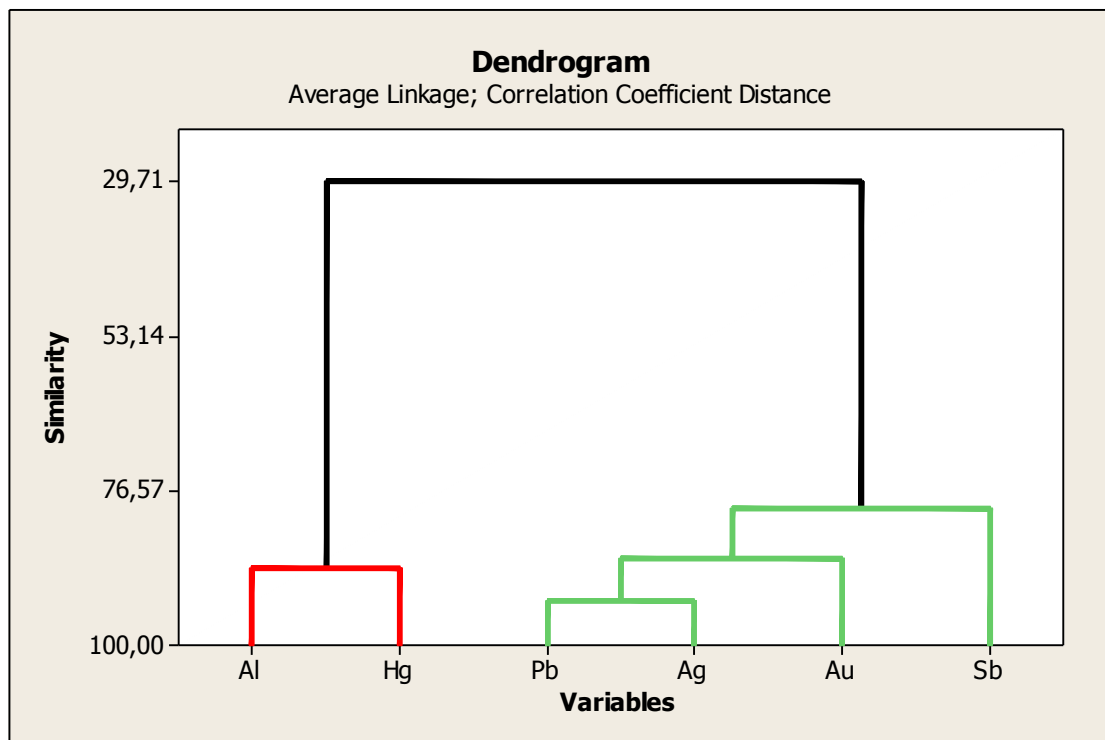
Supplementary Figure 2/ Macroscopic and SEM images of sulfide-sulfate minerals from Champagne . a, hand specimen with gypsum acicular crystals grown onto sulphide-sulphate matrix, b, SEM image of external surface of the sample showing botryoidal aggregates of pyrite and/or marcasite, associated with euhedral crystals of gypsum and barite, c, local aggregates of twinned chalcopyrite crystals with barite aggregates and galena precipitates, d, mount piece with brassy chalcopyrite



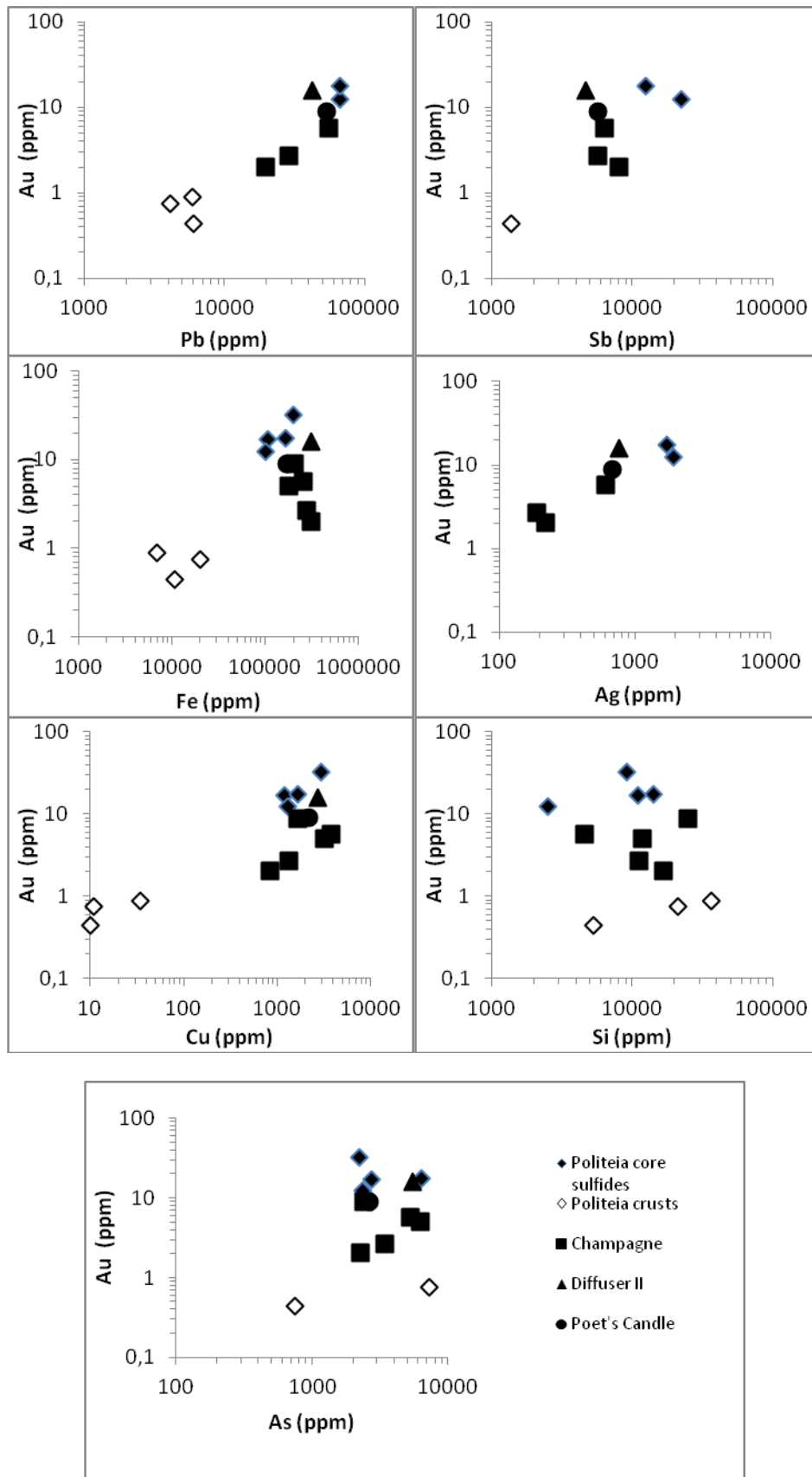
Supplementary Figure 3 | SEM image of phases lining open conduits of *Politeia spire*. a, K-Mg-Al-silicates (dark grey features, b, overgrown amorphous Sb-Zn sulfide aggregates, c, barite crystal.



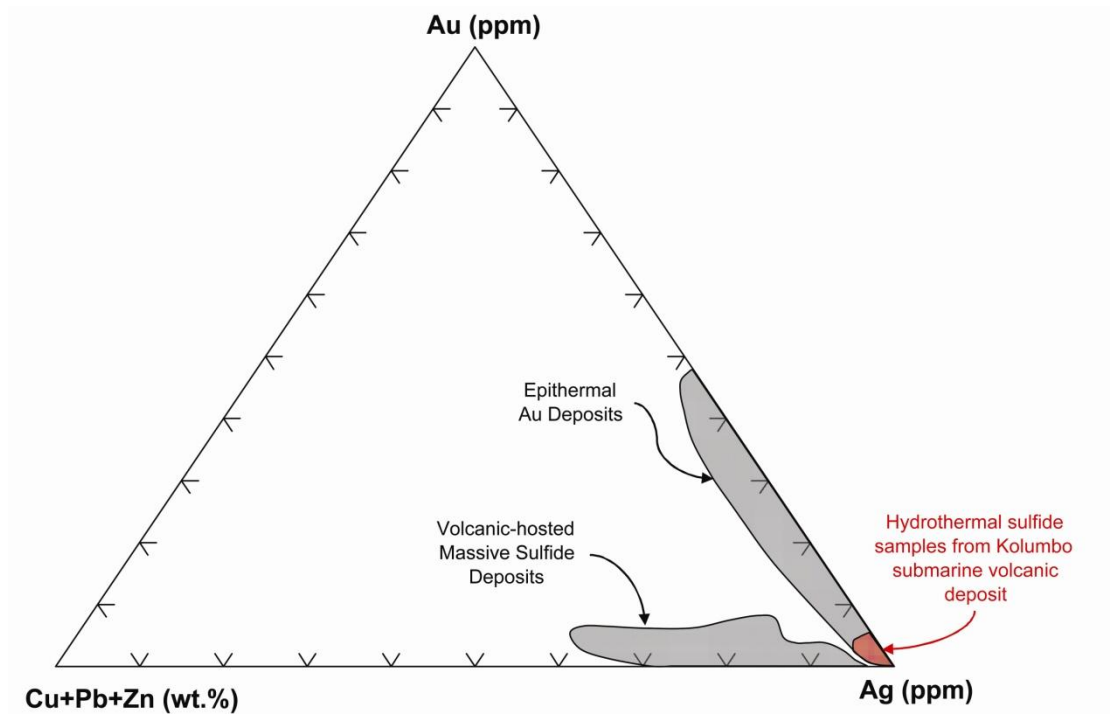
Supplementary Figure 4/ Geochemical spidergram comparing the Kolumbo vent samples with other seafloor hydrothermal deposits from various tectonic settings. Concentrations are normalized to Upper Continental Crust (UCC)¹ for selected noble (Ag, Au), potentially life-essential (Cu, Zn) and potentially toxic (Sb, Hg, Cd, As, Tl) elements. The average and maximum concentrations of Tl (510 ppm and >,1000 ppm respectively) and Sb (8,333 ppm and 2.2 wt %, respectively) are among the highest reported from modern seafloor hydrothermal systems. Average Sunrise deposit², Sunrise Myojin knoll¹⁷, Sunrise Myojinsho¹⁷, Sunrise Sujo Seamount¹⁷, Brothers¹⁷, Rumble II¹⁷, Average JADE site³, Izena cauldron¹⁷, Average JADE⁴, Franklin Seamount¹⁷, Tyrrhenian sea Palinuro¹⁷, Tyrrhenian sea Palinuro mean^{5,6}, Lake Taupo massive sulfides⁷, Lake Taupo pseudochimney⁷, Lake Taupo red-yellow material⁷, Conical seamount-mineralized samples average³⁴, Conical seamount- gold-rich samples average³⁴.¹⁷ or ³⁴; see ref. 17, or 34, in the main article



Supplementary Figure 5| Dendrogram based on statistical correlation of elements in Kolumbo samples. Variables are clustered into 2 groups according to similarity level. The first group includes Hg and Al with similarity level 88% and the second group includes Au, Pb, Ag and Sb with similarity level >79%. The relationships suggest that Au and Ag may be associated with sulfide mineral phases while Hg may be associated with aluminosilicate phases.



Supplementary Figure 6| Log/log plots of selected elements versus Au. Clustering of samples is observed according to vent complex, signifying different physicochemical conditions of formation. Relative enrichment of Politeia sulfides in Au, Ag, Sb and Pb is also observed.



Supplementary Figure 7 | Comparison of average Au, Ag and base-metal (Cu+Pb +Zn) content of samples from Kolumbo hydrothermal field and other sea-floor sulfides deposits. Compositional fields of typical epithermal gold deposits and volcanogenic massive sulfides are also shown (see Ref. 35).

Supplementary Table S1

Average content in ppm (mg kg^{-1}) of selected elements in samples from Kolumbo compared with other modern seafloor volcanogenic massive sulfide-style and epithermal-style hydrothermal deposits. Ref. XX: see reference XX in the main article.

	<i>n</i>	Si	Al	Fe	Pb	Sr	As	Sb	Bi	Zn	Cu	Cd	Hg	Tl	Ag	Au	Refs
Average Kolumbo deposit	14	14100	5890	166000	35000	10400	3810	8330	0.05	10200	1640	276	397	389	871	9	This study
Mid-ocean ridges:																	
S. Explorer Ridge	51	44409		252000	1000		575	42	2.0	54000	32000	200	11	43	125	0.72	Ref. 17
Endeavour Segment Main Field	83	42539		301000	5000		356	42	0.2	64000	27000	250	8	28	267	0.11	Ref. 17
Cleft segment, South cleft East Pacific Rise 11N, EPR	16	16361		186000	1000		360	18	0.1	309000	11000	615	2	23	230	0.11	Ref. 17
Galapagos rift	18	12621		205000	1000		330	26	0.3	266000	16000	885	2	19	37	0.15	Ref. 17
Mid-Atlantic Ridge TAG, surface and core	128	118267		283000	500		120	10	1.1	35000	45000	140	4	12	37	0.29	Ref. 17
Volcanic arcs:	310	50953		272000	500		55	28	9.0	65000	49000	232	9	13	92	1.8	Ref. 17
Average Sunrise deposit	12	89753	3705	116808	63700	1704	3050	2037	10.2	150800	48700	808	166	94	128	14.6	2
Sunrise Myojin knoll	37	40669		105000	23000		5045	3565		219000	55000	1860			1215	20	Ref. 17
Average Sunrise deposit	37	40576		100480	20270		5044	3564		210890	50540	1858			1213	20	2
Suiyo seamount	13			150000	0.7		1168	585			128000				162	27.7	Ref. 39
Brothers	9			74000	2000		2155			33000	28000	105					Ref. 17
Rumble II	1			125000	500		380			1000	98000	2.5					Ref. 17
Conical seamount	40			83000	10000		3200	612		17000	3000		39		216	25	Ref. 34
Lake Taupo massive sulphides	1			253000	8.2		588	108		62.5	4.2		27	137	<0.1	<0.005	7
Back arc rifts:																	
Average JADE site		19634	3175	62251	110800	1592	17500	6710	35.6	200200	33000	794	108	19	2300	31	3
Izena couldron	40	47214		62000	118000		17500	6710	25.0	202000	33000	820	190	345	2305	3	Ref. 17
Back arc basins:																	
Tyrrhenian Sea Panarea	5	118735		105000	28000		505			62000	500	255			11		Ref. 17
Tyrrhenian Sea Palinuro	15			151000	86000		3400	750		179000	4000		1400		270	3.4	Ref. 17
Manus Basin (intraoceanic)	26			149000	1.7		11000	1130		269000	109000		17		230	15	Ref. 17

Supplementary Table S2

Average content in ppm (mg kg^{-1}) or otherwise mentioned units of selected elements in hydrothermal vent samples from the Kolumbo deposit

Sample	Sr	V	Cr	Ni	Cd	% TOC	% TOT/S
NA014-003 Politeia spire-1 (ISSC)	10900	12	55	<20	682		24
NA014-003 Politeia spire-1 (OAsL)	21700	12		55	26		
NA014-003 Politeia spire-1 (SFeC)	35200	30	123	<20	7		13
NA014-003 Politeia spire-1 composite	1030	<10	4	7	629	5.82	
NA014-005 Diffuser II	1610	<10	6	2	50	5.71	
NA014-007 Champagne active mount (base)	1180	10	5	4	44	5.77	
NA014-016 Poet's Candle sulfide	1160	<10	4	15	210	3.86	
NA014-027 Champagne active mount-1 (N=2)	11400	<8	5	38	126	5.91	30
NA014-028 Champagne active mount -2 (N=2)	11900	<8	6	5	226	5.86	30
NA014-039 Politeia spire-2 (ISSC)	4570	15	27	<20	1025		34
NA014-039 Politeia spire-2 (SFeC)	41300	43	21	<20	4		12
NA014-039 Politeia spire-2 composite	1010	<10	4	7	489	4.14	
AVERAGE	10400	20	24	20	276	5.30	24
MAX	41300	43	123	55	1025	5.91	34
N	14	6	11	10	14	7	6

Supplementary Table S3

Microbial taxonomy of the produced sequences for the four samples by using the RDP classifier of the Ribosomal Database Project. The most abundant observed species (OTUs) were further compared to GenBank entries using BLAST (Basic Local Alignment Search Tool, National Center for Biotechnology Information, Bethesda, MD, USA) in order to confirm their phylogenetic affiliation. The most abundant OTU closely affiliated to *Nitrosopumilus maritimus* SCM1 (99% sequence similarity) is presented in grey background.

NA014_003	NA014_007	NA014_016	NA014_042	Consensus Lineage
39	27	27	90	Archaea unclassified
615	91	347	198	<i>Thaumarchaeota;Nitrosopumilales;Nitrosopumilaceae;Nitrosopumilus</i>
0	0	23	81	Crenarchaeota;Thermoprotei
0	0	0	3	Crenarchaeota;Thermoprotei;Thermoproteales;Thermofilaceae;Thermofilum
9	3	5	23	Euryarchaeota
0	0	0	1	Euryarchaeota;Methanomicrobia
2	0	4	5	Euryarchaeota;Thermoplasmata;Thermoplasmatales
1096	1573	550	1333	Bacteria;unclassified
0	1	16	21	Acidobacteria
1	3	10	2	Acidobacteria;Acidobacteria_Gp10;Gp10
0	0	0	1	Acidobacteria;Acidobacteria_Gp2;Gp2
0	3	18	13	Acidobacteria;Acidobacteria_Gp21;Gp21
2	5	11	7	Acidobacteria;Acidobacteria_Gp22;Gp22
1	10	0	0	Acidobacteria;Acidobacteria_Gp23;Gp23
0	1	1	2	Acidobacteria;Acidobacteria_Gp26;Gp26
0	1	13	12	Acidobacteria;Acidobacteria_Gp6;Gp6
0	0	1	4	Acidobacteria;Acidobacteria_Gp9;Gp9
0	0	0	1	Acidobacteria;Holophagae
1	0	3	14	Actinobacteria
0	0	1	0	Actinobacteria;Acidimicrobiales
0	0	0	1	Actinobacteria;Acidimicrobiales;Iamiaceae;Iamia
0	0	1	0	Actinobacteria;Actinomycetales;Brevibacteriaceae;Brevibacterium
0	1	5	1	Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium
0	2	0	0	Actinobacteria;Actinomycetales;Geodermatophilaceae
0	1	1	0	Actinobacteria;Actinomycetales;Micrococcaceae;Micrococcus
0	0	1	0	Actinobacteria;Actinomycetales;Nocardioideae;Nocardioideae
0	4	8	6	Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium
174	72	20	9	Bacteroidetes
1	10	1	0	Bacteroidetes;Bacteroidetes_incertae_sedis;Fulvivirga
0	0	1	0	Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella
7	3	0	0	Bacteroidetes;Flavobacteria;Flavobacteriales
1	1	5	0	Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae
78	8	166	1	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae
1	0	0	0	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Elizabethkingia
0	2	3	0	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Gaetbulibacter
0	0	1	0	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Lacinutrix
1	0	10	0	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Lutimonas
1	3	1	0	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Muricauda
13	16	9	2	Bacteroidetes;Sphingobacteria;Sphingobacteriales
0	0	0	1	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae
4	9	5	0	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Rhodothermaceae
1	1	0	0	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Rhodothermaceae;Rhodothermus
4	1	5	0	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Saprospiraceae
0	0	1	1	BRC1;BRC1_genera_incertae_sedis
1	0	0	0	Caldiserica;Caldisericia;Caldisericales;Caldiseriaceae;Caldisericum

6	1	3	17	Chlamydiae;Chlamydiae;Chlamydiales
0	0	0	3	Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae
0	8	0	1	Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Parachlamydia
0	11	0	0	Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Simkania
0	1	1	1	Chlamydiae;Chlamydiae;Chlamydiales;Waddliaceae;Waddlia
0	2	0	12	Chloroflexi
0	26	0	6	Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae
0	0	0	1	Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea
0	0	0	12	Chloroflexi;Dehalococcoidetes
0	0	0	6	Chloroflexi;Dehalococcoidetes;Dehalogenimonas
0	0	0	1	Cyanobacteria;Cyanobacteria;Family II;GpIIa
0	1	2	1	Deinococcus-Thermus;Deinococci;Deinococcales;Trueperaceae;Truepera
1	0	0	0	Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Oceanithermus
0	0	0	4	Firmicutes
0	0	0	1	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus
0	0	1	0	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Gemella
0	0	1	0	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus
0	0	1	0	Firmicutes;Bacilli;Lactobacillales
1	2	1	1	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus
0	1	9	3	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus
0	0	2	0	Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Finegoldia
0	1	0	0	Firmicutes;Clostridia;Clostridiales;Peptococcaceae
0	0	1	0	Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium
0	0	1	1	Firmicutes;Clostridia;Clostridiales;Veillonellaceae
1	1	0	0	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella
0	0	1	0	Lentisphaerae;Lentisphaeria;Lentisphaerales;Lentisphaeraceae;Lentisphaera
66	0	0	0	Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae
0	5	8	0	Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira
68	15	0	0	OD1;OD1_genera_incertae_sedis
155	281	79	106	Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae
3	31	9	5	Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula
0	0	1	0	Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pirellula
25	17	5	0	Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces
2	1	2	1	Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Rhodopirellula
206	58	85	33	Proteobacteria
197	101	138	16	Alphaproteobacteria
34	19	33	0	Alphaproteobacteria;Caulobacterales;Hyphomonadaceae
1	0	0	0	Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;Maricaulis
5	2	6	0	Alphaproteobacteria;Parvularculales;Parvularculaceae;Parvularcula
3	0	17	1	Alphaproteobacteria;Rhizobiales
0	0	0	4	Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae
0	0	1	0	Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Afipia
0	0	1	1	Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae
1	0	2	0	Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium
1	0	2	0	Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae
0	0	0	2	Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rhizobium
42	13	33	1	Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae
1	6	0	0	Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Lutimaribacter
0	0	0	1	Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus
0	0	5	0	Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseovarius
0	41	0	1	Alphaproteobacteria;Rhodospirillales
12	20	62	9	Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae
0	0	2	0	Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Thalassobaculum
2	0	0	0	Alphaproteobacteria;Rickettsiales;SAR11;Pelagibacter
0	7	1	0	Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
36	0	3	0	Betaproteobacteria
0	1	0	0	Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia
0	0	0	2	Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium

0	1	0	0	Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas
0	0	1	0	Betaproteobacteria;Neisseriales;Neisseriaceae
0	1	0	0	Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae
0	1	1	0	Betaproteobacteria;Rhodocyclales;Rhodocyclaceae
8	59	16	21	Deltaproteobacteria
4	0	0	0	Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Bacteriovorax
24	6	0	16	Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae
0	1	0	0	Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiferula
5	31	0	0	Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae
0	0	2	0	Deltaproteobacteria;Desulfuromonadales
0	0	1	0	Deltaproteobacteria;Desulfuromonadales;Geobacteraceae
2	1	2	1	Deltaproteobacteria;Myxococcales
0	2	0	0	Deltaproteobacteria;Myxococcales;Haliangiaceae;Haliangium
1	1	1	0	Deltaproteobacteria;Myxococcales;Nannocystaceae
0	0	6	0	Epsilonproteobacteria;Campylobacterales
32	1	0	0	Epsilonproteobacteria;Campylobacterales;Campylobacteraceae
4	0	0	0	Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum
17	1	3	0	Epsilonproteobacteria;Campylobacterales;Helicobacteraceae
98	1	5	0	Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas
1	0	0	0	Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Wolinella
626	369	332	35	Gammaproteobacteria
2	1	0	0	Gammaproteobacteria;Alteromonadales
3	3	0	1	Gammaproteobacteria;Chromatiales
23	0	7	0	Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae
0	3	0	2	Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae
0	2	1	0	Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella
0	5	0	0	Gammaproteobacteria;Gammaproteobacteria_incertae_sedis
1	2	0	1	Gammaproteobacteria;Gammaproteobacteria_incertae_sedis;Sedimenticola
1	0	0	0	Gammaproteobacteria;Legionellales;Legionellaceae
0	0	10	0	Gammaproteobacteria;Methylococcales;Methylococcaceae
32	0	5	0	Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas
0	0	4	3	Gammaproteobacteria;Pasteurellales;Pasteurellaceae
0	1	0	0	Gammaproteobacteria;Pseudomonadales;Moraxellaceae
0	1	9	0	Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter
0	0	1	0	Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter
2	19	186	22	Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas
8	0	0	0	Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Thiomicrospira
0	1	0	1	Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas
16	0	0	2	Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta
1	3	2	3	TM7;TM7_genera_incertae_sedis
3	1	0	0	Verrucomicrobia
5	1	0	2	Verrucomicrobia;Opitutae
1	0	0	0	Verrucomicrobia;Opitutae;Opitutales;Opitutaceae
1	0	0	0	Verrucomicrobia;Opitutae;Puniceococcales;Puniceococcaceae
5	11	2	0	Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae
0	1	0	0	WS3;WS3_genera_incertae_sedis
33	14	4	24	Unclassified

Supplementary Table S4

Bray-Curtis similarities of microbial community composition among the four investigated samples at an OTU (observed species) level and phylum level.

	NA014_003	NA014_007	NA014_016
<i>OTU level</i>			
NA014_007	0		
NA014_016	25.53	0	
NA014_042	0	7.15	0
<i>Phylum level</i>			
NA014_007	66.25		
NA014_016	82.06	60.03	
NA014_042	52.47	72.12	50.44

Supplementary References

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