1 SUPPLEMENTARY MATERIAL

Supplementary Figure S1. Alpha diversity indexes for the five SH communities.
Supplementary Figure S2. Co-occurrence network analysis of the SH bacterial communities. The size of each node (representing ASVs) is proportional to the number of connections (degrees), the color of the edges connecting nodes represents the interaction type, the node color indicates the taxonomic affiliation at the phylum level and node labels are at the lowest available taxonomic classification.
Supplementary Figure S3. MEBS analysis heatmap displaying the completeness of N, Fe, S and CH₄ pathways, as a whole (first top section) and for each particular pathway (bottom four sections). The color gradient shows the percentage of completion for each pathway (from lowest to highest) and the values shown in the top section represent the corresponding MEBS score (* FDR ≤ 0.01).
**Supplementary Table S1.** Physicochemical parameters and measured characteristics of the five SH sampled sites, as published previously in Castro-Severyn et al., 2020 [8].

| Site | pH  | Altitude (masl) | Sampling Temperature (°C) | As [mg/kg] | Salinity (%) | Conductivity (mS) | Suspended Solids (gr/L) | Coordinates          |
|------|-----|----------------|--------------------------|------------|--------------|-------------------|------------------------|----------------------|
| H0   | 8.8 | 3792           | 14.6                     | 9          | 11.9         | 6.082             | 3.006                  | 20º15'48.8"S, 68º52'28.4"W |
| H1   | 9.4 | 3785           | 14                       | 16.3       | 8.1          | 4.076             | 2.039                  | 20º16'27.7"S, 68º53'3"W |
| H3   | 8.5 | 3783           | 19.9                     | 49.2       | 2.2          | 1.122             | 0.560                  | 20º16'59.2"S, 68º53'16.7"W |
| H4   | 8.4 | 3787           | 18.8                     | 155        | 77.2         | 38.20             | 19.40                  | 20º17'40.9"S, 68º53'17.3"W |
| H5   | 9.2 | 3781           | 24.3                     | 321        | 84.5         | 42.12             | 21.12                  | 20º18'37"S, 68º52'42"W  |
| Phylum                        | H0    | H1    | H3    | H4    | H5    |
|------------------------------|-------|-------|-------|-------|-------|
| Proteobacteria               | 29.067| 40.343| 36.431| 41.857| 33.732|
| Bacteroidetes                | 19.051| 11.293| 26.303| 25.570| 33.257|
| Cyanobacteria                | 33.987| 11.488| 6.932 | 16.001| 14.524|
| Deinococcus-Thermus          | 2.038 | 0.078 | 5.236 | 5.286 | 2.901 |
| Chloroflexi                  | 1.176 | 8.489 | 6.072 | 1.614 | 2.996 |
| Actinobacteria               | 0.647 | 4.050 | 3.712 | 2.539 | 3.213 |
| Gemmatimonadetes             | 1.137 | 1.752 | 5.949 | 0.169 | 2.920 |
| Patescibacteria              | 2.940 | 2.687 | 2.409 | 0.989 | 1.858 |
| Verrucomicrobiota            | 1.313 | 1.986 | 1.131 | 1.393 | 1.100 |
| Firmicutes                   | 2.646 | 1.051 | 1.377 | 0.586 | 0.626 |
| Euryarchaeota                | 0.647 | 1.051 | 1.229 | 1.302 | 0.891 |
| Spirochaetes                 | 1.999 | 1.713 | 0.172 | 0.169 | 0.436 |
| Planctomycetes               | 0.764 | 2.414 | 1.278 | 0.000 | 0.265 |
| Kiritimatiellaeota           | 0.921 | 0.701 | 0.344 | 0.404 | 0.147 |
| Acidobacteria                | 0.039 | 2.687 | 0.688 | 0.000 | 0.133 |
| Tenericutes                  | 0.353 | 0.156 | 0.049 | 0.833 | 0.190 |
| Epsilonibacteraeota          | 0.274 | 0.701 | 0.000 | 0.286 | 0.683 |
| Nanoarchaeaeota              | 0.039 | 2.843 | 0.049 | 0.052 | 0.076 |
| Halanaerobiota               | 0.000 | 0.000 | 0.074 | 0.703 | 0.284 |
| Fibrobacteres                | 0.294 | 0.389 | 0.049 | 0.000 | 0.000 |
| Omnitrophicaeota             | 0.039 | 0.818 | 0.000 | 0.000 | 0.000 |
| Latescibacteria              | 0.000 | 0.234 | 0.123 | 0.152 | 0.000 |
| LCP-89                       | 0.039 | 0.156 | 0.049 | 0.052 | 0.000 |
| Lentisphaerae                | 0.000 | 0.078 | 0.147 | 0.052 | 0.000 |
| Caldiserica                  | 0.176 | 0.078 | 0.000 | 0.000 | 0.000 |
| Chlamydiae                   | 0.000 | 0.000 | 0.078 | 0.095 | 0.000 |
| Cloacimonetes                | 0.176 | 0.000 | 0.000 | 0.038 | 0.000 |
| Crenarchaeota                | 0.000 | 0.428 | 0.000 | 0.000 | 0.000 |
| Nitrospirae                  | 0.000 | 0.428 | 0.000 | 0.000 | 0.000 |
| WS1                          | 0.059 | 0.000 | 0.074 | 0.065 | 0.000 |
| Hydrogenedentes              | 0.098 | 0.078 | 0.074 | 0.000 | 0.000 |
| TA06                         | 0.000 | 0.350 | 0.000 | 0.000 | 0.000 |
| Rokubacteria                 | 0.000 | 0.234 | 0.000 | 0.000 | 0.000 |
| Altiaarchaeota               | 0.000 | 0.195 | 0.000 | 0.000 | 0.000 |
| BRC1                         | 0.039 | 0.000 | 0.000 | 0.000 | 0.038 |
| Fusobacteria                 | 0.000 | 0.156 | 0.000 | 0.000 | 0.000 |
| WS4                          | 0.000 | 0.156 | 0.000 | 0.000 | 0.000 |
| Calditrichaeota              | 0.000 | 0.117 | 0.000 | 0.000 | 0.000 |
| Acetothermia                 | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| Armatimonadetes              | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| Asgardaeota                  | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| Atribacteria                 | 0.039 | 0.000 | 0.000 | 0.000 | 0.000 |
| Chrysiogenetes               | 0.000 | 0.000 | 0.000 | 0.000 | 0.038 |
| Dependentiae                 | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| Diapherotorites              | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| Elusimicrobia                | 0.000 | 0.000 | 0.000 | 0.000 | 0.038 |
| Entothioneellaeota           | 0.000 | 0.000 | 0.049 | 0.000 | 0.000 |
| Modulibacteria               | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| WOR-1                        | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
| Zixibacteria                 | 0.000 | 0.078 | 0.000 | 0.000 | 0.000 |
**Supplementary Table S4.** Statistical values of the SH co-assembly, representing the five metagenomes.

| Contigs Stats          | SH Coassembly Contigs.db |
|------------------------|--------------------------|
| Total Length           | 1,859,591,865             |
| Num Contigs            | 994,545                  |
| Num Contigs > 2.5 kb   | 148,394                  |
| Num Contigs > 5 kb     | 31,221                   |
| Num Contigs > 10 kb    | 6,178                    |
| Num Contigs > 20 kb    | 870                      |
| Num Contigs > 50 kb    | 23                       |
| Num Contigs > 100 kb   | 1                        |
| Longest Contig         | 101,53                   |
| Shortest Contig        | 1                        |
| Num Genes (prodigal)   | 2,382,438                |
| L50                    | 281,061                  |
| L75                    | 583,991                  |
| L90                    | 817,245                  |
| N50                    | 1,859                    |
| N75                    | 1,305                    |
| N90                    | 1,103                    |

**Raw number of HMM Hits**

| Ribosomal_RNAs          | 227                      |
| Protista_83             | 2,396                    |
| Archaea_76              | 19,304                   |
| Bacteria_71             | 35,392                   |

**Approx. number of genomes**

| eukarya (Protista_83)   | 3                        |
| archaea (Archaea_76)   | 9                        |
| bacteria (Bacteria_71) | 356                      |
Supplementary Table S6. Indexes of relative abundance and detection of each recovered MAG across the five SH metagenomes.

| MAGs    | Relative Abundance | Detection |
|---------|--------------------|-----------|
|         | H0        | H1        | H3        | H4        | H5        | H0        | H1        | H3        | H4        | H5        |
| SH-MAG111 | 0        | 0         | 0,72168791 | 0         | 0,27831209 | 0,00441  | 0,00554  | 0,99771   | 0,07316   | 0,95468   |
| SH-MAG116 | 0        | 0         | 0,54889132 | 0,00013961 | 0,45096907 | 0,00295  | 0,00133  | 0,99243   | 0,12853   | 0,97785   |
| SH-MAG12  | 0        | 0         | 0,54493692 | 0,11609335 | 0,33896972 | 0,0025   | 0,00193  | 0,99281   | 0,78714   | 0,9599    |
| SH-MAG129 | 0        | 0         | 0,69848999 | 0,1220407  | 0,17946932 | 0,00313  | 0,02087  | 0,99531   | 0,74521   | 0,8047    |
| SH-MAG130 | 0        | 0         | 0,38686291 | 0,14428399 | 0,4688531  | 0,00382  | 0,00389  | 0,97836   | 0,86299   | 0,98158   |
| SH-MAG131 | 7,77E-06 | 0,99980086 | 0,0001669  | 0         | 2,45E-05   | 0,04034  | 0,99712  | 0,12015   | 0,02857   | 0,07146   |
| SH-MAG143 | 0,90041192 | 8,62E-05 | 0,07427925 | 2,36E-05   | 0,02519905 | 0,99706  | 0,09119  | 0,89824   | 0,11717   | 0,62849   |
| SH-MAG144 | 0        | 0         | 0,10728277 | 0,6230292  | 0,26951431 | 0,02051  | 0,01057  | 0,91627   | 0,99847   | 0,99011   |
| SH-MAG148 | 0        | 0         | 0,00210879 | 0,72287575 | 0,27501545 | 0,00406  | 0,00258  | 0,23134   | 0,99751   | 0,97311   |
| SH-MAG162 | 0        | 0         | 0,33797659 | 0,28950365 | 0,37251977 | 0,00712  | 0,0053   | 0,99119   | 0,99081   | 0,9919    |
| SH-MAG169 | 0,53828526 | 0,38203929 | 0,04537899 | 4,69E-07   | 0,03429599 | 0,98488  | 0,84044  | 0,60269   | 0,03486   | 0,50812   |
| SH-MAG192 | 0        | 0         | 0,3072886  | 0,22118822 | 0,47152318 | 0,00512  | 0,00153  | 0,98227   | 0,96535   | 0,99039   |
| SH-MAG193 | 0        | 0         | 0,64640238 | 0         | 0,35359762 | 0,00147  | 0,00092  | 0,99165   | 0,05107   | 0,91743   |
| SH-MAG29  | 0,99997034 | 0         | 5,39E-07   | 4,01E-06   | 2,51E-05   | 0,9993  | 0,00676  | 0,99412   | 0,32832   | 0,15348   |
| SH-MAG3   | 0        | 0         | 0,00864616 | 0,78123545 | 0,00068058 | 0,20943781 | 0,0037  | 0,2329   | 0,99661   | 0,082    | 0,87538   |
| SH-MAG78  | 0,00106885 | 0,0007131 | 0,73245797 | 0,0097231 | 0,25578776 | 0,0717  | 0,03031  | 0,9989    | 0,66337   | 0,99825   |
| SH-MAG89  | 0        | 0         | 0,63255005 | 0,00085958 | 0,36659037 | 0,00305  | 0,00202  | 0,99812   | 0,22902   | 0,98909   |
| SH-MAG93  | 0        | 0         | 0,48897198 | 0,15399497 | 0,35703306 | 0,00783  | 0,01217  | 0,98689   | 0,85548   | 0,96376   |
| SH-MAG96  | 0        | 0         | 0,63205353 | 3,97E-06   | 0,36794251 | 0,00293  | 0,00202  | 0,99801   | 0,08462   | 0,98806   |
| MAG ID       | Gene presence and copy number |   |   |   |   |   |   |
|--------------|------------------------------|---|---|---|---|---|---|
| SH-MAG111    | 1 1 1                        | 1 | 2 |   |   |   |   |
| SH-MAG12     | 1 1 1                        | 1 | 2 |   |   |   |   |
| SH-MAG116    | 2 1 1 1                      | 1 | 2 |   |   |   |   |
| SH-MAG130    | 1                            | 1 | 2 |   |   |   |   |
| SH-MAG193    | 1                            | 1 | 2 |   |   |   |   |
| SH-MAG148    | 2                            |   |   | 3 |   |   |   |
| SH-MAG143    | 1                            |   |   | 3 |   |   |   |
| SH-MAG93     | 1                            | 1 | 2 |   |   |   |   |
| SH-MAG129    | 1 1 3                        | 1 | 3 |   |   |   |   |
| SH-MAG144    | 1 1 1 1                      | 1 | 1 | 1 |   |   |   |
| SH-MAG29     | 1 3 1 1                      | 2 | 3 |   |   |   |   |
| SH-MAG3      | 1 3                          |   |   | 1 |   | 3 |   |
**Supplementary Table S3.** Abundance and taxonomic classification of the 3801 ASVs detected in SH communities.

**Supplementary Table S5.** Statistical evaluation of enriched functional categories (SEED subsystem 1) for each of the five communities with respect to the other four (according to Welch’s t-test).

**Supplementary Table S7.** Completion index of all detected KEGG modules in each analyzed MAG.