

Supplementary Information

**Analysis of Marine Microbial Communities Colonizing Various
Metallic Materials and Rust Layers**

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33 Table S1 Relative abundance of bacterial and archaeal 16S rRNA gene sequences obtained from
34 surface, seawater and sea mud samples at the class level (Relative abundance >1%)

Class	Fe	Cu	Al	SW	YB	SM	OL	ML	IL
Bacteria ^a									
Deltaproteobacteria	7.5	4.9	5.8	3.3	12.2	24.1	10.5	75.1	30.7
Alphaproteobacteria	21.5	32.0	24.1	35.3	29.9	11.3	21.5	3.6	14.9
Gammaproteobacteria	27.5	14.6	19.2	11.3	17.1	14.8	15.1	3.3	15.1
Epsilonproteobacteria	0.4	2.8	2.0	1.1	0.7	19.4	0.3	0.04	0.4
Clostridia	9.9	5.6	5.9	2.1	9.3	2.1	18.4	8.1	12.5
Acidimicrobiia	12.2	3.0	5.6	15.1	6.3	6.3	5.0	0.9	3.4
Unidentified Cyanobacteria	0.8	3.8	0.8	14.6	0.5	0.2	0.5	0.1	0.2
Bacilli	3.1	7.8	5.7	3.2	1.5	1.8	1.0	2.3	0.3
Archaea ^b									
Methanococci	0.0	0.1	0.0	0.5	4.0	0.2	82.0	97.8	68.5
Unidentified Thaumarchaeota	88.1	18.9	94.3	15.3	76.5	24.1	14.6	1.6	28.9
Thermoplasmata	0.0	0.0	0.0	0.0	0.0	7.5	0.0	0.0	0.0
Thaumarchaeota SCG	3.1	0.3	1.4	6.2	0.1	0.3	0.3	0.0	0.3
Methanomicrobia	0.7	0.1	0.0	0.7	0.1	5.3	0.1	0.0	0.2
Thaumarchaeota SAGMCG-1	0.0	0.0	0.0	3.4	0.0	0.0	0.0	0.0	0.0
Methanobacteria	0.1	0.0	0.0	1.0	0.1	0.0	0.0	0.0	0.1

35 Abbreviations : Fe, biofilm of carbon steel; Cu, biofilm of copper alloy; Al, biofilm of aluminum
36 alloy; SW, seawater; YB, yellow blister of carbon steel; SM, sea mud; OL, outer layer of rust from
37 carbon steel; ML, middle layer of rust from carbon steel; IL, inner layer of rust from carbon steel.

38 ^a The proportion of major bacterial classes related sequences in the total bacterial sequences.

39 ^b The proportion of major archaeal classes related sequences in the total archaeal sequences.

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41 Table S2 Relative abundance of bacterial and archaeal 16S rRNA gene sequences obtained from
 42 surface, seawater and sea mud samples at the family level (Relative abundance >2%)

Family	Fe	Cu	Al	SW	YB	SM	OL	ML	IL
Bacteria ^a									
Rhodobacteraceae	8.2	22.5	8.9	20.1	8.5	2.0	5.5	1.4	2.7
Unidentified Chloroplast	0.7	8.5	2.6	0.4	1.2	0.1	1.1	0.3	0.6
Lactobacillaceae	2.2	5.7	1.5	0.5	0.3	1.3	0.4	1.4	0.0
JTB255 marine benthic group	6.7	4.0	3.6	0.5	4.4	4.2	3.3	0.5	1.9
Helicobacteraceae	0.3	2.7	2.0	1.1	0.6	19.4	0.3	0.0	0.2
Pseudomonadaceae	4.9	2.3	1.4	0.5	0.2	0.6	2.4	1.1	1.5
Flammeovirgaceae	1.3	2.3	1.4	0.3	0.9	0.4	1.0	0.2	0.7
Lachnospiraceae	2.2	2.0	1.3	0.5	2.7	0.8	0.4	2.5	0.1
OM1 clade	6.8	1.9	2.7	14.3	2.8	5.0	2.3	0.4	1.6
Rhodospirillaceae	4.7	1.6	4.5	2.0	7.8	4.8	4.3	0.6	3.5
Bacillaceae	0.6	1.5	3.0	1.7	0.5	0.2	0.5	0.4	0.2
Clostridiaceae 1	4.9	1.2	2.2	0.9	4.1	0.4	1.0	1.2	0.1
Haliaceae	3.7	0.8	2.7	2.2	1.7	0.6	1.3	0.2	1.1
Sva0996 marine group	3.0	0.7	1.5	0.4	1.9	0.5	1.1	0.2	0.9
Peptococcaceae	0.5	0.6	0.7	0.0	0.4	0.0	16.2	2.6	11.3
Desulfovibrionaceae	0.4	0.5	0.7	0.1	3.0	0.0	2.6	3.1	13.3
Burkholderiaceae	0.4	0.4	0.5	0.0	0.3	0.3	0.1	0.1	2.2
Desulfobacteraceae	0.7	0.3	0.4	0.5	1.9	12.6	2.4	0.5	12.1
FamilyI	0.5	0.2	0.5	14.6	0.3	0.2	0.3	0.0	0.2
Methylobacteriaceae	0.2	0.2	0.2	0.0	0.2	0.0	3.0	0.1	0.9
Vibrionaceae	0.4	0.2	0.9	2.1	0.8	0.2	0.4	0.1	0.2
Desulfobulbaceae	0.4	0.1	0.2	0.2	1.1	3.6	0.6	0.0	0.2
Surface 1	0.0	0.0	1.2	8.3	0.0	0.9	0.0	0.0	0.0
SAR86 clade	0.0	0.0	1.2	2.2	0.0	0.6	0.0	0.0	0.0
Archaea ^b									
Unidentified Thaumarchaeota	86.1	18.6	87.0	15.3	74.5	13.8	14.1	1.6	27.1
Methanococcaceae	0.0	0.1	0.0	0.5	4.0	0.2	82.0	97.8	68.5
MBG D and DHVEG-1	0.0	0.0	0.0	0.0	0.0	7.1	0.0	0.0	0.0
Cenarchaeaceae	0.2	0.2	1.5	0.0	0.5	6.8	0.0	0.0	0.4
Methanomicrobiaceae	0.0	0.0	0.0	0.0	0.0	2.6	0.0	0.0	0.0
Methanosarcinaceae	0.0	0.1	0.0	0.3	0.0	2.2	0.1	0.0	0.0
Unidentified SAGMCG-1.	0.0	0.0	0.0	1.9	0.0	0.0	0.0	0.0	0.0
Methanobacteriaceae	0.1	0.0	0.0	1.0	0.1	0.0	0.0	0.0	0.1

43 The abbreviations of the samples are the same as those used in Table S1.

44 ^a The proportion of major bacterial family related sequences in the total bacterial sequences.

45 ^b The proportion of major archaeal family related sequences in the total archaeal sequences.

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48 **Figure legends**

49 **Fig. S1** Rarefaction curves of sequencing reads of 16S rRNA genes from nine samples
50 for **a** bacteria and **b** archaea at 97% sequence similarity cutoff value. Abbreviations:
51 Cu, biofilm of copper alloy; Al, biofilm of aluminum alloy; Fe, biofilm of carbon steel;
52 YB, yellow blister of carbon steel; OL, outer layer of rust from carbon steel; ML,
53 middle layer of rust from carbon steel; IL, inner layer of rust from carbon steel; SW,
54 seawater; SM, sea mud.

55 **Fig. S2** Venn diagram of bacteria for all surface and seawater samples (**a**), and for all
56 samples taken from carbon steel (**b**) based OTUs. The values indicate the number of
57 OTUs. The abbreviations of the samples are the same as those used in Fig. S1.

58 **Fig. S3** Venn diagram of archaea for all surface and seawater samples (**a**), and for all
59 samples taken from carbon steel (**b**) based OTUs. The values indicate the number of
60 OTUs. The abbreviations of the samples are the same as those used in Fig. S1.

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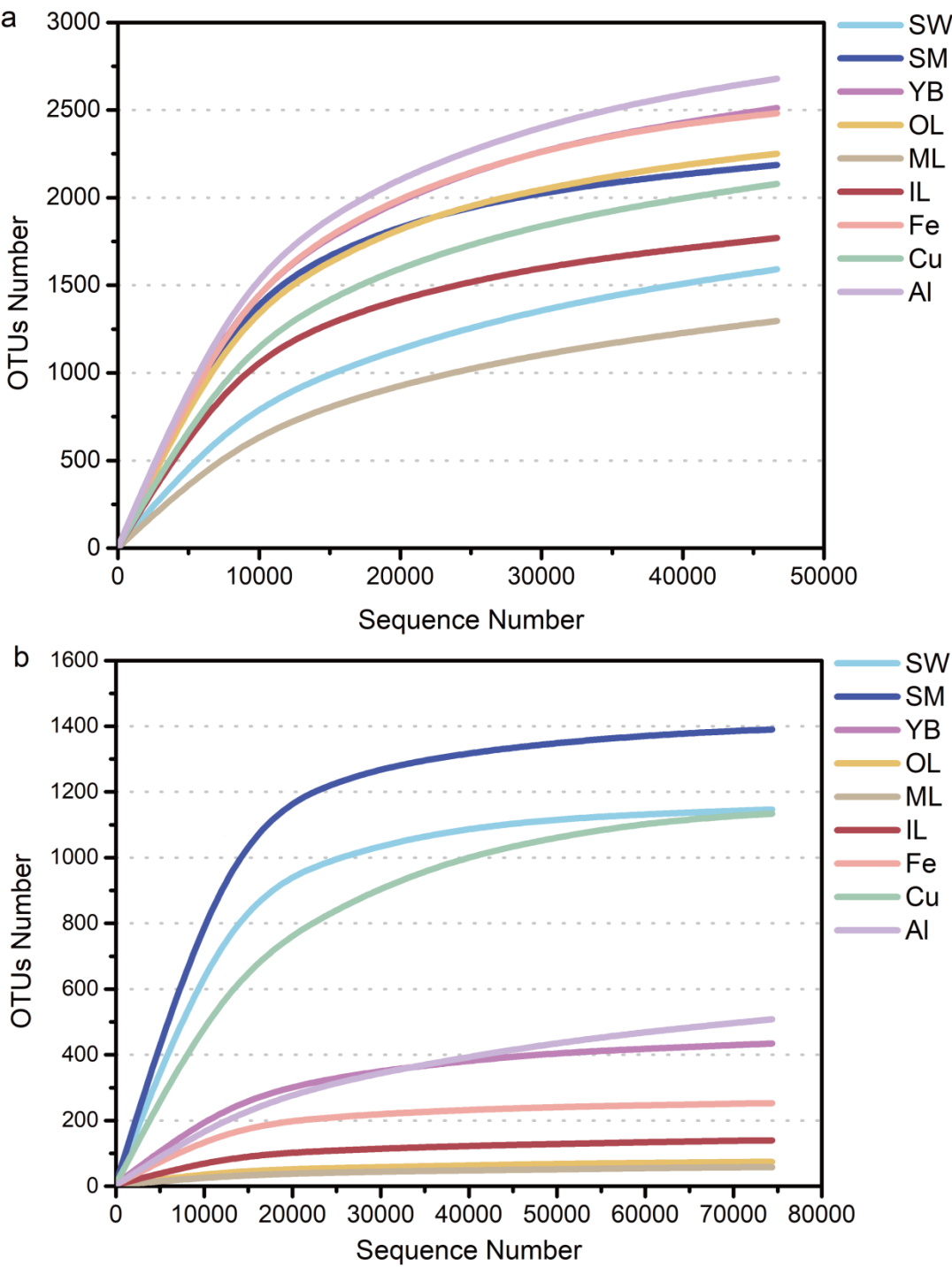


Figure S1

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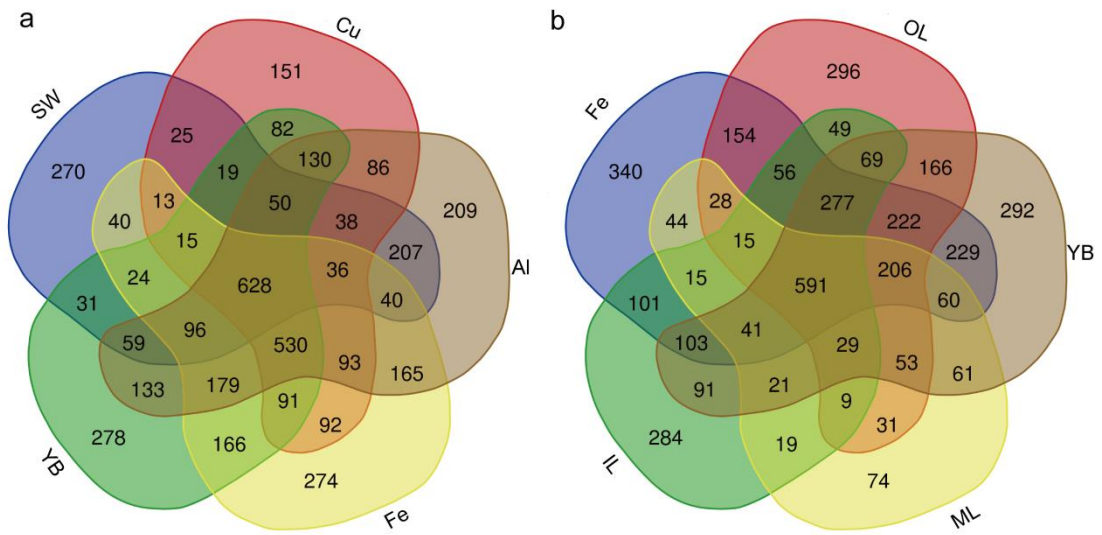


Figure S2

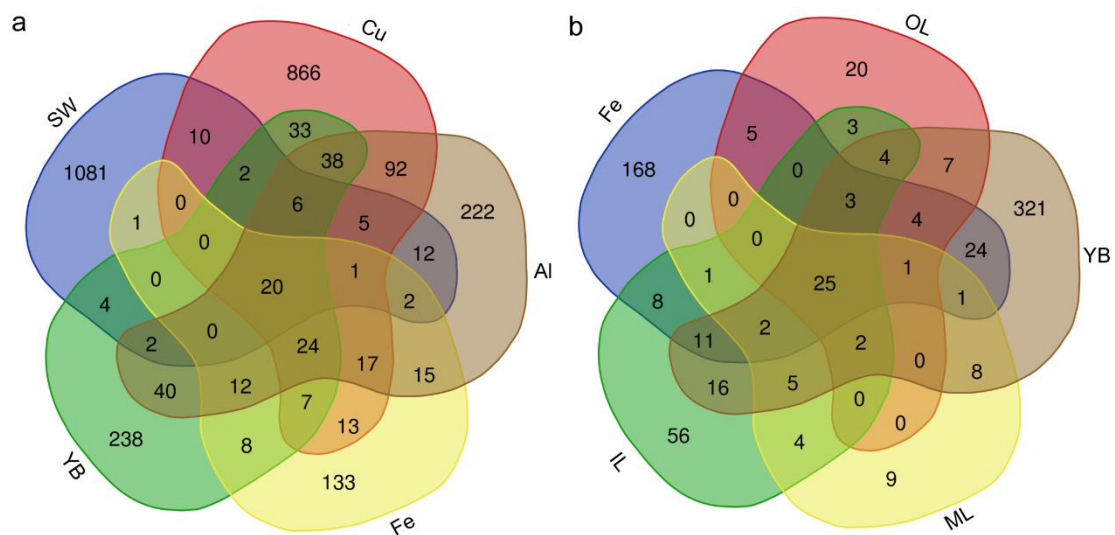


Figure S3