Microbial succession during the transition from active to inactive stages of deep-sea hydrothermal vent sulfide chimneys

Jialin Hou, Stefan M. Sievert, Yinzhao Wang, Jeff S. Seewald, Vengadesh Perumal Natarajan Fengping Wang*, Xiang Xiao*

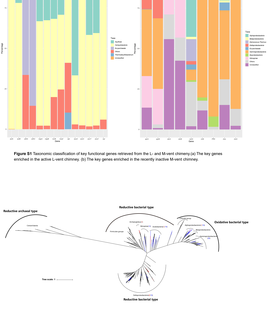

Figure S1 Taxonomic classification of key functional genes retrieved from the L and M-vent chimney.(a) The key genes enriched in the active L-vent chimney. (b) The key genes enriched in the recently inactive M-vent chimney.

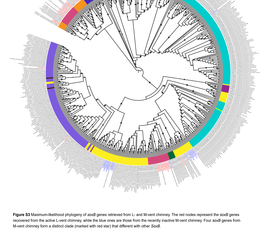

Figure S2 Maximum-likelihood phylogeny of dsrA genes retrieved from L- and M-vent chimney. The red branches represent the dsrA genes recovered from the active L-vent chimney, while the blue ones are those from recently inactive M-vent chimney. Numbers of dsrA gene for each sample are displayed in the parentheses after the clade name.

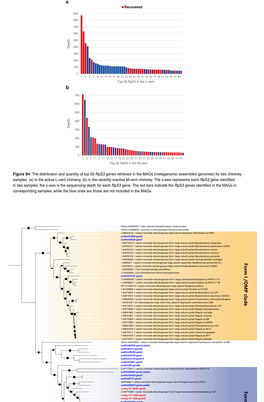

Figure S3 Maximum-likelihood phylogeny of dsrB genes retrieved from L- and M-vent chimney. The red branches represent the dsrB genes recovered from the active L-vent chimney, while the blue ones are those from recently inactive M-vent chimney. Four dsrB genes from M-vent chimney form a distinct clade (marked with red star) that different with other DsrB

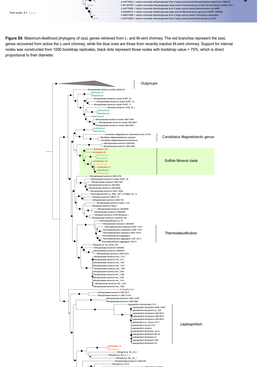

Figure S4 The distribution and quantity of top 50 RpS3 genes retrieved in the MAGs (metagenomic assembled genomes) for two chimney samples. (a) In the active L-vent chimney. (b) In the recently inactive M-vent chimney. The x-axis represents each RpS3 gene identified in two samples, the y-axis is the sequencing depth for each RpS3 gene. The red bar is the sample the RpS3 genes identified in the MAGs in corresponding samples, while the blue ones are those are not included in the MAGs.

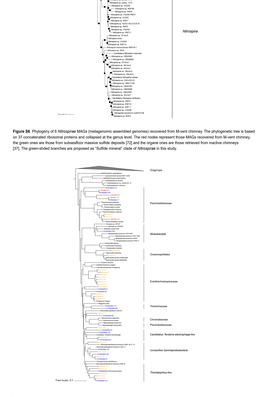

Figure S5 Maximum-likelihood phylogeny of cbsL genes retrieved from L- and M-vent chimney. The red branches represent the cbsL genes recovered from the active L-vent chimney, while the blue ones are those from recently inactive M-vent chimney. Sequence for internal nodes was constructed from 1000 bootstrap replicates, black dots represent those nodes with bootstrap value > 70%, which is direct proportional to their diameter.

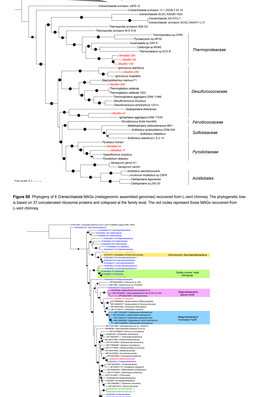

Figure S6 Phylogeny of 6 Nitrospirae MAGs (metagenomic assembled genomes) recovered from M-vent chimney. The phylogenetic tree is based on 37 concatenated ribosomal proteins and collapsed at the family level. The red nodes represent those MAGs recovered from M-vent chimney. Sequence for internal nodes was constructed from 1000 bootstrap replicates, black dots represent those nodes with bootstrap value > 70%, which is direct proportional to their diameter. The green ones are those from subsediment massive sulfide deposits [72] and the organe ones are those retrieved from inactive chimneys [37]. The green-ended branches are proposed as "Sulfide mineral" clade of Nitrospirae in this study.

Figure S7 Phylogeny of 22 Gammaproteobacteria MAGs (metagenomic assembled genomes) recovered from M- and L-vent chimney. The phylogenetic tree is based on 37 concatenated ribosomal proteins and collapsed at the genus level. The red nodes represent those MAGs recovered from L-vent chimney, and blue for M-vent chimney. The organe ones are those retrieved from inactive chimneys [37].

Figure S8 Phylogeny of 6 Crenarchaeota MAGs (metagenomic assembled genomes) recovered from L-vent chimney. The phylogenetic tree is based on 37 concatenated ribosomal proteins and collapsed at the family level. The red nodes represent those MAGs recovered from L-vent chimney.

Figure S9 Maximum-likelihood phylogeny of cyc2 genes retrieved from L- and M-vent chimney. The red branches represent the cyc2 genes recovered from the active L-vent chimney while the blue ones are those from recently inactive M-vent chimney. the green ones are those from subsediment massive sulfide deposits [72] and the organe ones are those retrieved from inactive chimneys. [37] The other reference sequences are come from Kato et al., 2013 [76]. Sequence for internal nodes was constructed from 1000 bootstrap replicates, black dots represent those nodes with bootstrap value > 70%, which is direct proportional to their diameter.