**Virologica Sinica**

**Supplementary Data**

**Isolation and characterization of a novel linear-plasmid phage from the sediment of the Mariana Trench**

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**Supplementary Materials**

**Material and Methods**

**Sample collection and bacterial isolation**

The deep-sea sediment sample was obtained from the Mariana Trench in the western Pacific Ocean (11°11.6988' N, 141°48.7008' E, water depth of 8636 m) during the TS01 hadal trench cruise carried out by the *R/V Tan Suo Yi Hao* in August 2016. Initially, the sample was diluted with artificial seawater and plated on 2216E marine agar (5 g/L tryptone, 1 g/L yeast extract, 0.1 g/L FePO4, 34 g/L NaCl). Subsequently, single colonies were picked, and pure culture was obtained after three rounds of [plate](javascript:;) [streaking](javascript:;). The genomic DNA of the isolated strain was extracted by the QIAamp Genomic DNA Kit (Qiagen, Hilden, Germany) following the manufacturer’s instructions. The 16S rRNA gene was amplified by PCR using the universal primer pair 27F/1492R, and the PCR product was sequenced by Personal Biotechnology (Shanghai, China).

**Prophage induction**

Culture of *Halomonas* sp. MT08-1 was grown in 200 mL 2216E medium at 15°C with a shaking speed of 200 rpm. Growth was detected using turbidity measurements at 600 nm. When reaching the early exponential growth phase, 100 mL of each culture was separated and used as a control. The remaining culture was treated with mitomycin C at a final concentration of 1 μg/mL. Prophage induction was considered to have occurred when a drop in cell density of the induced culture in comparison with the control was detected.

**Quantification of viral-like particles (VLPs)**

The VLPs were quantified as previously described ([Jian et al. 2019](#_ENREF_10)). Briefly, approximately 2 ml of bacterial culture was centrifugated at 10,000 × g for 1 min. After centrifugation, the supernatant was filtered with a 0.02 μm pore-size Anodisc Al2O3 filter (Whatman, Kent, UK), and the filter were stained with 25× SYBR Green I (Invitrogen, Carlsbad, CA, USA) for 15 min in dark. After rinsing with 0.02 μm filter-autoclaved MilliQ H2O, each filter was mounted on a glass slide with 0.1% (v/v) *p*-phenylenediamine dihydrochloride anti-fade mounting medium (Sangon Biotech, Shanghai, China). VLPs on the filter were observed with a fluorescence microscope (Nikon Eclipse 90i, Melville, NY, USA). For each sample, the number of VLPs was counted in at least 10 microscopic fields, with a total number above 200.

**Phage particle purification**

To concentrate and purify phage particles from the induction experiments, the cells were pelletized by centrifugation at 10000 × *g* for 30 min, and the supernatant was mixed with polyethylene glycol (PEG8000) at a final concentration of 10% (wt/vol). After the mixture was incubated at 4°C for 12 h, the phage particles were pelletized by centrifugation at 10000 ×*g* for 10 min, and the pellet was resuspended in SM buffer (100 mmol/L NaCl, 8 mmol/L MgSO4, 0.01% gelatine, 50 mmol/L Tris-HCl, pH 7.5). The concentrated phage particle extract was further purified in 0.75 g/mL CsCl by isopycnic gradient centrifugation (200,000 ×*g*, 20 h, 4°C) (Beckman Coulter, CA, USA).

**Electron microscopy observation**

For transmission electron microscopy (TEM) observation, the purified phage extracts were placed onto a carbon-coated grid (200 mesh) and stained with 0.5% (wt/vol) phosphotungstic acid (PTA). The grid was air dried and examined under a Tecnai G2 Spirit BioTwin microscope (FEI Company, Eindhoven, Netherlands).

**Genome sequencing, assembly and annotation**

The phage DNA was extracted with Mag-Bind Viral DNA kit (Omega Bio-Tek, Norcross, USA) according to manufacturer’s instructions. The complete genomes were sequenced using the Oxford Nanopore GridION platform (Nextomics, Wuhan, China). The coverage depths were calculated, and the raw reads were filtered by nanofilt (https://github.com/wdecoster/nanofilt) ([Coster et al. 2018](#_ENREF_3)) using the following parameters: -q 7 -l 1000. The Flye version 2.6 (https://github.com/fenderglass/Flye) assembler ([Kolmogorov et al. 2019](#_ENREF_12)) was used to assemble these clean reads into a complete genome using the following parameters: –nano-raw. Pilon v1.23 (parameters: default) was used to correct these results until the complete sequence was obtained by splicing (https://github.com/broadinstitute/pilon) ([Walker et al. 2014](#_ENREF_25)). Prodigal v2.6.3 was used to predict coding genes (https://github.com/hyattpd/Prodigal) ([Hyatt et al. 2010](#_ENREF_8)).

**Plaque assays**

The *Halomonas* strains were cultivated in 2216E medium at 15°C to early exponential growth phase. To test the infectivity and host range of HMP1, 10 μL of the 10-fold serially diluted phage lysate (1011 VLPs/mL) was spotted onto a lawn of each *Halomonas* strain in soft-agar overlay plate, and incubated at 15°C for 4–5 days. The *E. coli* K-12 strain MG1655 and its lytic phage vB\_EcoS\_SH2 (NCBI genome accession number [NC\_047828](https://www.genome.jp/dbget-bin/get_linkdb?refseq:NC_047828)) was tested in parallel as the positive control.

**Availability of data**

The complete genome sequence of HMP1 generated from the current study has been deposited in the NODE (The National Omics Data Encyclopedia) database under the Accession number OER181318.

**说明: 绿色的球

描述已自动生成**

**Figure S1.** Quantification of viral-like particles (VLPs) derived from MMC+ (**A**) and MMC- (**B**) treated *Halomonas* sp. MT08-1 cultures by epifluorescence microscopy. For each sample, the number of VLPs was counted in at least 10 microscopic fields. Scale bar = 5 μm.

**说明: 日程表

描述已自动生成**

**Figure S2.** Comparison of HMP1 and ΦHAP-1 genomes by Easyfig ([Sullivan et al. 2011](#_ENREF_23)). The regions sharing homology between adjacent genomes are indicated by shared areas. The bar for percent nucleotide identity is outlined on the right, and the proposed functions of the encoded proteins are indicated in the colour panels at the bottom of the figure.

**说明: 图示

描述已自动生成**

**Figure S3.** The nucleotide sequence of the 36-bp inverted repeat identified in the region between the *parA* and *telN* genes of HMP1. The predicted cut site of the protelomerase is indicated by scissors. The sequences below the repeat are the predicted right and left telomeric ends of HMP1.

说明: 图片包含 文本

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**Figure S4.** (A) Schematic representation of the two conformations of the HMP1 genome. The cut sites of restriction enzymes are indicated by vertical arrows. Predicted fragment sizes are shown below each map. Figures are not drawn to scale. (B-C) Gel electrophoresis of *Halomonas* sp. MT08-1 plasmid DNA (B) and its restriction enzyme digested products (C). The desired fragments are indicated by arrows. M. GeneRulerTM High Range DNA Ladder.

**说明: 图片包含 图示

描述已自动生成**

**Figure S5.** (A) In silico analysis of the restriction enzyme cutting sites in the HMP1 genome. (B) Simulated gel electrophoresis of HMP1 genomic DNA after digestion with different restriction enzymes. The analyses were performed by DNAMAN software (Lynnon Biosoft) and Restriction Analyzer (https://molbiotools.com/restrictionanalyzer.php), respectively.

**说明: 图表, 条形图, 瀑布图

描述已自动生成**

**Figure S6.** Comparison of the average nucleotide identity (ANI) between all isolated linear plasmid phages. The ANI values were calculated by pyani (v0.2.8) ([Pritchard et al. 2019](#_ENREF_17)) and demonstrated as heatmap.

**说明: 图表, 条形图

描述已自动生成**

**Figure S7.** Comparison of the virion size between HMP1 and ΦHAP-1. The data of ΦHAP-1 phage particle is from the previous publication([Mobberley et al. 2008](#_ENREF_15)). The Student’s *t* test was performed to evaluate the difference significance. \*\*\* *P*<0.001; \*\* *P*<0.01.

**说明: 图形用户界面, 文本, 应用程序

描述已自动生成**

**Figure S8.** Genome-based phylogenetic analysis of all isolated linear plasmid phages by VICTOR ([Meier-KolthoffandGӧker 2017](#_ENREF_14)). The recommended VICTOR tree (formula *d6*) is shown and the numbers shown above the branches are Genome-BLAST Distance Phylogeny (GBDP) pseudo-bootstrap support values from 100 replications.

说明: 日程表

描述已自动生成

**Figure S9.** Recruitment analysis of HMP1-like phages in the marine virome. Recruitment plots are computed using metagenomic raw reads from the Pacific Ocean virome (POV) with water depths <1000 m (upper panel) and ≥1000 m (lower panel). The recruitment analyses were performed by BLASTn with an e-value cutoff of ≤10-3. Only reads that hit with ≥50% identity (nucleic acid) and query coverage were considered.

**说明: 一群不同颜色的碗

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**Figure S10.** Plaque assay of HMP1 against 17 marine *Halomonas* strains.Ten microliters each of a tenfold serial dilution (1011–104) of HMP1 phage was spotted ontoa lawn of each *Halomonas* strain.The *E. coli* K-12 strain MG1655 and its lytic phage vB\_EcoS\_SH2 were tested in parallel as the positive control.

**Table S1**. Isolated linear plasmid phages.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage** | **Taxonomy** | **Host** | **Environment** | **Genome size (bp)** | **ORFs** | **GC%** |  | **Accession number** | **Reference** |
| HMP1 | *Myoviridae* | *Halomonas* sp. MT08-1 | Deep-sea sediment | 38,130 | 52 | 59.70 |  | OER181318 | This study |
| ΦHAP-1 | *Myoviridae* | *Halomonas aquamarina* | Marine surface water | 39,245 | 46 | 59.00 |  | NC\_010342 | ([Mobberley et al. 2008](#_ENREF_15)) |
| VP882 | *Myoviridae* | *Vibrio parahaemolyticus* | Marine | 38,197 | 71 | 56.95 |  | NC\_009016 | ([Lan et al. 2009](#_ENREF_13)) |
| PY54 | *Siphoviridae* | *Yersinia enterocolitica* | unknown | 46,339 | 67 | 44.60 |  | NC\_005069 | ([Hertwig et al. 2003](#_ENREF_5)) |
| N15 | *Siphoviridae* | *Escherichia coli* | unknown | 46,363 | 59 | 51.20 |  | NC\_001901 | ([Ravin et al. 2000](#_ENREF_21)) |
| ΦKO2 | *Siphoviridae* | *Klebsiella oxytoca* | Mineral oil water | 51,601 | 64 | 51.90 |  | NC\_005857 | ([Casjens et al. 2004](#_ENREF_2)) |
| ΦARM81ld | *Myoviridae* | *Aeromonas* sp. ARM81 | Waste water | 47,457 | 61 | 58.60 |  | KT898133 | ([Dziewit and Radlinska 2016](#_ENREF_4)) |
| VHML | *Myoviridae* | *Vibrio harveyi* | Larvae of *Panaeus monodon* | 43,198 | 57 | 52.00 |  | NC\_004456 | ([Oakey et al. 2002](#_ENREF_16)) |
| vB\_VpaM\_MAR | *Myoviridae* | *Vibrio parahaemolyticus* | Seawater | 41,351 | 62 | 51.30 |  | JX556417 | ([Villa et al. 2012](#_ENREF_24)) |
| Vp58.5 | *Myoviridae* | *Vibrio parahaemolyticus* | Human | 42,612 | 58 | 50.90 |  | FN297812 | ([Zabala et al. 2009](#_ENREF_27)) |
| xhp1 | *Siphoviridae* | *Actinomyces odontolyticus* | Human oral cavity | 35,031 | 54 | 65.29 |  | MG941013 | ([Shen et al. 2018](#_ENREF_22)) |

**Table S2**. Putative ORFs identified in the HMP1 genome.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **ORFs** | **Strand** | **Start** | **End** | **Length** | **BLASTp against RefSeq Viruses** | | | **eggNOG annotation** | | **Predicted function** |
| **Top BLAST hit** | **Identity** | **E-value** | **Description** | **E-value** |
| 1 | - | 608 | 57 | 551 | hypothetical protein HAPgp46 [Halomonas virus HAP1] | 98.6 | 3.8E-73 | - | - | hypothetical protein |
| 2 | - | 1240 | 605 | 635 | hypothetical protein HAPgp45 [Halomonas virus HAP1] | 100 | 2.2E-117 | Glycosyl hydrolase 108 | 1.5e-115 | Glycosyl hydrolase |
| 3 | - | 1551 | 1237 | 314 | hypothetical protein HAPgp44 [Halomonas virus HAP1] | 100 | 4E-19 | - | - | hypothetical protein |
| 4 | + | 1709 | 2233 | 524 | - | - | - | - | - | hypothetical protein |
| 5 | - | 2400 | 2071 | 329 | - | - | - | - | - | hypothetical protein |
| 6 | - | 3005 | 2397 | 608 | transcription antiterminator [Halomonas virus HAP1] | 98 | 6.2E-117 | Phage antitermination protein Q | 4.1e-115 | transcription antiterminator |
| 7 | - | 3279 | 3043 | 236 | hypothetical protein HAPgp41 [Halomonas virus HAP1] | 81.3 | 7.9E-28 | - | - | hypothetical protein |
| 8 | - | 3619 | 3350 | 269 | hypothetical protein HAPgp40 [Halomonas virus HAP1] | 71.1 | 2.9E-10 | - | - | hypothetical protein |
| 9 | - | 3876 | 3622 | 254 | - | - | - | - | - | hypothetical protein |
| 10 | - | 4490 | 3879 | 611 | prophage antirepressor [Halomonas virus HAP1] | 96 | 2.5E-110 | - | - | prophage antirepressor |
| 11 | + | 4630 | 5274 | -644 | putative repressor protein [Vibrio virus VP882] | 35 | 5.9E-33 | - | - | repressor |
| 12 | + | 5628 | 9611 | 3983 | replication protein RepA [Halomonas virus HAP1] | 97.4 | 0 | hydrolase activity, acting on acid anhydrides | 0.0 | replication protein RepA |
| 13 | + | 9662 | 9949 | 287 | hypothetical protein HAPgp35 [Halomonas virus HAP1] | 97.9 | 1.1E-44 | - | - | hypothetical protein |
| 14 | - | 11487 | 9925 | 1562 | protelomerase [Halomonas virus HAP1] | 95.6 | 3.1E-277 | Pfam:Telomere\_res | 2e-275 | protelomerase |
| 15 | + | 12074 | 12709 | 635 | ParA-like protein [Halomonas virus HAP1] | 99.5 | 3.4E-118 | - | - | ParA-like protein |
| 16 | + | 12702 | 13001 | 299 | hypothetical protein HAPgp32 [Halomonas virus HAP1] | 100 | 7.9E-49 | - | - | hypothetical protein |
| 17 | + | 13078 | 13227 | 149 | - | - | - | - | - | hypothetical protein |
| 18 | + | 13224 | 13490 | 266 | hypothetical protein HAPgp31 [Halomonas virus HAP1] | 96.6 | 1.4E-41 | - | - | hypothetical protein |
| 19 | + | 13608 | 13949 | 341 | tape measure protein [Caulobacter phage CcrSC] | 42.4 | 3.7E-10 | - | - | tape measure protein |
| 20 | + | 13946 | 14158 | 212 | - | - | - | - | - | hypothetical protein |
| 21 | + | 14265 | 14678 | 413 | hypothetical protein HAPgp29 [Halomonas virus HAP1] | 94.9 | 1E-75 | - | - | hypothetical protein |
| 22 | + | 15261 | 15353 | 92 | - | - | - | - | - | hypothetical protein |
| 23 | - | 16151 | 15396 | 755 | DNA adenine methyltransferase [Halomonas virus HAP1] | 98.8 | 5.5E-147 | D12 class N6 adenine-specific DNA methyltransferase | 3.6e-145 | DNA adenine methyltransferase |
| 24 | - | 17317 | 16292 | 1025 | tail protein [Halomonas virus HAP1] | 96.5 | 1E-188 | Phage late control gene D protein (GPD) | 6.7e-187 | tail protein |
| 25 | - | 17526 | 17308 | 218 | hypothetical protein phiCTXp09 [Pseudomonas virus phiCTX] | 44.1 | 0.00000032 | Tail protein | 3.9e-12 | Tail protein |
| 26 | - | 17908 | 17492 | 416 | putative tail tape measure [Halomonas virus HAP1] | 97.8 | 1.2E-71 | Phage P2 GpU | 4.9e-35 | tail tape measure protein |
| 27 | - | 20793 | 17908 | 2885 | putative tail tape measure [Halomonas virus HAP1] | 73.5 | 6.5E-249 | amidase activity | 4.3e-247 | tail tape measure protein |
| 28 | + | 20796 | 21017 | 221 | - | - | - | - | - | hypothetical protein |
| 29 | - | 21544 | 20909 | 635 | hypothetical protein HAPgp22 [Halomonas virus HAP1] | 70.5 | 5.4E-79 | Pfam:Phage\_TAC\_7 | 3.5e-77 | hypothetical protein |
| 30 | - | 22131 | 21625 | 506 | putative tail tube protein [Halomonas virus HAP1] | 71.9 | 1.1E-66 | Phage tail tube protein FII | 7.2e-65 | tail tube protein |
| 31 | - | 23301 | 22135 | 1166 | major tail sheath protein [Halomonas virus HAP1] | 91 | 8.9E-205 | Phage tail sheath protein | 5.8e-203 | major tail sheath protein |
| 32 | - | 23498 | 23301 | 197 | - | - | - | - | - | hypothetical protein |
| 33 | - | 23880 | 23575 | 305 | hypothetical protein HAPgp19 [Halomonas virus HAP1] | 91.1 | 3E-51 | - | - | hypothetical protein |
| 34 | - | 24356 | 23877 | 479 | putative tail fiber assembly protein [Halomonas virus HAP1] | 66 | 3.7E-48 | - | - | tail fiber assembly protein |
| 35 | - | 25199 | 24372 | 827 | hypothetical protein HAPgp17 [Halomonas virus HAP1] | 44.6 | 4.9E-16 | - | - | hypothetical protein |
| 36 | - | 25870 | 25205 | 665 | hypothetical protein VPVV882\_gp24 [Vibrio virus VP882] | 56.7 | 1.3E-59 | - | - | hypothetical protein |
| 37 | - | 26176 | 25874 | 302 | hypothetical protein HAPgp15 [Halomonas virus HAP1] | 60.5 | 1.5E-23 | - | - | hypothetical protein |
| 38 | - | 26531 | 26169 | 362 | hypothetical protein HAPgp14 [Halomonas virus HAP1] | 96.7 | 5.4E-60 | - | - | hypothetical protein |
| 39 | - | 27058 | 26540 | 518 | putative tail protein [Halomonas virus HAP1] | 98.3 | 1.2E-89 | virus tail, fiber | 8.1e-88 | tail fiber protein |
| 40 | - | 27787 | 27062 | 725 | putative tail protein [Halomonas virus HAP1] | 93.1 | 1.4E-99 | Phage tail protein (Tail\_P2\_I) | 9.2e-98 | tail protein |
| 41 | - | 28776 | 27784 | 992 | baseplate assembly protein [Halomonas virus HAP1] | 96.1 | 2.7E-178 | Baseplate J-like protein | 1.8e-176 | baseplate assembly protein |
| 42 | - | 29108 | 28776 | 332 | putative baseplate assembly protein [Halomonas virus HAP1] | 97.2 | 9.7E-56 | - | - | baseplate assembly protein |
| 43 | - | 29728 | 29105 | 623 | putative baseplate assembly protein V [Halomonas virus HAP1] | 88.4 | 6.6E-106 | Phage-related baseplate assembly protein | 4.3e-104 | baseplate assembly protein V |
| 44 | - | 30287 | 29736 | 551 | hypothetical protein HAPgp08 [Halomonas virus HAP1] | 92.3 | 2.6E-98 | - | - | hypothetical protein |
| 45 | - | 30798 | 30268 | 530 | hypothetical protein HAPgp07 [Halomonas virus HAP1] | 96.8 | 2.1E-81 | virus tail | 1.4e-79 | tail protein |
| 46 | - | 31135 | 30776 | 359 | hypothetical protein HAPgp06 [Halomonas virus HAP1] | 97.5 | 3.3E-65 | - | - | hypothetical protein |
| 47 | - | 31350 | 31135 | 215 | - | - | - | - | - | hypothetical protein |
| 48 | - | 33375 | 31417 | 1958 | putative phage-related protein [Vibrio virus VP882] | 58.4 | 2.7E-206 | N-acetylmuramoyl-L-alanine amidase activity | 1.8e-204 | N-acetylmuramoyl-L-alanine amidase |
| 49 | - | 34834 | 33320 | 1514 | putative phage-related protein [Vibrio virus VP882] | 57.5 | 6.2E-158 | virion assembly | 4.1e-156 | virion assembly protein |
| 50 | - | 35361 | 34834 | 527 | hypothetical protein HAPgp03 [Halomonas virus HAP1] | 58.4 | 4.1E-48 | - | - | hypothetical protein |
| 51 | - | 37364 | 35364 | 2000 | putative terminase large subunit [Halomonas virus HAP1] | 95.1 | 0 | Phage terminase large subunit (GpA) | 0.0 | terminase large subunit |
| 52 | - | 37908 | 37333 | 575 | putative terminase small subunit [Halomonas virus HAP1] | 99 | 5.5E-99 | Phage DNA packaging protein Nu1 | 3.6e-97 | terminase small subunit |

**Table S3**. *Halomonas* strains used for the plaque assay of HMP1.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **NCBI accession** | **Geographic origin** | **Isolation environment** | **Depth (m)** | **Reference/Source** |
| ***Halomonas* sp. NH62J** | JABFTQ000000000 | South China Sea | Deep sea sediment | 1,000 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. NH67M** | JABFTR000000000 | South China Sea | Deep sea sediment | 1,000 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. NH67N** | JABFTS000000000 | South China Sea | Deep sea sediment | 1,000 | Wang and Shao, *Front Microbiol*, 2021 |
| ***H. zhangzhouensis* CXT3-11** | JABFTT000000000 | China: Zhangzhou City | Sediments from shrimp culture pond | 5 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. CYD-5** | JABFTU000000000 | China: Taiwan Strait | Coastal water | 5 | Wang and Shao, *Front Microbiol*, 2021 |
| ***H. aerodenitrificans* CYD-9** | JABFTV000000000 | China: Taiwan Strait | Coastal water | 5 | Wang and Shao, *Front Microbiol*, 2021 |
| ***H. sulfidoxydans* CYN-1-2** | CP053381 | China: Taiwan Strait | Surface sediments in coastal sea | 0 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. CYQ2-2-1** | JABFTW000000000 | China: Xiamen City | Sewage from municipal wastewater treatment plant | 2 | Wang and Shao, *Front Microbiol*, 2021 |
| ***H. ethanolica* CYT3-1-1** | JABFTX000000000 | China: Zhangzhou City | Sediments from shrimp culture pond | 5 | Wang and Shao, *Front Microbiol*, 2021 |
| ***H. sulfidivorans* NLG\_F1E** | CP053383 | Pacific Ocean | Deep sea sediment | 1,618 | Wang and Shao, *Front Microbiol*, 2021 |
| ***H. tianxiuensis* BC-M4-5** | CP035042 | Northwest Indian Ocean | Sulfide from Tianxiu hydrothermal vent | 3,440 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. BC-M4-4** | JABFTZ000000000 | Northwest Indian Ocean | Sulfide from Tianxiu hydrothermal vent | 3,440 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. 1A13316** | CP053382 | Pacific Ocean | Deep sea sediment | 1,618 | Wang and Shao, *Front Microbiol*, 2021 |
| ***Halomonas* sp. MT08-1** | ND | Pacific Ocean | Hadal sediment | 8,636 | Lab stock |
| ***Halomonas* sp. MT11-5** | ND | Pacific Ocean | Hadal sediment | 11,094 | Lab stock |
| ***Halomonas* sp. ARCS81** | ND | Pacific Ocean | Hadal sediment | 6,300 | Lab stock |
| ***Halomonas* sp. D1** | ND | Pacific Ocean | Hadal sediment | 8,636 | Lab stock |

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