

UNIVERSIDAD AUTÓNOMA DE BAJA CALIFORNIA
FACULTAD DE CIENCIAS MARINAS
INSTITUTO DE INVESTIGACIONES OCEANOLÓGICAS



ESTUDIO DE LA DIVERSIDAD DE BACTERIAS TERMÓFILAS
EN ZONAS HIDROTERMALES DE LA CUENCA PESCADERO
EN EL GOLFO DE CALIFORNIA

T E S I S

QUE PARA CUBRIR PARCIALMENTE LOS REQUISITOS NECESARIOS PARA
OBTENER EL GRADO DE

DOCTOR EN CIENCIAS EN OCEANOGRAFÍA COSTERA

PRESENTA

MANET ESTEFANÍA PEÑA SALINAS

ENSENADA, BAJA CALIFORNIA, MÉXICO. JULIO 2024.

**FACULTAD DE CIENCIAS MARINAS
INSTITUTO DE INVESTIGACIONES OCEANOLÓGICAS
POSGRADO EN OCEANOGRAFÍA COSTERA**

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EN ZONAS HIDROTERMALES DE LA CUENCA PESCADERO EN
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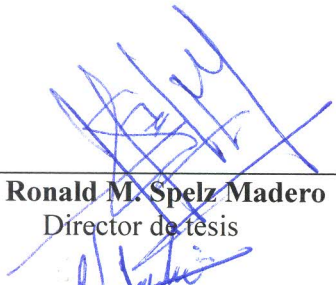
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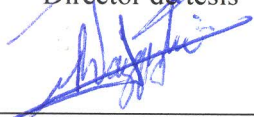
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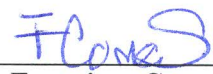
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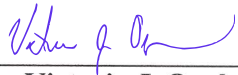
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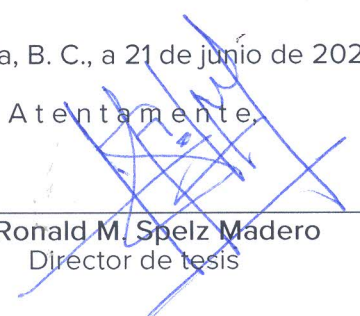
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HIDROTERMALES DE LA CUENCA PESCADERO EN EL GOLFO DE CALIFORNIA

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El trabajo exhibe una sólida base teórica, una metodología rigurosa y una presentación coherente de los hallazgos. Las referencias bibliográficas están actualizadas y pertinentes, y las figuras y tablas son claras y respaldan eficazmente los argumentos del texto. La sección de conclusiones proporciona un resumen sólido de los resultados y sus implicaciones, las referencias y citas están actualizadas y son pertinentes.

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Atentamente,



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Director de tesis

c.c.p. Expediente

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Dr. Francisco Correa Sandoval
Sinodal

c.c.p. Expediente

RESUMEN GENERAL

Desde el descubrimiento de las ventilas hidrotermales en los años 70, los esfuerzos por estudiar estos ecosistemas extremos han aumentado. La exploración del Golfo de California ha llevado al descubrimiento de campos de ventilas hidrotermales al sur de la Cuenca Pescadero. En octubre de 2018, se llevó a cabo la expedición oceanográfica FK181031 a bordo del buque de investigación *Falkor* a la Cuenca Pescadero para investigar los campos de ventilas hidrotermales de *Auka* y *JaichMaa 'ja 'ag*, recientemente descubiertos a 3,670 m de profundidad, los sistemas de ventilas hidrotermales más profundos conocidos en el Océano Pacífico. La exploración de estos campos hidrotermales se realizó mediante el vehículo sumergible *Subastian*, con el cual se recolectaron un total de 33 núcleos de sedimentos. Posteriormente, se tomaron submuestras de diferentes profundidades del núcleo de sedimento para realizar estudios geoquímicos, extracción de ADN, amplificación del gen 16S rRNA, secuenciación y análisis bioinformático. El objetivo de este trabajo es investigar las comunidades de bacterias termófilas que habitan en los sedimentos asociados a las ventilas hidrotermales de la Cuenca Pescadero. Además, en el campo de la astrobiología, las ventilas hidrotermales han sido propuestas como sitios análogos para estudiar ambientes potencialmente habitables fuera de la Tierra. Por lo tanto, en este trabajo también se exploran las perspectivas astrobiológicas de las ventilas hidrotermales del Golfo de California como base para el desarrollo de un modelo de habitabilidad de Europa, luna de Júpiter.

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CAPÍTULO 1

Introducción General

1.1 Antecedentes

La exploración del fondo marino ha revelado la gran diversidad de seres vivos que existen en nuestro planeta. Entre los ecosistemas de mayor interés para la investigación de organismos capaces de sobrevivir en condiciones fisicoquímicas extremas, conocidos como extremófilos, se encuentran las ventilas hidrotermales. Desde su descubrimiento en la década de los 70 ([Ballard, 1977](#)), los esfuerzos para estudiar estos ecosistemas profundos y extremos han ido en aumento.

Las ventilas hidrotermales son fisuras en el fondo oceánico a través de las cuales se expulsan fluidos calentados geotérmicamente y enriquecidos con los minerales de las rocas circundantes. La formación de la estructura geológica de la ventila hidrotermal ocurre debido a la precipitación de los minerales cuando los fluidos entran en contacto con el agua de mar ([Soto & Estradas, 2013](#)). Numerosos estudios sobre ecosistemas de ventilas hidrotermales han destacado la relevancia de los microbios como mediadores de los ciclos biogeoquímicos en el fondo marino ([Dick et al., 2013](#); [Holden et al., 2012](#); [Orcutt et al., 2011](#); [Zeng et al., 2021](#)). Sin embargo, aún queda mucho por investigar con respecto a la composición y estructura de estas comunidades microbianas, particularmente en términos de los factores espaciales, físicos y biogeoquímicos que influyen en su diversidad ([Meier et al., 2017](#); [Reysenbach et al., 2020](#); [Sogin et al., 2006](#); [Speth et al., 2022](#)).

El Golfo de California, un estrecho mar marginal formado como resultado de la separación continental de la península de Baja California del territorio continental de México hace aproximadamente 12.3 millones de años ([Stock y Hodges, 1989](#); [Atwater y Stock, 1998](#); [Fletcher et al., 2007](#)), destaca como un entorno distintivo para la investigación y exploración en curso. Este interés se ve impulsado por el creciente número de sistemas hidrotermales profundos que albergan diversos conjuntos de comunidades faunísticas y microbianas ([Goffredi et al., 2017](#); [Michel et al., 2018](#); [Soule et al., 2018](#); [Salcedo et al., 2019](#); [Speth et al., 2021](#)). La estructura, la geomorfología

del fondo marino y la evolución del sistema de rift del Golfo de California han sido objeto de investigación durante más de 40 años (por ejemplo, [Lonsdale et al., 1980](#); [Lonsdale, 1989](#); [González-Fernández et al., 2005](#); [Lizarralde et al., 2007](#); [Fletcher et al., 2007](#); [Sutherland et al., 2012](#); [Ferrari et al., 2013](#); [van Wijk et al., 2017](#); [Umhoefer et al., 2018](#); [Ramírez-Zerpa et al., 2022](#)). La exploración de fallas de transformes y centros de dispersión del piso oceánico, cruciales para acomodar la deformación tectónica entre la placa del Pacífico y la placa de América del Norte a lo largo del eje del Golfo, ha revelado continuamente nuevos campos de ventilas hidrotermales ([Prol-Ledesma et al., 2013](#); [Prol-Ledesma et al., 2016](#); [Neumann et al., 2017](#); [Negrete-Aranda et al., 2021](#); [Peña-Domínguez et al., 2022](#); [Neumann et al., 2023](#)). Entre estos descubrimientos se encuentran los nuevos sitios de ventilas identificados en la cordillera de Alarcón y las fallas transformes adyacentes de Pescadero y Tamayo, así como la Cuenca del Sur de Pescadero en el Complejo de la Cuenca de Pescadero ([Clague et al., 2018](#); [Paduan et al., 2018](#)).

En 2015, en la Cuenca Pescadero, se descubrió el campo de ventilas hidrotermales de *Auka* a 3670 m debajo del nivel del mar. Este campo es el más profundo conocido hasta la fecha en el Pacífico oriental ([Goffredi et al., 2017](#); [Paduan et al., 2018](#)). Las ventilas hidrotermales, cubiertas por sedimentos, consisten en calcita y anhidrita, con temperaturas máximas registradas del fluido cercanas a los $\sim 300^{\circ}\text{C}$ ([Goffredi et al., 2017](#)). La diversidad microbiana que habita en los sedimentos de *Auka* ha sido recientemente estudiada ([Espinosa-Asuar et al., 2020](#); [Speth et al., 2022](#); [Wu et al., 2022](#)) y se reportó que aproximadamente el 20% de estas especies se comparten con la Cuenca de Guaymas ([Speth et al., 2022](#)). Además, se han desarrollado investigaciones sobre las condiciones térmicas al sur de la Cuenca Pescadero ([Negrete-Aranda et al., 2021](#)).

En 2018 se descubrió un nuevo campo de ventilas hidrotermales al sur de Cuenca Pescadero durante la expedición FK181031 a bordo del R/V Falkor. Situado a sólo ~ 2 km al sureste de *Auka*, *JaichMaa 'ja 'ag* comparte similitudes en términos del tamaño y la estructura de los montículos hidrotermales, la temperatura de los respiraderos hidrotermales y las comunidades

faunísticas ([Schmidt Ocean Institute, 2018](#)). El estudio de estos nuevos sitios de ventilas y la comparación con aquellos previamente encontrados en la cuenca vecina de Guaymas y la Elevación del Pacífico Este al norte y al sur, respectivamente, no solo profundiza nuestra comprensión de los intrincados procesos geológicos, sino que también proporciona conocimientos cruciales sobre la interacción dinámica entre la tectónica y los ecosistemas marinos profundos en el Golfo de California.

El estudio de las ventilas hidrotermales ofrece la oportunidad de establecer un vínculo entre la oceanografía y la astrobiología. La astrobiología investiga el origen, distribución, evolución y futuro de la vida en el universo ([Des Marais et al. 2008](#)). Examina las condiciones ambientales que facilitan el origen de la vida en la Tierra, comprende los mecanismos de la evolución, determina los límites ambientales para la vida, busca entornos habitables dentro del Sistema Solar y trata de identificar bioseñales en otros planetas ([Chyba & Hand, 2005](#)).

Los sistemas de ventilas hidrotermales en el fondo del océano terrestre están íntimamente relacionados con la formación y evolución planetaria y el origen de la vida en la Tierra ([Martin et al., 2008](#)). Son ejemplos destacados de sitios análogos a otros ambientes planetarios, las condiciones extremas de alta presión, temperatura y composición química en estas ventilas proporcionan un modelo para comprender cómo podría sostenerse la vida en entornos similares en otros lugares del Sistema Solar ([McCollom, 1999](#)). Uno de los mundos oceánicos de interés es Europa, la luna del planeta Júpiter, la cual se caracteriza por su corteza de hielo, un océano subsuperficial y la posible existencia de actividad hidrotermal en el fondo marino ([Hand et al., 2007](#); [Kargel et al., 2000](#)).

Al estudiar cómo la vida puede persistir en estos ecosistemas extremos, podemos obtener información crucial sobre los procesos fundamentales que rigen la supervivencia y adaptación de los organismos, los límites de la vida y la posibilidad de encontrar mundos habitables más allá de la Tierra.

1.2 Objetivos

1.2.1 *Objetivo General*

Evaluar la diversidad taxonómica basada en el gen 16S rRNA y determinar la estructura poblacional de las bacterias termófilas que habitan en los sedimentos del campo de ventilas hidrotermales de *JaichMaa 'ja 'ag* recientemente descubierto en la Cuenca Pescadero del Golfo de California.

1.2.2 *Objetivos Específicos*

- Realizar la descripción del nuevo campo de ventilas hidrotermales de *JaichMaa 'ja 'ag* en la Cuenca Pescadero del Golfo de California, que incluya las características físicas y geoquímicas más relevantes como la composición de los sedimentos, la temperatura del fluido hidrotermal y la biota relacionada.
- Determinar la diversidad taxonómica basada en el gen 16S rRNA de las comunidades microbianas presentes en los sedimentos del nuevo campo de ventilas hidrotermales de *JaichMaa 'ja 'ag* en la Cuenca Pescadero del Golfo de California.
- Evaluar la similitud entre los campos de ventilas hidrotermales de *Auka* y *JaichMaa 'ja 'ag* en la Cuenca Pescadero con respecto a las características fisicoquímicas y a la composición de las comunidades microbianas extremófilas.
- Analizar la densidad, frecuencia relativa y patrones de distribución del phylum de bacterias termófilas Thermotogota asociado a los sedimentos y fluidos hidrotermales de los campos hidrotermales de *Auka* y *JaichMaa 'ja 'ag* en la Cuenca Pescadero.
- Proponer un modelo de estudio sobre la habitabilidad de Europa, satélite de Júpiter, basado en las características de los campos de ventilas hidrotermales de las Cuencas de Guaymas y Pescadero en el Golfo de California.

1.3 Hipótesis

En los ecosistemas de ventilas hidrotermales profundas en la Cuenca de Guaymas y Cuenca Pescadero del Golfo de California, encontraremos una diversidad de comunidades microbianas adaptadas a condiciones ambientales extremas de presión, anoxia, pH, temperatura, luz y disponibilidad de nutrientes. El estudio de la estructura y composición de estas comunidades de bacterias y arqueas termófilas nos proporcionará información valiosa sobre la diversidad microbiana y su metabolismo para sobrevivir en estos ambientes extremos. Además, nos ayudará a conocer más sobre los límites de la vida en la Tierra y nos permitirá proponer un modelo de estudio sobre la habitabilidad de Europa, la luna congelada de Júpiter, para la posible existencia de vida más allá de nuestro planeta.

1.4 Justificación

La exploración del fondo marino del Golfo de California ha llevado al descubrimiento de los campos de ventilas hidrotermales de *Auka* y *JaichMaa 'ja 'ag* al sur de la Cuenca Pescadero. Sin embargo, las interacciones entre los procesos geológicos, fisicoquímicos y biológicos en las zonas hidrotermales todavía no son comprendidos por completo.

Esta investigación proporciona información valiosa sobre las características fisicoquímicas, geológicas y microbiológicas de los campos de ventilas hidrotermales en la Cuenca Pescadero; en particular, sobre la ecología de las bacterias termófilas que habitan en los sedimentos de *Auka* y *JaichMaa 'ja 'ag*.

El estudio de estos ecosistemas extremos es fundamental para una mejor comprensión de la biósfera del mar profundo y para explorar los límites de la vida en la Tierra. Además, ofrece perspectivas importantes en la astrobiología para investigar la habitabilidad de otros cuerpos celestes, como las lunas heladas del Sistema Solar.

1.5 Estructura de la Tesis

Capítulo 1: Este capítulo introduce el tema de investigación y proporciona los antecedentes necesarios para entender el contexto del estudio. Se presentan los objetivos, la hipótesis y la justificación del trabajo, se destaca la importancia de la exploración y estudio de los ecosistemas hidrotermales en el Golfo de California.

Capítulo 2: Aquí se describe detalladamente el nuevo campo de ventilas hidrotermales de *JaichMaa 'ja 'ag* en la Cuenca Pescadero, Golfo de California. Se analizan las características físicas y geoquímicas del campo, así como la estructura y composición de las comunidades microbianas, con un enfoque en las bacterias y arqueas termófilas presentes en los sedimentos y fluidos hidrotermales de los campos de ventilas hidrotermales de *Auka* y *JaichMaa 'ja 'ag*.

Capítulo 3: Este capítulo se describen las perspectivas de la Astrobiología con respecto a cómo el estudio de los sistemas de ventilas hidrotermales puede aportar información para determinar la habitabilidad de Europa, luna del planeta Júpiter.

Capítulo 4: En el capítulo final, se resumen los hallazgos principales de la investigación, con el fin de avanzar en el conocimiento de los ecosistemas hidrotermales y su relación con la astrobiología.

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CAPÍTULO 2

**Thermotogota diversity and distribution patterns revealed in
Auka and *JaichMaa* 'ja 'ag hydrothermal vent fields in the
Pescadero Basin, Gulf of California**

2.1 Abstract

Discovering new deep hydrothermal vent systems is one of the biggest challenges in ocean exploration. They are a unique window to elucidate the physical, geochemical, and biological processes that occur on the seafloor and are involved in the evolution of life on Earth. In this study, we present a molecular analysis of the microbial composition within the newly discovered hydrothermal vent field, *JaichMaa* 'ja 'ag, situated in the Southern Pescadero Basin within the Gulf of California. During the cruise expedition FK181031 in 2018, 33 sediment cores were collected from various sites within the Pescadero vent fields and processed for 16S rRNA amplicon sequence variants (ASVs) and geochemical analysis. Correlative analysis of the chemical composition of hydrothermal pore fluids and microbial abundances identified several sediment-associated phyla, including Thermotogota, that appear to be enriched in sediment horizons impacted by hydrothermal fluid flow. Comparative analysis of Thermotogota with the previously explored *Auka* hydrothermal vent field situated 2 km away displayed broad similarity between the two locations, although at finer scales (e.g., ASV level), there were notable differences that point to core-to-core and site-level factors revealing distinct patterns of distribution and abundance within these two sediment-hosted hydrothermal vent fields. These patterns are intricately linked to the specific physical and geochemical conditions defining each vent, illuminating the complexity of this unique deep ocean chemosynthetic ecosystem.

2.2 Introduction

The discovery of hydrothermal vents in the deep ocean is fundamental to understanding our planet and its extreme ecosystems. As microbes dominate the deep-sea biosphere, exploring the environmental factors influencing microbial diversity is essential for gaining insights into their distribution in terms of biogeographic patterns.

Nevertheless, there is still much to unravel concerning the composition and structure of these microbial communities and the biogeochemical factors influencing their high diversity (Meier et al., 2017; Reysenbach et al., 2020; Sogin et al., 2006; Speth et al., 2022).

2.2.1 *The Gulf of California*

The Gulf of California (GoC) stands as a distinctive environment for ongoing research. The exploration of transform faults and spreading centers has continuously revealed new hydrothermal vent fields (Goffredi et al., 2017, 2021; Michel et al., 2018; Negrete-Aranda et al., 2021; Neumann et al., 2017, 2023; Paduan et al., 2018; Peña-Domínguez et al., 2022; Prol-Ledesma et al., 2013, 2016; Soule et al., 2018). Noteworthy among these discoveries are the newly identified vent sites at the Alarcon Rise and the adjacent Pescadero and Tamayo transform faults, and the South Pescadero Basin in the Pescadero Basin Complex (inset Fig. 1; Clague et al., 2018; Paduan et al., 2018). Since their discovery, the study of these new vent sites not only deepens our understanding of the intricate geological processes but also provides crucial insights into the dynamic interplay between tectonics and deep marine ecosystems in the GoC.

2.2.2 *The South Pescadero Basin and the newly discovered hydrothermal vent sites*

The South Pescadero Basin is the smallest of three tectonic basins that collectively form the Pescadero Basin Complex (Bischoff & Niemitz, 1980; Ramírez-Zerpa et al., 2022). The *Auka*

hydrothermal vent field was discovered in 2015 at a depth of 3,670 m. This vent field stands as the deepest hydrothermal vent system known to date in the eastern Pacific (Fig. 1; Paduan et al., 2018). The sediment-hosted chimneys in *Auka* consist of calcite and anhydrite, with recorded maximum fluid temperatures nearing ~300 °C (Goffredi et al., 2017). Various studies have been conducted to gain a comprehensive understanding of its geological, geophysical, and biological context (Goffredi et al., 2017; Negrete-Aranda et al., 2021; Paduan et al., 2018; Ramírez-Zerpa et al., 2022; Salcedo et al., 2019).

Despite these efforts, the microbial diversity of the microorganisms inhabiting the sediments surrounding the hydrothermal vents in *Auka* has been relatively understudied until recent years (Espinosa-Asuar et al., 2020; Speth et al., 2022; Wu et al., 2022). Phylogenetic studies have unveiled highly diverse microbial communities in *Auka*, exhibiting a variety of metabolisms enabling them to thrive in extreme conditions. Interestingly, approximately 20% of these species overlap with those found in the nearby Guaymas Basin (Speth et al., 2022).

Notably, a novel hydrothermal vent field was recently discovered in 2018 in the South Pescadero Basin. The new vent field, named *JaichMaa 'ja 'ag*, was confirmed and sampled using the Remote Operated Vehicle (ROV) *Subastian* during expedition FK181031 aboard the *R/V Falkor* in the Gulf of California (Fig. 1; Schmidt Ocean Institute, 2018). Situated only ~2 km southeast from *Auka*, *JaichMaa 'ja 'ag* shares similarities with *Auka* in terms of the size and structure of the hydrothermal mounds, the temperature and composition of the hydrothermal vent fluids, and the dominant faunal communities. Baker and colleagues (2016) previously estimated the average distance between hydrothermal discharges (plumes or vents) along spreading ridges, typically ranging from 3 to 20 kilometers. In this context, *JaichMaa 'ja 'ag* offers a valuable opportunity to assess the dispersion and spatial patterns of microbial communities between two closely located hydrothermal vent fields within the South Pescadero Basin.

Expanding on prior research concerning thermal conditions in the South Pescadero Basin (e.g., [Negrete-Aranda et al., 2021](#)) and predicted optimal growth temperatures (OGT) of *Auka* microbes ([Speth et al., 2022](#)), we conducted a detailed investigation to elucidate the impact of temperature on the composition and distribution of microbial communities within the recently discovered *JaichMaa 'ja 'ag* hydrothermal field.

In this study, we present the first microbial ecology analysis of the *JaichMaa 'ja 'ag* vent field, including a comparative assessment with *Auka* in terms of microbial diversity and distribution patterns in the south Pescadero Basin, utilizing 16S rRNA analysis. Additionally, we explored thermophilic microbial groups related to hydrothermal diffuse fluids within sediments, focusing on the generally thermophilic phylum Thermotogota. These findings offer valuable insights into our understanding of hydrothermal vent systems and the influence of biogeochemical drivers, such as vent fluid availability, on the formation of sediment microbial communities.

2.3 Materials & Methods

2.3.1 High-resolution bathymetry data

Bathymetry data at 40-m and 1-m resolution, respectively, were collected and processed during the cruise expedition FK181031 in November 2018 ([Fig. 1 and 2](#)) using the R/V *Falkor's* 30 kHz hull-mounted Kongsberg EM302 multibeam sonar, and MBARI's D. Allan B. Autonomous Underwater Vehicle (AUV) equipped with a Reson 400 kHz 7125 multibeam sonar, an Edgetech 110-kHz chirp sidescan (e.g., [Caress et al., 2019](#); [Caress et al., 2022](#)). Raw and processed bathymetry data collected are archived and openly accessible at the Marine Geoscience Data System, MGDS (<https://www.marine-geo.org/>).

2.3.2 Sampling

Using the ROV *SuBastian* aboard *R/V Falkor*, a total of ten 30 cm long sediment push cores were collected across the *JaichMaa 'ja 'ag* vent field during dives S0195, S0197, and S0199 ([Supplementary Data S1](#)). The sediments analyzed were specifically taken from areas covered with microbial mats and exhibiting visible hydrothermal fluid flow ([Fig. 2](#)). Pore water geochemistry was obtained from the same core used for DNA extraction where possible except for 11 cores, which were only sampled for DNA, lacking geochemical data. Subsequent to core collection, temperature-depth profiles were measured whenever possible in proximity to the coring sites. Temperature measurements were recorded for each site at depths ranging from 15 to 30 centimeters below the seabed (cmbsf). Post-recovery, all sediment cores were extruded and sectioned into 1–3 cm horizons onboard the ship for pore water geochemical analysis following [Speth et al., 2022](#). Furthermore, 2 mL of sediment from each horizon were subsampled with a sterile cutoff 1 cc syringe and immediately frozen at -80°C for subsequent DNA analysis.

Sample collection permits were granted by la Dirección General de Ordenamiento Pesquero y Acuícola, Comisión Nacional de Acuacultura y Pesca (CONAPESCA: Permiso de Pesca de Fomento No. PPFE/DGOPA-200/18) and la Dirección General de Geografía y Medio Ambiente, Instituto Nacional de Estadística y Geografía (INEGI: Autorización EG0122018), with the associated Diplomatic Note number 18-2083 (CTC/07345/18) from la Secretaría de Relaciones Exteriores - Agencia Mexicana de Cooperación Internacional para el Desarrollo / Dirección General de Cooperación Técnica y Científica.

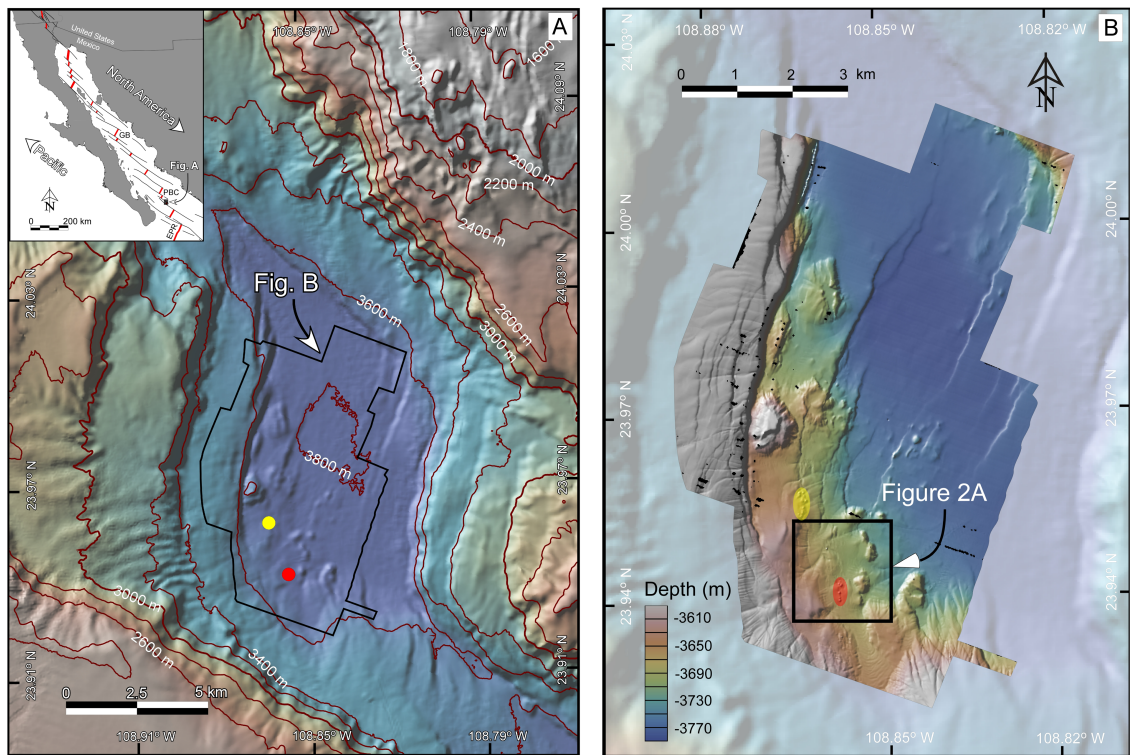


Figure 1. Bathymetric map at 40-m resolution of the South Pescadero Basin indicating the location of the newly discovered hydrothermal vent fields. **A)** *Auka* and *JaichMaa 'ja 'ag*, marked by yellow and red dots, respectively. The Inset provides an overview of the study area within the regional tectonic context of the Gulf of California, a narrow continental-margin rift system formed between the Pacific and North American plates. The Gulf of California is characterized by a series of narrow pull-apart basins (thick red lines) interconnected by transform faults (thin black lines). South Pescadero Basin is the deepest and southernmost basin among a set of three closely spaced basins collectively referred to as the Pescadero Basin Complex (PBC). The PBC is flanked by other hydrothermal vent fields in the Guaymas Basin (GB), the Alarcon Rise (AR), and the East Pacific Rise (EPR). **B)** AUV multibeam bathymetry with a lateral resolution of 1-m overlaid on shaded 40-m resolution ship-surveyed bathymetry. The black box delineates the *JaichMaa 'ja 'ag* hydrothermal vent field and its surrounding area. Data source credit: Schmidt Ocean Institute.

2.3.3 *Geochemical analysis*

Pore water was extracted from sediments using a pneumatic sediment squeezer (KC Denmark A/S, Silkeborg, Denmark) under an argon gas headspace following [Green-Saxena et al., 2014](#). Approximately 15 mL of pore water was extracted for 1 cm horizons, and ~50 mL for 3 cm horizons. The extracted pore water was filtered through a 0.22 μm pore size filter. A volume of 0.25 mL was preserved in a 0.5M zinc acetate solution for sulfide analysis and stored at room temperature and 0.25 mL was stored at -20°C for ion chromatography. Ion chromatography (IC) was performed at the Environmental Analysis Center, Caltech, using a Dionex ICS-2000 system (Dionex, Sunnyvale, CA, USA) equipped with parallel anion and cation columns. Samples, diluted at a ratio of 1:50 in 18M Ω deionized water, were introduced via an autosampler and passed through an LC-Pak polisher (MilliporeSigma, Burlington, MA, USA) in series. Subsequently, the samples were loaded onto a 10 μL sample loop for both the anions and cations channels. The columns and detectors were maintained at 30°C. For ion separation, a 2 mm Dionex IonPac AS19 analytical column protected by a 2 mm Dionex IonPac AG19 guard column (ThermoFisher, Waltham, MA, USA) was employed. A potassium hydroxide eluent generator cartridge was employed to generate a hydroxide gradient, which was pumped at 0.25 mL min⁻¹. The gradient remained constant at 10 mM for 5 minutes, increased linearly to 48.5 mM at 27 minutes, and then further increased to 50 mM at 40 minutes. Suppressed conductivity was detected using a Dionex AERS 500 suppressor operated in recycle mode with an applied current of 30 mA. For cation analysis, a 4 mm Dionex IonPac CS16 analytical column paired with a 4 mm Dionex IonPac CG16 guard column was utilized. An eluent generator cartridge, using methane-sulfonic acid, produced a gradient delivered at a flow rate of 0.36 mL min⁻¹. The gradient was held constant at 10 mM for 5 minutes, then non-linearly increased to 20 mM at 20 minutes (Chromleon curve 7, concave up), and further increased non-linearly to 40 mM at 40 minutes (Chromleon curve 1, concave down). A Dionex

CERS 2 mm suppressor with an applied current of 32 mA was used for suppressed conductivity detection. Chromatographic peaks integration was performed using Chromeleon 7.2 software with the Cobra algorithm. Concentrations were determined with correlation to known standards. The detection thresholds were approximately 10 μM for bromide and thiosulfate, 50 μM for ammonium, and 100 μM for calcium, potassium, and sulfate. Magnesium had a detection threshold of 400 μM . The IC data produced pore water concentrations for fluoride, acetate, formate, chloride, bromide, nitrate, sulfate, thiosulfate, lithium, sodium, ammonium, potassium, magnesium, and calcium ([Supplementary Data S1](#)). We focused on the magnesium and ammonium findings as correlates of hydrothermal fluid concentration ([Edmond & Damm, 1983](#)).

Sulfide measurements, following the Cline reaction assay ([Cline, 1969](#)), included sample dilution, Cline reagent addition, and a 1-hour reaction at room temperature in 96-well plates. Measurements, compared to a replicated 12-point standard sulfide curve, were conducted using a Tecan Sunrise 4.2 plate reader. For additional procedural details, please refer to [Speth et al., 2022](#).

2.3.4 DNA extraction, 16S rRNA sequencing, and bioinformatics

For the isolation of microbial genomic DNA, a Qiagen Dneasy PowerSoil kit (Valencia, CA, USA) was employed to extract DNA from 80 subsamples taken from the 10 sediment cores, along with samples from microbial mats collected in the *JaichMaa* 'ja 'ag hydrothermal vent field. The DNA purification process followed the manufacturer's protocol for 0.25 g of sediment, incorporating a series of six cleaning solutions; except that the lysis of cells was performed utilizing MP Biomedicals FastPrep-24 (Irvine, CA, USA). For the PCR amplification, the targeted region was the V4-V5 segment of the 16S rRNA gene, utilizing the 515f/926r primer set ([Walters et al., 2016](#)) modified with Illumina (San Diego, CA, USA) adapters on the 5' end (515F 5'-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG-GTGYCAGCMGCCGCGGTAA-3' and 926R 5'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-

CCGYCAATTYMTTTRAGTTT-3'). PCR reactions were performed in duplicate for every sample using Q5 Hot Start High-Fidelity 2x Master Mix (New England Biolabs, Ipswich, MA, USA). The reactions were conducted in a 15 µL volume with annealing at 54°C for 28 cycles. In cases where no product was obtained, the number of cycles was increased as indicated in the sample metadata ([Supplementary Data S1](#)). Subsequently, the PCR duplicates were pooled and barcoded using Illumina Nextera XT index 2 primers, which included unique 8-bp barcodes (P5 5'-AATGATACGGCGACCACCGAGATCTACAC-XXXXXXXXX-TCGTCGGCAGCGTC-3' and P7 5'-CAAGCAGAAGACGGCATACGAGAT-XXXXXXXXX-GTCTCGTGGGCTCGG-3').

Barcoded primers were employed for amplification using the Q5 Hot Start PCR mixture. The total reaction volume was 25 µL with 2.5 µL of product. Annealing occurred at 66°C and the process was cycled 10 times. Purification of the products was performed using the Millipore-Sigma (St. Louis, MO, USA) MultiScreen Plate MSNU03010 with a vacuum manifold. Quantification was carried out with the ThermoFisher Scientific (Waltham, MA, USA) QuantIT PicoGreen dsDNA Assay Kit P11496 on the BioRad CFX96 Touch Real-Time PCR Detection System. Equimolar quantities of barcoded samples were combined and purified using the Qiagen PCR Purification Kit 28104 with the addition of 15-20% PhiX. Samples were sequenced on a MiSeq (Illumina San Diego, CA, USA) with a 2x300bp chemistry protocol (Laragen Inc., Culver City, CA, USA). All raw data are available at NCBI BioProject PRJNA1045058, accession numbers SAMN38428873 through SAMN38428956.

Microbial community identifications from *Auka* samples were previously published by Speth et al. (2022) and publicly available at NCBI BioProject PRJNA713414; these were combined with the newly obtained *JaichMaa* 'ja' 'ag' data for a combined analysis.

Amplicon sequence variants (ASVs) were obtained with DADA2 v.1.22 following the developer's recommendations (Callahan et al., 2016). A reproducible workflow with full details

is available as [Supplementary Data S2](#). In brief, primers were trimmed with cutadapt (v3.4) to a mean depth of 26,315 reads per sample, discarding read pairs lacking amplicon primers. Reads were then trimmed to 240 and 200 bp for forward and reverse reads, respectively, and reads with more than 2 expected errors were excluded. The pool='pseudo' flag was used in the dada denoising step to increase sensitivity for potentially rare organisms. Forward and reverse sequences were merged before removing chimeras with default settings, resulting in a mean of 12,256 pairs retained per sample. Taxonomy was assigned to each ASV with the IDTAXA function ([Murali et al., 2018](#)) in the DECIPHER package in R using a custom database of SILVA 138 expanded with previously obtained but unpublished full-length 16S sequences from methane seep sites. Contaminant ASVs were identified and removed with the decontam package using the 'prevalence' method ([Davis et al., 2018](#)); a total of 36 ASVs were removed this way, resulting in a final count of 26,162 ASVs. ASVs were named in rank order by family, e.g., Thermotogaceae__2 is the second-most abundant Thermotogaceae ASV. The next-lowest taxon level was used if the ASV could not be confidently assigned a family-level designation ([Supplementary Data S3 and S4](#)).

2.3.5 Statistical analysis

To assess the degree of similarity between the newly introduced *JaichMaa* 'ja 'ag hydrothermal vent system and its microbial communities with *Auka* ([Speth et al., 2022](#)), a Non-Metric Multidimensional Scaling (NMDS) analysis was performed. This analysis was based on Bray-Curtis distances calculated with the ASV relative frequency data aggregated at the family level. *Juwak Yuum*, another site outside of the vent field with low activity in the S. Pescadero Basin (see [Fig. 2](#)), was included in the analysis to account for any potential outliers. Confidence ellipses were calculated with the ordiellipse function from the vegan package ([Oksanen et al., 2022](#)) a 95% confidence level.

Following Speth et al. (2022), we used magnesium concentration as a proxy for mixing of hydrothermal fluids in the pore water as increased fluid temperatures result in a depletion of magnesium (Edmond & Damm, 1983). The relative frequency of reads of different phyla was then correlated with magnesium concentrations in pore fluids from sediments. Phyla were only included with at least 0.5% abundance in at least 75 samples. For the ASV-level analysis of *Thermotogota*, abundant and prevalent ASVs were defined as ASVs that accounted for at least 20% of total *Thermotogota* abundance in at least one sample and were detectable (>1% of *Thermotogota*) in at least 12 samples.

The phylogenetic tree combining *Thermotogota* ASV sequences and Genome Taxonomy Database (GTDB, Parks et al., 2022) reference genomes was constructed by identifying 16S rRNA genes in GTDB reference genomes with the anvi-run-hmms program (Eren et al., 2020), exported, and trimmed to the V4-V5 region with cutadapt v3.4. A single sequence was chosen arbitrarily from *Thermotogota* reference genomes if more than one 16S rRNA sequence was detected. Sequences were then aligned with muscle v5.1 (Edgar, 2022). A maximum likelihood phylogeny was then constructed using IQ-TREE v2.1.2 with 1000 bootstraps and the model GTR+F+I+G4 as selected by ModelFinder. The resultant phylogeny was midpoint rooted and displayed with the R package ggtree (Yu et al., 2017).

2.4 Results

2.4.1 *JaichMaa 'ja 'ag: A new hydrothermal vent field*

The recently discovered *JaichMaa 'ja 'ag* vent field (Figs. 1 and 2) was confirmed and sampled using the ROV *Subastian* during expedition FK181031 aboard the R/V *Falkor* in the Gulf of California (Schmidt Ocean Institute, 2018). Situated at approximately 23.9402°N, 108.8556°W, roughly ~2 km south of *Auka*, and at a depth of ~3,700 m, this new vent field unveiled intriguing features. AUV mapping revealed a series of mounds emerging from the sediment-covered basin, showcasing both active and inactive zones of hydrothermal vent fluids (Fig. 2). *JaichMaa 'ja 'ag* hydrothermal vent field covers an area of approximately 0.05 km² (70–100 m wide by 400 m long). The nomenclature *JaichMaa 'ja 'ag*, roughly translating to ‘Liquid Metal’ from the dialect of the Kiliwa ethnic group that continues to live in northern Baja California, was chosen to reflect the interplay of light on the interface of hydrothermal fluid ponded in the roof of a cavern and the reflections of coarsely crystalline calcite covering the cavern walls. *JaichMaa 'ja 'ag* shares similarities with *Auka* in terms of the size and structure of the hydrothermal mounds, the temperature and composition of the hydrothermal vent fluids, and the dominant faunal communities. The new field comprises a series of mounds/hills, with hydrothermal edifices reaching heights up to ~25 meters.

The northernmost mounds include *Tay Mpáan* (Big Sister) to the southeast and the smaller *Muutp Mpáan* (Little Sister) to the northwest, both featuring inactive or diffuse venting areas covered with bacterial mats and various marine organisms (Fig. 2A). Moving south there is a small hill of carbonate called *Abuelita* (Fig. 2B) with an actively venting area displaying gray and white bacterial mats on the north flank, accompanied by *Oasisia* tubeworm colonies, *Ostiactis* anemones (Goffredi et al., 2021), *Peinaleopolynoe orphanae* and scale worms (Hatch et al., 2020), largely consistent with the fauna described previously from *Auka* (Goffredi et al., 2017). The largest

central mound in the hydrothermal field is *Tay Ujaa* (Big Cave), a substantial mound with flanges where the hydrothermal fluid is ponded at the roof, forming a distinct optical interface (Fig. 2C). Between this mound and the next mound to the south, the area is populated by a vast field of clams buried in sediments and various bacterial mats. The southernmost feature is *Weey 'kual* (Red Hill), a mound named for the exuberant coverage with *Oasisia* tubeworms around its summit (Fig. 2E).

Another noteworthy site in the vicinity of *JaichMaa 'ja 'ag* is *Juwak Yuum* (Two Eyes; Fig. 2A), located approximately 700 meters to the N-NE. The site comprises two adjacent circular depressions, each measuring 3 meters in depth and width, one of which was discharging shimmering water. The area is covered with sediment and adorned with patches of blue and yellow bacterial mats, as well as frenulates and anemones on the slopes, and *Oasisia* tubeworms at the bottom.

Furthermore, about 500 meters east of *Juwak Yuum*, there is *Maija awi*, an isolated actively venting mound located midway between *Auka* and *JaichMaa 'ja 'ag* (Figs. 1B and 2A). Named after the divine serpent of water in the creation myth of the indigenous Kumiai culture, *Maija awi* was first explored during dive S0473 of the ROV *Subastian* on expedition FK210922 aboard the *R/V Falkor* in 2021 (Caress et al., 2023; Schmidt Ocean Institute, 2018). This mound teems with life, dominated by polychaetes (*Oasisia* colonies, Dorvilleids, and *Peinaleopolynoe orphanae* scale worms), and *Ostiactis* anemones. The prominent chimney exhibits bright white hydrothermal calcite-anhydrite precipitates in the form of a dragon's head, inspiring the vent's name. Surrounding this unique structure are delicate spires and numerous flanges with shimmering water. Samples from this site are not included in the present paper.

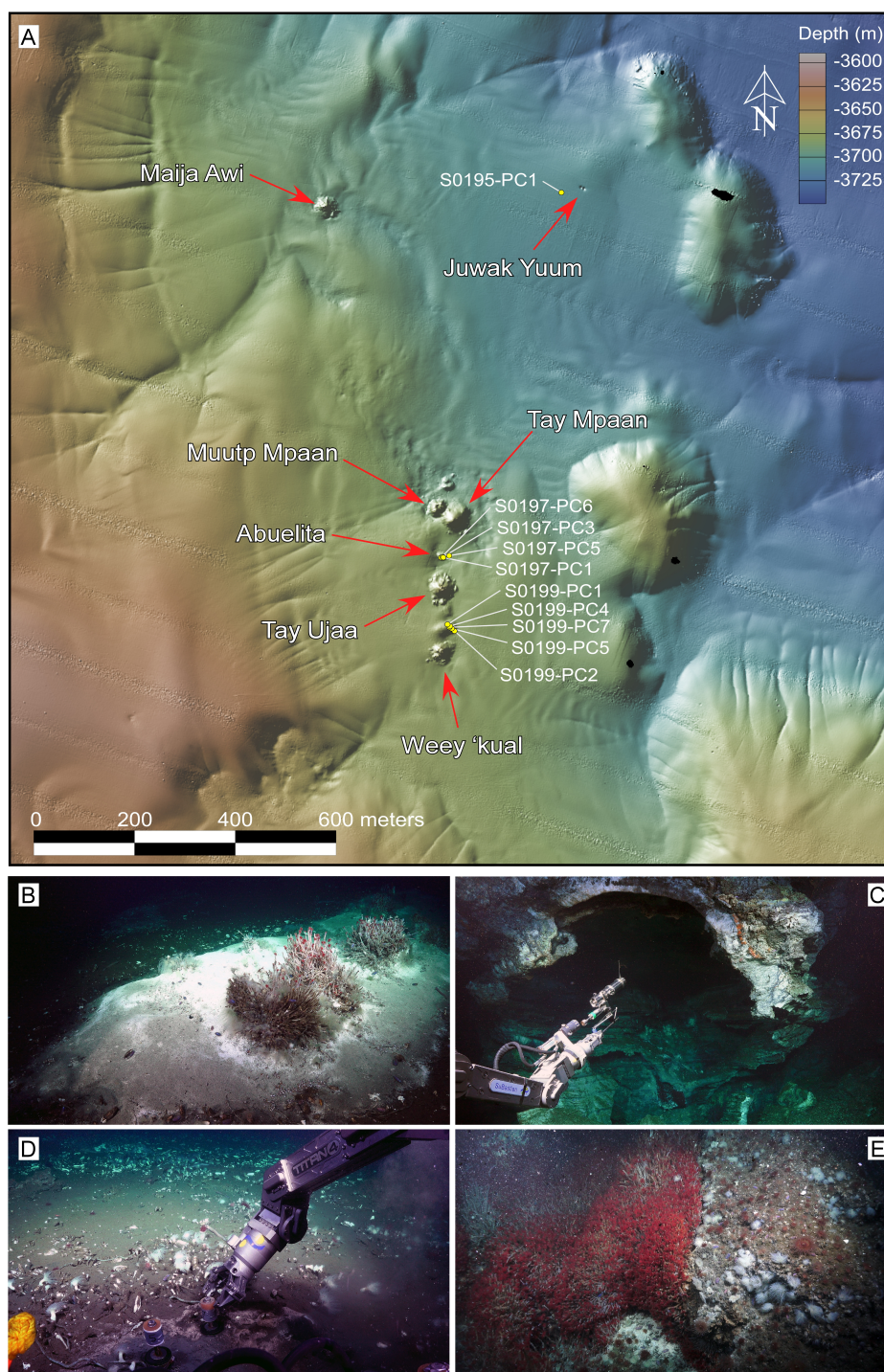


Figure 2. Overview of the sampling area and selected frame grabs of the *JaichMaa 'ja 'ag* vent field and adjacent vent sites.

A) High-resolution (1-m) bathymetric map of the study area. The *JaichMaa 'ja 'ag* vent field (bottom) comprises distinct mounds and chimneys, labeled with names*, extending 400 m in a north-south direction. Other vent features north of *JaichMaa 'ja 'ag*, including *Maija awi* and *Juwak Yuum*, are shown. Sampling locations of push cores collected during expedition FK181031, analyzed in this study, are marked.

B) Top of a carbonate mound, informally referred to as *Abuelita* ('Grandma'), covered in a white and gray bacterial mats with discrete clusters of *Oasisia sp.* tubeworms, *Clavularia* anemones and *P. orphanae* scale worms around a localized spot of hydrothermal fluid discharge (top right).

C) ROV *SuBastian*'s manipulator arm holding a gastight water bottle used to sample the hydrothermal fluids ponded in the roof of *Tay Ujaa* ('Big Cave'), the largest central mound in the vent field. Note the reflection of light from coarse calcite crystals lining the cavern walls.

D) Push coring in sediment-covered bacterial mat surrounded by a broad vesicomid clam bed located between *Tay Ujaa* and *Weey 'kual* vent sites.

E) *Weey 'kual* ('Red Hill') displaying a rich colony of *Oasisia sp.* capping the mound's summit.

* Most vents' names are derived from ancient indigenous Yuman tribes' words, inhabitants of Baja California, Sonora (Mexico), and California and Arizona (United States).

* The name of the reported hydrothermal vent field of *JaichMaa 'ja 'ag* mentioned in this paper has been updated to reflect the accurate representation in the Kiliwa language. This revision supersedes the earlier reference in Negrete-Aranda et al., 2021.

2.4.2 *Overlapping microbial communities in the Southern Pescadero Basin vent fields*

Microbial community composition was investigated at each site by sequencing the V4-V5 region of the 16S rRNA gene from sediments taken from *JaichMaa 'ja 'ag* and combined with previously published data from *Auka* (Speth et al., 2022). Each core was sectioned into 1-3cm horizons from which DNA was extracted separately. Cores were generally dominated by microbes known to be associated with hydrothermal vents, such as Halobacterota, Desulfobacterota, Thermoplasmatota, Crenarchaeota, and more (Supplementary Fig. S1). However, substantial compositional variation was observed across the dataset, leading us to investigate potential differences within and across the two vent fields.

We conducted a Non-Metric Multidimensional Scaling (NMDS) on family-level abundances. This ordination revealed a distinct cluster where most *Auka* sites (Diane's vent, Matterhorn, north and south sides of Z vent), and *JaichMaa 'ja 'ag* sites (*Abuelita* and the chemosynthetic clam field between *Tay Ujaa* and *Weey 'kual*) converged, indicating a high level of similarity between microbial community composition across the two vent fields (Fig. 3). Within this analysis, the south side of Z vent in the *Auka* vent field shows the greatest scatter between data points, likely due to the larger number of samples from this site (n= 96 samples from 13 pushcores; Supplementary Data S5). This variation is likely attributed to intra-core variation in community composition associated with core depth and steep physico-chemical gradients (as previously reported in Speth et al., 2022). The microbial communities from the low activity *Juwak Yuum* location plotted separately from samples collected within the hydrothermally active areas (Fig. 3A).

As hydrothermal fluids tend to exhibit lower magnesium concentrations compared to seawater, here we use lower magnesium levels as a proxy for the increased proportion of hydrothermal fluid within sediment pore waters (Von Damm et al., 1985; [Supplementary Data S5](#)). Magnesium concentrations were superimposed on the NMDS plot, showing a strong correlation between the variation in community composition and magnesium concentration ([Fig. 3B](#)).

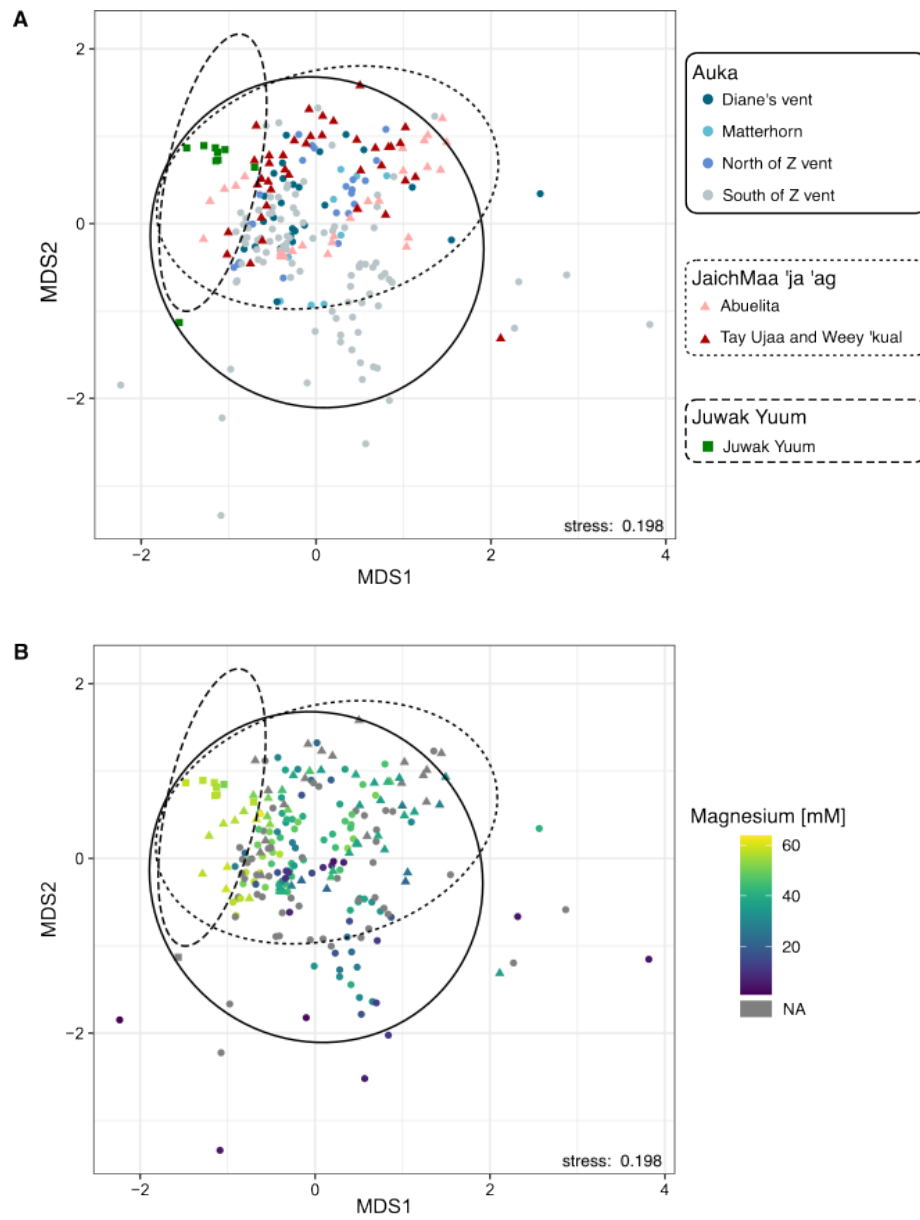


Figure 3. Non-metric Multidimensional Scaling (NMDS) plot based on 16S rRNA amplicon sequence variants of bacteria and archaea across the two vent sites *Auka* and *JaichMaa 'ja 'ag*, and the third *Juwak Yuum* in the Pescadero Basin. Ellipses denote 95% confidence limits for each location based on the observed samples. **A)** Colors indicate the site from which the sample was collected during FK181031. **B)** Colors indicate magnesium concentrations [mM] in the pore water.

2.4.3 Diffuse fluids revealed abundant thermophilic groups in the *S. Pescadero vent fields*

To identify the taxonomic group(s) associated with vent fluid, we examined the correlation between phylum-level relative frequency of reads and pore water magnesium concentration (Supplementary Data S4 and S5). The correlation coefficients were used as preliminary indicators to identify candidates for closer investigation. Top candidates included Desulfobacterota, Crenarchaeota, and other putative thermophilic phyla (e.g., Thermoplasmatota, Halobacterota, Nanoarchaeota, and Caldatribacteriota) previously reported to be associated with active hydrothermal vents, including the neighboring sedimented vent system in Guaymas Basin (Supplementary Fig. S2; Dombrowski et al., 2018; Huber, 2006; Laso-Pérez et al., 2023; Murphy et al., 2021; Shiotani et al., 2020; Speth et al., 2022; Teske et al., 2014; Zeng et al., 2021). Other community members were affiliated with microbial taxa described from other sedimented hydrothermal ecosystems, including sulfate-reducing bacteria, anaerobic methanotrophic archaea (ANME), and various taxa capable of sulfur oxidation, hydrogen oxidation, iron oxidation, sulfate reduction, and methane oxidation, among others (Supplementary Fig. S1; Supplementary Data S4).

In both *Auka* and *JaichMaa 'ja 'ag*, the Thermotogota phylum was highly ranked by correlation coefficient and occurred across a range of magnesium concentrations. At both vent sites, the Thermotogota relative frequency of reads was highest in samples with low magnesium, i.e., samples inferred to have higher levels of mixing with vent fluid. Interestingly, magnesium concentrations at *Auka* started at low concentrations near 1mM, whereas at *JaichMaa 'ja 'ag* they started at 20 mM (Fig. 4). Such overlapping but distinct vent fluid regimes may influence the representation of different lineages of Thermotogota across the vent fields. As the ecology of the Thermotogota has not been extensively studied in hydrothermal vent sediments, we chose to

highlight this phylum as an example of the dynamics within microbial communities in hydrothermal sediments across the different sites of the S. Pescadero Basin sites.

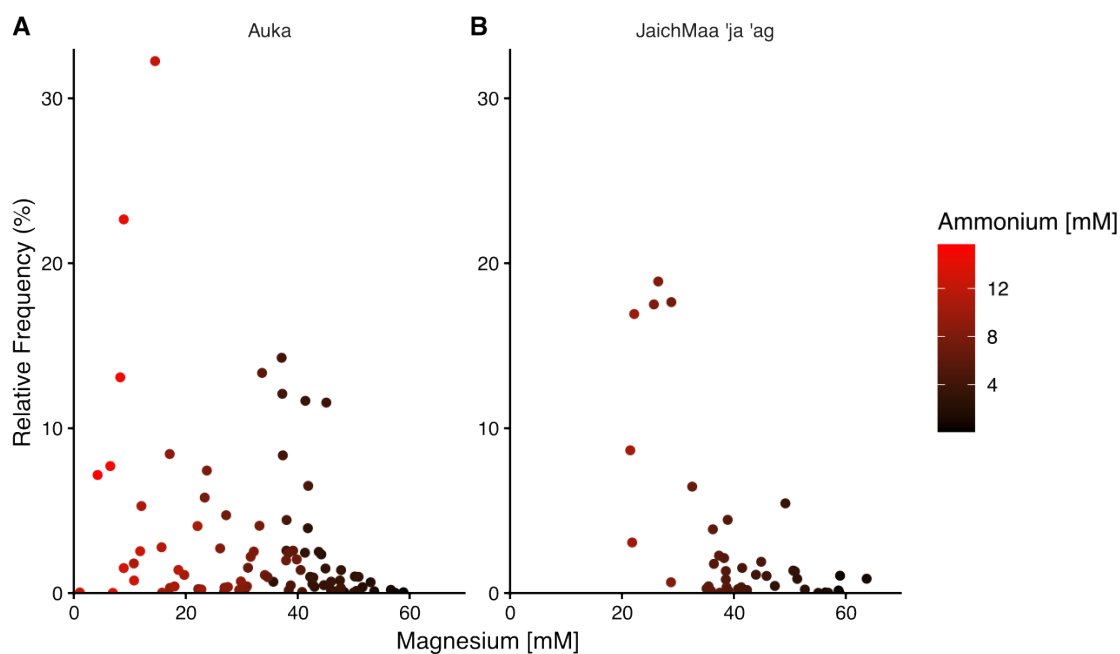


Figure 4. Relative frequency of reads corresponding to *Thermotogota* plotted against magnesium concentration (mM) in pore water sediment samples from the **A)** *Auka*, and **B)** *JaichMaa 'ja 'ag* hydrothermal vent fields. Color coding denotes ammonium concentrations (mM) in the pore water.

2.4.4 *Spatial patterns of Thermotogota sequence variants*

The phylum Thermotogota was commonly recovered in sediments from both hydrothermal vent fields and shown to be strongly correlated with low magnesium concentrations (our hydrothermal fluid proxy). Here, we examined the diversity within this deeply branching bacterial lineage, along with their relative frequency of reads and distribution patterns across the Southern Pescadero vents. Of the total of 26,162 microbial ASVs, 153 unique ASVs were affiliated with Thermotogota across all sites. Specific tracking of all Thermotogota ASVs showed high variation both with core depth and site location for some ASVs, ranging from below detection to up to 32% of the total reads in a sample (mean of $2.93\% \pm 5.1\%$ out of 135 samples). Members of the Thermotogaceae family were most diverse with 48 ASVs, followed by Mesoaciditogaceae (32 ASVs), Kosmotogaceae (16 ASVs), Fervidobacteriaceae (11 ASVs), and finally Petrotogaceae (4 ASVs). The remaining 42 Thermotogota ASVs could not be confidently assigned a family-level designation. To bolster the taxonomic assignment, we constructed a phylogeny using the Thermotogota ASV sequences and reference 16S rRNA sequences obtained from the Genome Taxonomy Database (GTDB, [Parks et al., 2022](#)) species references for Thermotogota ([Supplementary Fig. S4](#)). ASV and GTDB sequences were generally consistent by taxonomy. The most notable exception is the apparent paraphyly of Thermotogaceae; however, this observation could be due to the limited information available in the short V4-V5 region as well as the fact that no GTDB references for Thermotogaceae contained suitable 16S rRNA genes. Nonetheless, the phylogenetic comparison of *Auka* and *JaichMaa* 'ja 'ag ASV suggests substantial phylogenetic diversity, underscoring the importance of exploring the evolution and ecology of these new hydrothermal vent sites.

These Thermotogota families were represented throughout the sampled regions of S. Pescadero Basin, however distinct distribution patterns were observed within the *Auka* and

JaichMaa 'ja 'ag vent sites. 18 ASVs display the highest abundance and prevalence across the different cores obtained from the S. Pescadero Basin (Fig. 5A). These ASVs belong to the families Mesoaciditogaceae, Kosmotogaceae, Thermotogaceae, and Fervidobacteriaceae. In general, these 18 ASVs are extensively distributed across all sites within both hydrothermal vent fields, with their relative frequency of reads varying in relation to the sediment depth.

As shown in Fig. 5A, the ASVs from Mesoaciditogaceae exhibit a significantly higher level of prevalence at the South of Z vent and *Abuelita* locations within a range of 0 to 17 cmbsf. When detected, Mesoaciditogaceae ASVs tended to dominate other Thermotogota, and occurred across all core depths, particularly in samples from the *Auka* vent field. Furthermore, Mesoaciditogaceae_1 and Mesoaciditogaceae_2 rarely co-exist in the same samples despite occurring in similar depths in different cores obtained from the same site. For instance, in the case of cores south of Z vent at *Auka*, where Mesoaciditogaceae_1 is abundant, Mesoaciditogaceae_2 is not, and vice versa. This down-core consistency persists despite drastically different magnesium concentrations, e.g., Mesoaciditogaceae_1 in PC6 from dive S0196 spanned nearly the full range of magnesium concentrations. Over this gradient, the abundance of Thermotogota relative to the entire community ranged from approximately 0.5% to 30% (Supplementary Fig. S1), with one ASV (a Mesoaciditogaceae) dominant among the Thermotogota ASVs despite the presumed difference in hydrothermal fluid mixing.

In contrast, other Thermotogota ASVs peaked in abundance at the surface and diminished with depth, or vice versa (Fig. 5A). Most frequently, the ASV was replaced with an ASV from a different family, e.g., Kosmotogaceae_1 and Thermotogaceae_2 at *Tay Ujaa* and *Weey 'kual*. Thermotogaceae ASVs tended to be more abundant at depth than at the surface, e.g., Thermotogaceae_1 in PC6 from *Abuelita*, Thermotogaceae_2 in PC1 and PC2 from *Tay Ujaa* and *Weey 'kual*, etc. However, there were exceptions to this trend, such as in PC5 collected from a

blue-tinged mat on the flank of Diane's vent in *Auka*, where Thermotogaceae_1 was abundant in the first few sediment horizons and disappeared with depth.

Eight of Thermotogota ASVs were abundant and prevalent yet could not be assigned confidently to a taxon (Thermotogae_1 through Thermotogae_8). By using the percent identity of the sequenced 16S rRNA V4-V5 region as a rough proxy for their phylogenetic relatedness, we found that all were more similar to Thermotogaceae ASVs (sharing approximately 90% sequence identity) than to Kosmotogaceae or Mesoaciditogaceae ASVs (Fig. 5B). These ASVs also illustrated down-core dynamics, most notably in PC4 from north of Z vent where Thermotogae_4, Thermotogae_5, and Thermotogae_6 were all detectable in the same core but with abundance peaks at different depths (Fig. 5A, Supplementary Fig. S3). Interestingly, Thermotogae_4 and Thermotogae_6 were closely related (>99% similarity over the sequenced region) but never were both abundant in the same horizon.

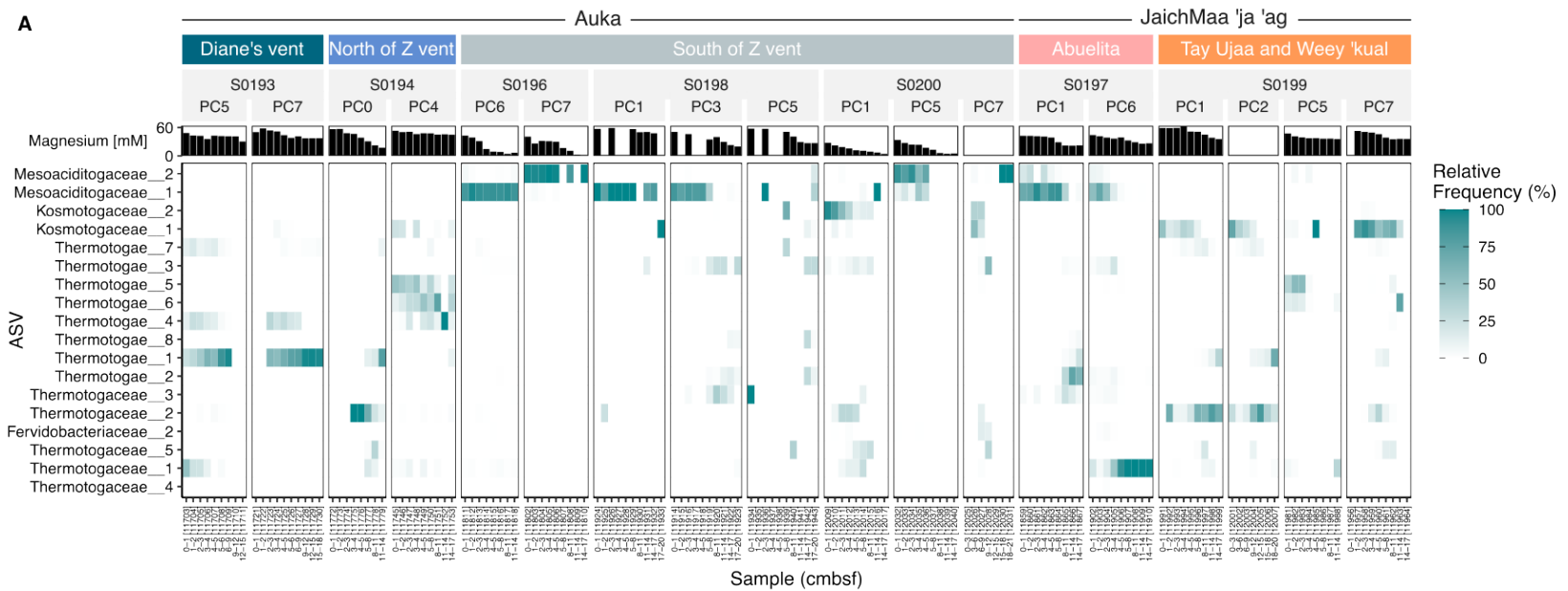
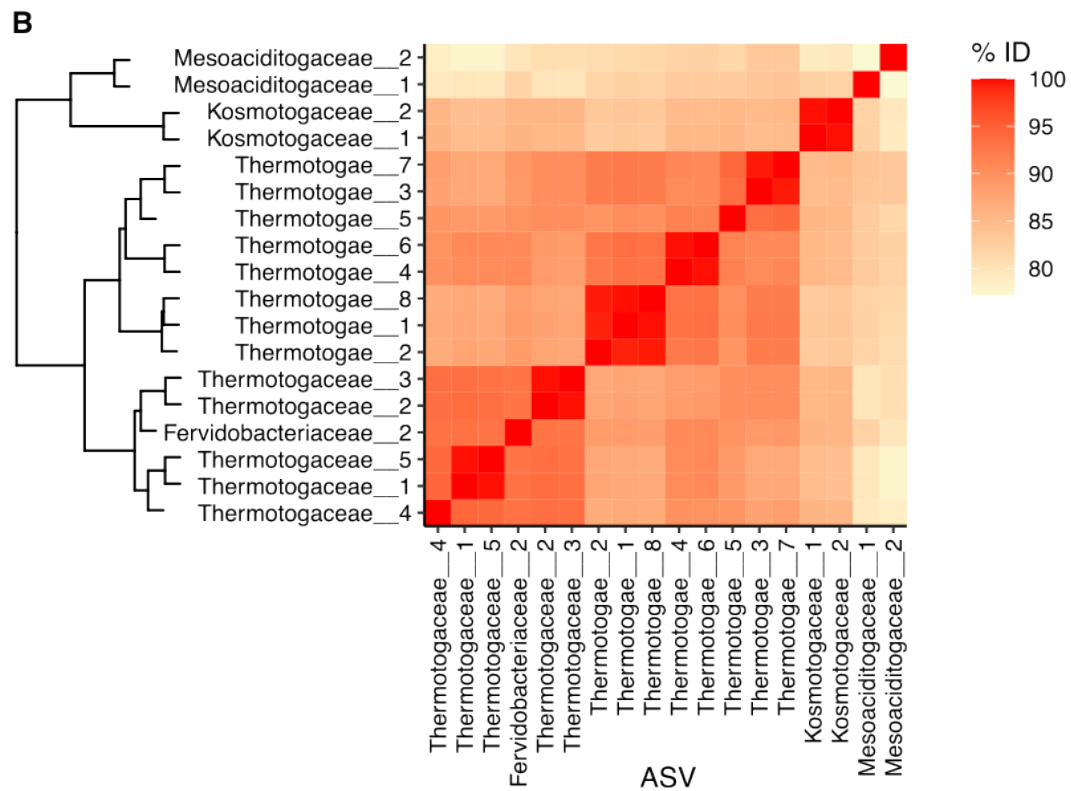


Figure 5. Microbial structure and composition of the phylum Thermotogota in the *Auka* and *JaichMaa 'ja 'ag* hydrothermal vent fields. **A)** Heatmap showing abundances of the 18 most abundant and prevalent Thermotogota amplicon sequence variants (rows) in each sediment horizon (columns), grouped by site, dive, and pushcore (nested columns). Note that the relative frequency is re-normalized to total Thermotogota abundance in a sample to better identify shifts among Thermotogota ASVs.



B) Heatmap showing the pairwise percent identity of the V4-V5 region of the 16S rRNA gene for the ASVs shown in A. The dendrogram clusters the Bray-Curtis distances computed on the percent identity matrix (hclust method='complete'). Abbreviations: PC: Pushcore; cmbsf: centimeters below seafloor.

2.5 Discussion

In this study, we introduce the discovery of *JaichMaa 'ja 'ag*, the second hydrothermal vent field located within the S. Pescadero Basin in the Gulf of California. The relatively close proximity of *JaichMaa 'ja 'ag* and the previously described *Auka* site, separated by 2 km, enable comparison of the degree of overlap in microbial community structure. Recent 16S rRNA and metagenomic characterization of the microbial diversity within the *Auka* vent field revealed substantial overlap at the species level between the archaea and bacterial lineages and viruses from *Auka* sediments and those previously described from sedimented vent system from Guaymas Basin, approximately 400 km to the north of the S. Pescadero Basin site ([Laso-Pérez et al., 2023](#); [Speth et al., 2022](#)).

The overall similarity of the bulk microbial community shared between *Auka* and *JaichMaa 'ja 'ag* fields is consistent with previous vent field comparisons ([Anderson et al., 2017](#); [Flores et al., 2011](#); [Namirimu et al., 2022](#); [Speth et al., 2022](#); [Urich et al., 2014](#)). Additionally, the intra-field variability in the sediment microbial assemblages observed at *JaichMaa 'ja 'ag* and their relationship with vent fluids (Mg concentration) suggest a strong response to the local physico-chemical conditions as previously noted by [Flores et al., 2012](#). Heat-flow measurements support *Auka* and *JaichMaa 'ja 'ag* as part of a connected system that shares a deep hydrothermal reservoir ([Negrete-Aranda et al., 2021](#)). Our results extend this connectivity to the microbial communities between fields.

To complement this community wide characterization, we additionally conducted a targeted analysis of the ASV-level diversity of members within the Thermotogota, a deeply branching bacterial phylum known to have cultured representatives spanning a broad temperature range. Analysis of the new vent field, *JaichMaa 'ja 'ag*, and previously described *Auka* site revealed distinct patterns in the composition, distribution, and abundance of Thermotogota ASVs

across the basin, highlighting the potential for distinct ecological adaptations between lineages in this physico-chemically heterogeneous system.

2.5.1 Diversity of Thermotogota in the S. Pescadero Basin hydrothermal vents

Thermotogota are a deep-branching bacterial phylum that includes hyperthermophilic, thermophilic and mesophilic heterotrophs adapted to organic-rich, anoxic environments.

Characterized members of Thermotogota all have a distinctive sheath-like toga structure surrounding the cell (Huber et al., 1986). Cultured representatives are all anaerobes and capable of fermentation or growing organotrophically with thiosulfate or elemental sulfur (Connors et al., 2006; Itoh et al., 2016). Members of this phylum have been detected from hydrothermal vents, geothermal environments, and petroleum reservoirs worldwide (Bhandari & Gupta, 2014b; Gupta & Bhandari, 2011; Itoh et al., 2016; Orphan et al., 2000; Reysenbach et al., 2013; Zeng et al., 2021). *Thermotoga maritima* MSB8 was the first described member of the Thermotogota isolated from coastal geothermal sediments in Italy, with an optimum growth temperature of 80°C (Huber et al., 1986). Subsequent characterization of other Thermotogota has expanded the physiological range to include mesophilic and thermo-acidophilic isolates (Belahbib et al., 2018).

All five families (Thermotogaceae, Fervidobacteriaceae, Kosmotogaceae, Petrotogaceae, and Mesoaciditogaceae; Bhandari & Gupta, 2014) have been reported within hydrothermal vents, highlighting the diversity of this phylum in these extreme environments, and matching our observations of their distribution across the *Auka* and *JaichMaa 'ja 'ag sites*. Only a single genus of the family Fervidobacteriaceae (*Thermosipho*) has been described in marine hydrothermal environments. This genus appears to have a widespread hydrothermal distribution including Djibouti, Africa (Huber et al., 1989), deep-sea hydrothermal vents in the Lau Basin (Antoine et al., 1997), the Iheya Basin (Takai & Horikoshi, 2000), the Mid-Atlantic Ridge (Podosokorskaya et al., 2011; Urios et al., 2004), the Suiyo Seamount in western Pacific Ocean (Kuwabara et al.,

2011), and in Guaymas Basin (Podosokorskaya et al., 2014). While we chose to focus on the most abundant Thermotogota ASVs as an example of the spatial distribution patterns of this phylum, phylogenetic analysis of all ASVs suggests that even greater diversity of the Thermotogota occurs within the S. Pescadero vents (Supplementary Fig. S4).

ASVs belonging to the families Thermotogaceae, Fervidobacteriaceae, Kosmotogaceae, and Mesoaciditogaceae were the most abundant members of the Thermotogota phylum in the hydrothermal vent fields of *Auka* and *JaichMaa 'ja 'ag*. Surprisingly, members of the Petrotogaceae, previously described from deep, hot oil reservoirs and vents (Alain et al., 2002; L'Haridon et al., 2019; Orphan et al., 2000; Postec et al., 2005), were only detected at low abundance despite the presence of sediment-associated hydrocarbons in the basin (Speth et al., 2022).

It is possible that members of the more abundant Kosmotogaceae, which also occur in deep subsurface oil reservoirs (DiPippo et al., 2009; Pollo et al., 2017; Swithers et al., 2011) may occupy hydrocarbon-rich niches in the S. Pescadero Basin rather than Petrotogaceae.

Thermophily appears to be a phylogenetically conserved trait among most Thermotogota families. For example, the Thermotogaceae consist of thermophilic and hyperthermophilic bacteria with optimum growth temperatures (OGTs) ranging from 60 to 80°C (Zhaxybayeva et al., 2019) with some members (e.g., *Thermotoga maritima* and *Thermotoga neapolitana*) as high as 90°C (Huber et al., 1989). In contrast, Mesoaciditogaceae are moderately thermophilic and acidophilic (pH 6.0), growing optimally around 55 to 60°C with a GC content of 39.9–40.6 mol% (Itoh et al., 2016). The distribution of Thermotogota families within the *JaichMaa 'ja 'ag* vent field in some samples appears to support these predictions. For example, the relative abundance of the ASV Thermotogaceae_1 was high at the *Abuelita* site, with the previously reported OGT values for this family falling within the recorded sediment temperatures for the site (Supplementary Data S5). Differences in thermotolerance among the Thermotogota may explain

some of down-core shifts in family-level representation, where sediment cores PC6 and PC1 from *Abuelita*, showing moderate gradients in Mg, were dominated by Mesoaciditogaceae_1 near the seafloor by up to 94% and transitioned to Thermotogaceae_1 or Thermotogae_2, respectively with depth. However, inferred temperature tolerance among Thermotogota does not appear to explain the complete distribution patterns of this phylum; for example, the Thermotogota in some cores (e.g., PC6 and PC7 from south of Z) were dominated by a single Mesoaciditogaceae ASV from top to bottom, although the total abundance of Thermotogota changed from 0.5% to 30% along with large gradients in Mg concentration. These observations likely point to factors other than temperature controlling community composition. Or perhaps this Mesoaciditogaceae ASV distribution may reflect greater diversity in optimal growth temperatures than currently recognized for this family, similar to other Thermotogota groups (e.g., Kosmotogaceae with an OGT range from 37 and 70°C, [Nesbø et al., 2021](#)). The overall agreement between family-level OGT values and observed distribution patterns point to temperature and vent fluid associated physico-chemical conditions as a major determinant of the Thermotogota distribution in *Auka* and *JaichMaa 'ja 'ag* vent fields. We also note that as this is a DNA-focused study, some of the recovered 16S rRNA gene diversity may also be affiliated with non-viable cells ([Li et al., 2017](#)). As such, we cannot rule out the possibility that the documented changes in Thermotogota ASVs down core may be attributed to mixing from bioturbation or active hydrothermal circulation in the sediments. Future analyses incorporating RNA analysis or targeted fluorescence in situ hybridization microscopy will assist with advancing our understanding of potential temperature-based niche differentiation among Thermotogota families in sedimented hydrothermal vents.

In addition to the physiological characterization of cultivated isolates, genome sequencing and environmental metagenomic assembled genomes (MAGs) can be used to infer optimal growth temperature based on GC content and amino acid composition for microbial groups that have not yet been physiologically characterized ([Li et al., 2019](#); [Sauer & Wang, 2019](#)). Previously, Speth

et al. (2022) used MAGs reconstructed from sediment-hosted microorganisms at the *Auka* vents for OGT predictions of representative bacterial and archaeal lineages. Eleven of these MAG's were affiliated with the Thermotogota, with estimated completeness ranging from 60 to 100 and estimated contamination ranging from 1.02 to 5.93%. OGT predictions were performed on these *Auka* MAGs and correlated with phylogeny, containing representatives from 3 of the 4 Thermotogota families along with other as yet uncharacterized lineages (Speth et al. 2022). This dataset was used to provide additional ecological context to the distribution of ASVs across the 246 samples in this study. Kosmotogaceae MAGs from *Auka* had a predicted OGT value of 44°C, consistent with characterized cultured isolates (Nesbø et al., 2021) and the lateral and down core distribution of Kosmotogaceae ASVs distribution in this study (Fig. 5A). The predicted OGT values of Thermotogaceae MAGs ranged between 46 to 65°C, while Fervidobacteriaceae had a predicted OGT value of 53°C. Both families had genome-based predicted OGT values lower than reported for cultured representatives (Bhandari & Gupta, 2014a; Farrell et al., 2021; Zhaxybayeva et al., 2019), possibly pointing to the potential for mesophilic members within the Thermotogales. This is consistent with previous reports suggesting that distinct Thermotogales lineages are distributed in low-temperature environments but are likely underreported (Nesbø et al., 2010). The remaining five MAGs within the Thermotogota phylum belonged to family level lineages without cultured representatives and thus lack empirical data to compare with the genomic OGT predictions. OGTs for these uncultured lineages ranged between 42 and 51°C, supporting the potential for a greater diversity of mesophilic representatives within the Thermotogota across the S. Pescadero Basin.

2.5.2 Biogeography and distribution of *Thermotogota* in the S. Pescadero Basin

We found 18 ASVs related to *Thermotogota* with different patterns of distribution and abundance across the S. Pescadero Basin, suggesting the ability of this phylum to inhabit the diverse niches in seafloor hydrothermal vent environments. These diverse niche environments provide opportunities for the colonization and adaptation of microbial lineages (Anderson et al., 2015). Our down-core trends on the centimeter scale extends previous insights into the occurrence patterns of distinct microbial lineages within hydrothermal vent sediments (Lagostina et al., 2021; Zhang et al., 2021).

Different ASVs are dominant at each Pescadero Basin site, yet several of the same ASVs were detected across several samples. This overlap suggests that the hydrothermal vent fields draw from a shared pool of ASVs, i.e., dispersal bridges the two vent fields. Indeed, several recent studies of the vent systems in the Gulf of California (S. Pescadero Basin and Guaymas Basin) have come to similar conclusions based on the microbial composition (Laso-Pérez et al., 2023; Speth et al., 2022; Wu et al., 2022) and geophysical attributes (Negrete-Aranda et al., 2021).

Assuming both *Auka* and *JaichMaa* 'ja' 'ag have sufficiently low barriers to dispersal, they represent an ecologically interesting pair as hydrothermal fluids appear more diffuse in *JaichMaa* 'ja' 'ag than *Auka* (inferred from magnesium concentrations). Indeed, *Auka* had the highest temperatures of 128°C at 30 cmbsf compared to a maximum temperature of 86°C in *JaichMaa* 'ja' 'ag. Thus, these environmental differences could play a role in shaping microbial communities at small scales (e.g., adjacent cores), contributing significantly to the spatial variation observed in microbial diversity as summarized by Martiny et al. (2006).

Beyond thermal variation, other drivers of community composition have been documented in large-scale geological settings (Galambos et al., 2019) where differential enrichments of sulfide, hydrogen, methane, or other hydrocarbons can occur (Amend et al., 2011;

Brazelton et al., 2006; Teske, 2020). Biotic drivers are also well-documented drivers of community structure in marine sediments (Holden & Adams, 2003; Thomas et al., 2021; Ulrich et al., 2014), and indeed recent work in the S. Pescadero Basin has highlighted the prevalence and eco-evolutionary impact of phage communities, associated with ANME-1 archaea or Heimdallarchaea (Laso-Pérez et al., 2023; Wu et al., 2022).

2.6 Conclusions

In this study, we report the microbial ecology of the recently discovered hydrothermal vent field of *JaichMaa 'ja 'ag* located in the Southern Pescadero Basin. The proximity of vents within the Pescadero Basin offers the opportunity to investigate complex microbial community dynamics and ecosystem functioning at different scales. Our ecological analyses comparing the diversity of ASV composition with the physicochemical characteristics of the basin suggest that both *Auka* and *JaichMaa 'ja 'ag* are components of a shared hydrothermal system. The microbial distribution patterns of Thermotogota, a phylum known for thermophily, in the Pescadero Basin appear to be influenced in part by the temperature gradients in the hydrothermal fluids. The identification of differences in the prevalence of the Thermotogota assemblages highlights the intricate variables within the hydrothermal ecosystem, underscoring the need for additional research to fully understand them. *JaichMaa 'ja 'ag* represents a remarkable advancement in exploring hydrothermal vent ecosystems at the Gulf of California, with the potential to enhance our knowledge of the physical, geochemical, and biological processes that shape the microbial communities in the deep-sea biosphere.

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CAPÍTULO 3

Perspectivas astrobiológicas en el estudio de ventilas hidrotermales en el Golfo de California

3.1 Abstract

Europa's subsurface ocean is considered one of the most promising environments for potentially harboring life. Predictions suggest that hydrothermal activity might occur on its seafloor, implying the presence of a warm, chemically enriched ocean that could support living organisms. Advances in space exploration over recent decades have greatly expanded our understanding of the cosmos and provided a more robust framework for investigating life on a universal scale. This progress has given rise to Astrobiology, a field dedicated to studying the origin, distribution, evolution, and future of life throughout the Universe. Hydrothermal vents on Earth have been proposed as analogous sites for studying potential habitats beyond our planet, particularly Europa moon. The exploration of these extreme environments has unveiled the extraordinary diversity of life that thrives under high pressure, temperature, and chemical conditions. Research campaigns using oceanographic vessels have yielded significant insights into the deep-sea biosphere. In the Gulf of California (GoC), the study of hydrothermal vents, such as those recently discovered in the Pescadero Basin and in Guaymas Basin, provides crucial information for developing models of habitability. These hydrothermal vents offer a unique opportunity to explore how life might exist in similar environments on other ocean worlds. By leveraging our knowledge of these terrestrial analogs, we can more precisely target our search for life on ocean worlds, develop models of habitability, and ultimately enhance our capability to detect and understand life beyond Earth.

3.2 Introduction

3.2.1 *The Search for Life in the Universe*

Astrobiology is a multidisciplinary scientific field that studies the origin, distribution, evolution, and future of life in the Universe (Des Marais et al., 2008). It aims to explore fundamental aspects of life within a planetary context; for example, the conditions of the primitive Earth, the evolution of life, the physical and chemical limits of life, the exploration and distribution of habitable environments in the Solar System, and the search for signs of life on exoplanets (Cottin et al., 2017; Des Marais et al., 2008). Earth is currently the only planet known to harbor life, from this perspective, astrobiology also involves the study of terrestrial biology (Chyba & Hand, 2005) but integrating various scientific disciplines, each contributing essential knowledge to understanding life on Earth and beyond.

One of the primary strategies in astrobiology is "Follow the Water" (Hand et al., 2020). This approach is predicated on the understanding that water is a crucial solvent for life as we know it (Cottin et al., 2017). By seeking out environments where liquid water is or was present, it is feasible to identify potential habitats that might support or have supported life. Therefore, planetary bodies with liquid water are prime candidates in the search for life beyond Earth (Lunine, 2017). Ocean worlds became particularly relevant to astrobiology in the late 20th and early 21st centuries, driven by groundbreaking discoveries from space missions and advancements in planetary science. Since then, identifying ocean worlds has been a top priority for astrobiological research (Hendrix et al., 2018).

The NASA Roadmap to Ocean Worlds (ROW) emphasizes understanding the characteristics of subsurface oceans and the geophysical processes that sustain them. Enceladus, Titan, and Europa have been identified as the highest-priority targets in the near term. Determining the dynamics of subsurface oceans and their chemical composition is essential for assessing their

potential to support life (Hendrix et al., 2018). Furthermore, exploring ocean worlds in the outer Solar System provides the opportunity to search for an independent origin of life (Hand & German, 2018).

Another strategy in Astrobiology is the exploration of terrestrial analogs to comprehend other environments beyond Earth (Des Marais et al., 2008). Hydrothermal vent systems on Earth's ocean floor are prime examples of such analogs (Joseph, 2023b). The extreme conditions of high pressure, temperature, and chemical composition at these vents provide a model for understanding how life might emerge in similar environments elsewhere in the Solar System, such as the subsurface oceans of icy moons (Russell et al., 2017).

The study of hydrothermal vents offers an opportunity to establish a link between the fields of oceanography and astrobiology. Oceanographic research into Earth's hydrothermal vent systems not only elucidates the conditions that can support life in extreme environments but also guides the design of future space missions (Hendrix et al., 2018). By studying how life can persist in these extreme ecosystems, we gain critical insights into where and how to search for life within and beyond our planet.

3.2.2 The Study of Europa: A Prominent Ocean World

Europa, one of the four largest satellites of Jupiter, was discovered by Galileo Galilei in 1610; and in the 1970s, the first close-up image of the moon was captured with the Voyager 2 spacecraft revealing interesting features like its surface is crossed by ridges and cracks with few records of meteorite craters (Smith et al., 1979). But it was not until 1995 with the Galileo mission that the satellite began to be studied in greater detail, providing great evidence of the characteristics of its liquid subsurface until today. Europa, one of the four largest Jupiter satellites, was discovered by Galileo Galilei in 1610 (Joseph, 2023a). In the 1970s, the first close-up image of the moon was

captured with the Voyager 2 spacecraft, revealing interesting features, such as its surface being crossed by ridges and cracks with few meteorite craters (Smith et al., 1979). However, it was not until 1995 with the Galileo mission that the satellite began to be studied in greater detail, providing great evidence of the characteristics of its liquid subsurface.

Europa is approximately 3160 km in diameter, about the size of Earth's moon, and is tidally locked to Jupiter, meaning that one hemisphere is constantly facing the planet (Joseph, 2023a). It has been confirmed that the satellite has a tenuous atmosphere, primarily composed of oxygen (Bagenal & Dols, 2020). The upper atmospheric layer, known as the ionosphere, consists of charged particles created by solar radiation and energetic particles from the magnetosphere of Jupiter (Kliore et al., 1997).

Gravity and magnetic data from the Galileo mission suggest that Europa is differentiated into a metallic iron-nickel core and a silicate mantle (Fig. 6; Anderson et al., 1998; Bhatia & Sahijpal, 2017; Showman & Malhotra, 1999). Infrared spectroscopy and albedo measurements have shown that water ice dominates the surface (Showman & Malhotra, 1999), and recent models have estimated a mean surface temperature of -183°C (Ashkenazy, 2019).

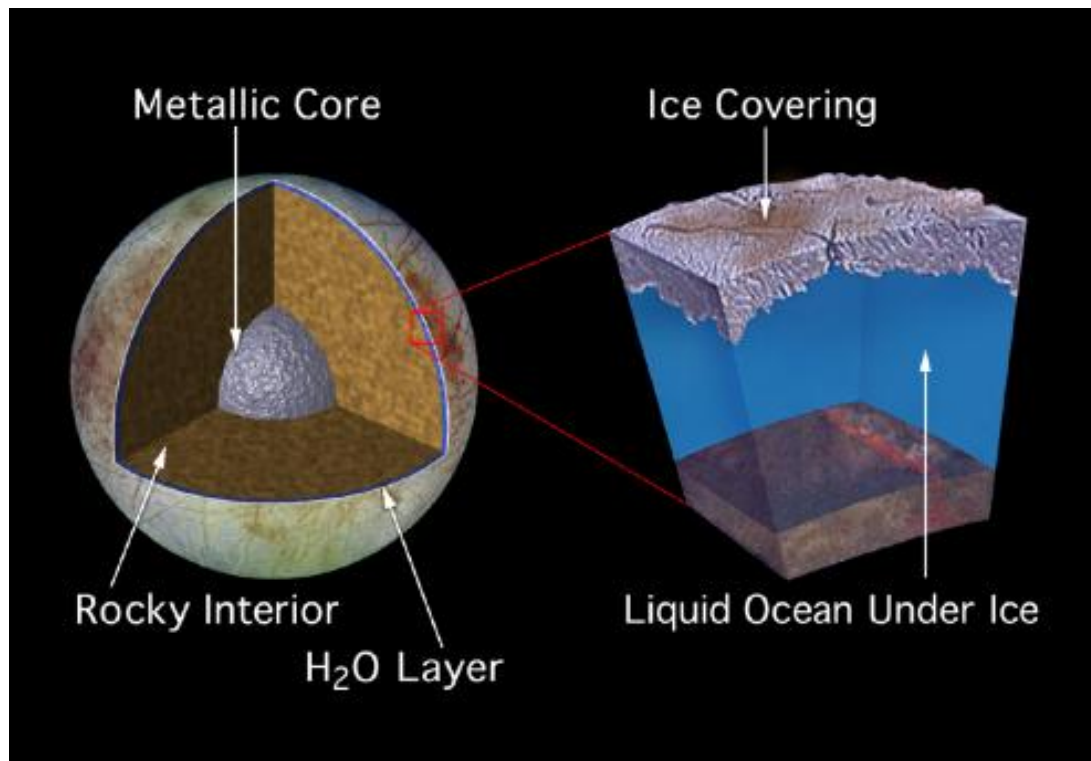


Figure 6. This illustration presents a proposed model of the subsurface structure of Europa, a satellite of Jupiter, based on data obtained from the Galileo mission. The model depicts a metallic core, a rocky mantle, and a liquid ocean beneath the icy crust. Credit: NASA/JPL.

The icy surface is covered by a global network of linear features, such as cracks, ridges, and bands, some of which extend up to 3000 km in length (Fig. 7; Greenberg et al., 1999; Joseph, 2023a). These fractures are largely attributed to tidal deformation induced by Jupiter's gravitational forces (Greenberg et al., 1998). Other features include pits, spots, domes, and disrupted terrain (Singer et al., 2021), which indicate a variety of processes occurring on the ice shell. For example, the presence of few craters suggests ongoing geological activity and crater dating has estimated a young surface age of approximately 10 million years (Showman and Malhotra, 1999). Furthermore, studies have revealed that subduction processes recycle surface material into the interior, suggesting that Europa may be the only body in the Solar System, other

than Earth, with plate tectonics (Kattenhorn & Prockter, 2014). Estimates indicate that the thickness of its icy crust is approximately 15 kilometers (Roberts et al., 2023). Additionally, analyses have shown that the dark, reddish streaks on Europa's surface contain precipitated salts such as magnesium sulfate (McCord et al., 1998).

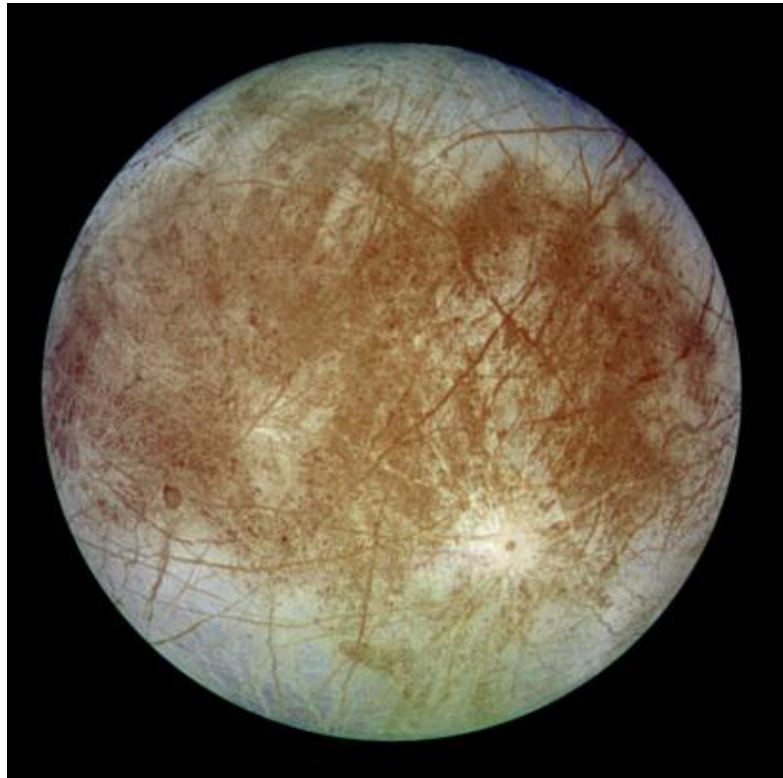


Figure 7. Image of Europa taken by the Galileo mission showing the approximate natural color of the moon and the long dark fractures in the crust. The orange color indicates the presence of sulfur compounds. The bright feature with a central dark spot in the lower third of the image is a young impact crater that is approximately 50 km in diameter. Credit: NASA/JPL/DLR.

According to Kivelson et al. (1997), substantial data support the hypothesis of a subsurface ocean on Europa, derived from the interaction between Europa's magnetic field and Jupiter's. The resulting induced magnetic field suggests the presence of a conductive layer beneath Europa's icy crust, likely composed of salty liquid water. The existence of Europa's subsurface water layer is confirmed by various pieces of evidence (Cassen et al., 1979; Pappalardo et al., 1999), with one of the most compelling being the eruption of water vapor plumes from its interior (Paganini et al., 2019).

Europa's internal heat, generated by tidal forces, may be sufficient to prevent the ocean from freezing (Showman and Malhotra, 1999). The potential global ocean is presumed to be ~60–160 km deep (Paganini et al., 2019). Little is known about Europa's ocean, with ongoing research efforts aiming to understand its characteristics better. The presence of salts on Europa's surface, coupled with magnetic field data, indicates that the subsurface water is likely salty. Still, the exact amount and composition of salts remain poorly understood (Lunine, 2017). This uncertainty underscores the importance of further investigation into Europa's ocean, especially for potentially discovering biosignatures beyond Earth.

The future Europa Clipper mission will extensively characterize the moon's surface. Its overarching goal is to establish Europa's habitability, which would not only allow for a direct search for life on another planetary body but also provide valuable information on the geological, geophysical, and chemical nature of the icy moon (Hendrix et al., 2018).

3.2.3 *Hydrothermal Vent Systems as Analog Sites*

The biosphere on Earth represents our most comprehensive knowledge of life within the Solar System; therefore, we use it as a point of comparison for studying life in the universe ([Weber et al., 2023](#)). Terrestrial analogs, such as extreme environments, play a crucial role in astrobiological research, where physical and chemical conditions closely resemble those of non-terrestrial habitats ([Arrigo, 2022](#); [Joseph, 2023b](#)). Consequently, astrobiology can explore questions about ocean worlds that would not be possible to investigate otherwise ([Arrigo, 2022](#)).

In the case of Europa, numerous lines of evidence indicate the presence of a subsurface ocean ([Carr et al., 1998](#); [Pappalardo et al., 1999](#)). Although its oceanic chemistry and geochemical cycles are largely unknown ([Joseph, 2023a](#)), estimates have been made regarding the processes occurring at the bottom of this satellite's ocean. Lowell and Dubose ([2005](#)) estimated that a subsurface ocean around ~100 km deep on Europa would likely lead to significant high-temperature hydrothermal activity. This activity would be primarily driven by radiogenic and tidal heat within the moon's rocky interior. Additionally, Vance et al. ([2007](#)) demonstrated that the fluctuating hydrostatic pressure caused by tidal forces on Europa's ice shell could induce hydrothermal fluid flow through the seafloor. The potential for hydrothermal activity on Europa suggests the existence of a warm, chemically rich subsurface ocean, offering an environment favorable for supporting life as we know it.

Evidence of life's existence on Earth is found in submarine hydrothermal vents located on the ocean floor, resulting from tectonic activity. These hydrothermal vents sustain a unique ecosystem composed entirely of chemosynthetic organisms, which thrive using chemical energy ([Arrigo, 2022](#)). Therefore, the similarities between Europa and Earth have led to the proposal of hydrothermal systems as analogs for life on early Earth and some other planets and their moons, such as Europa's subsurface ocean ([Chela-Flores, 1998](#)).

Submarine hydrothermal vents are globally distributed, occurring not only on seafloor spreading zones but also in various geological settings like mid-ocean ridges, back-arc basins, island arcs, and hot-spot environments (Pirajno, 2009). These geological formations protrude from fissures on the ocean floor, releasing fluid that has been heated to high temperatures through geothermal processes. As the heated seawater moves through the Earth's crust below the ocean floor, it gathers dissolved gases and various minerals. When this warm fluid mixes with cooler seawater, chemical separation occurs, leading to the emanation of reduced gases (like methane, hydrogen sulfide, and hydrogen) and precipitation and solidification of minerals into structures such as mounds, spires, and chimneys (Joseph, 2023b; Koschinsky, 2016). Most hydrothermal vents are located at depths of 1500 to 4000 meters and the hydrothermal fluid is heated to temperatures of 250°C to 450°C (Dover, 2000).

As mentioned, deep-sea hydrothermal environments are predominantly inhabited by chemoautotrophs. These organisms derive the energy necessary for synthesizing organic compounds by oxidizing sulfides like hydrogen sulfide (H_2S), as well as other reduced substrates such as hydrogen (H_2), iron (Fe^{2+}), or manganese (Mn^{2+}) emitted from vents (Joseph, 2023b). It has been suggested that several of these redox compounds could be present in Europa's ocean, and there is speculation that processes such as anaerobic methane oxidation and sulfate reduction might be occurring as well (Weber et al., 2023). Thus, extremophiles, are the life forms most closely resembling potential organisms that could exist on the subsurface of the icy moon (Joseph, 2023b).

Nevertheless, there is still much to investigate to comprehensively understand the interactions within terrestrial hydrothermal systems that could provide insights into Europa's oceanic environment. This includes, for example, comparing fluid compositions and analyzing the microbial communities commonly found in these hydrothermal settings (Weber et al., 2023).

3.3 Astrobiological Perspectives

3.3.1 *Considerations for Habitability Models*

Habitability is broadly defined as the set of environmental conditions required for sustaining life as we know it. These conditions include access to liquid water, the availability of essential nutrients, and energy sources to power life (e.g., chemical disequilibria) (Glass et al., 2022; Hand et al., 2020). The building blocks of life refer to the elements that are required by all known organisms, including carbon, hydrogen, nitrogen, oxygen, phosphorus, and sulfur (Hendrix et al., 2018). Additional critical environmental parameters shaping the limits of life on Earth include pressure, temperature, pH, and water activity (Dartnell, 2011).

Europa emerges as a leading candidate for habitability beyond Earth due to its subterranean liquid ocean beneath an icy crust, alongside the presence of essential chemical elements and energy sources (Chyba & Hand, 2005). While Europa's planetary features are broadly characterized, a quantitative evaluation of its habitability necessitates identifying specific physicochemical parameters essential for life support on this icy moon (Glass et al., 2022).

To evaluate potential habitats on Europa based on its planetary features, we can consider the environmental conditions of its outer icy crust, subsurface liquid ocean, and the interface between them, where material exchange between the interior and exterior of the satellite could occur (Culberg et al., 2022; Roberts et al., 2023). Given the focus of this study on oceanographic research in deep-sea environments, our attention will be directed solely towards Europa's subsurface ocean.

The habitability of Europa's ocean hinges on the presence of essential biological elements and suitable chemical energy sources (Hand et al., 2016). Existing knowledge indicates that the ocean includes salts like sulfate and chloride (Joseph, 2023b). Estimates propose that the seafloor

undergoes geochemical processes influenced by both high and low-temperature hydrothermal activity ([Hand et al., 2016](#); [Vance et al., 2016](#)).

Although the precise depth of Europa's ocean has not yet been determined, and the concentrations of its chemical compounds remain uncertain, inferring the habitability of this environment can draw from analogs found on Earth ([Hand et al., 2020](#)). Insights gained from terrestrial studies encompass a broad spectrum of physical (temperature, pressure, radiation levels) and chemical (pH, redox potential, salinity, elemental abundances) conditions conducive to life. Additionally, research on ecological succession and adaptation provides valuable understanding of how ecosystems establish and evolve under varying environmental conditions, shedding light on metabolic diversity and potential biomass production in oceanic environments ([Hendrix et al., 2018](#)).

Accumulating such data will facilitate the development of habitability models specifically tailored for oceanic worlds like Europa. These models are designed to explore the possibility of life beyond Earth and contribute to validating our understanding of critical planetary processes. Furthermore, they aid in refining sampling strategies, determining optimal locations for exploration, and identifying key parameters essential for designing effective future space missions ([Arrigo, 2022](#)).

3.3.2 Case Study: Hydrothermal Vents in the Gulf of California

The hydrothermal vent fields in the Gulf of California provide excellent environments for studying the processes occurring on the ocean floor. While hydrothermal systems have been proposed as analog sites for the seafloor of Europa ([Joseph, 2023b](#)), the hydrothermal systems of the Gulf of California (GoC) have not been thoroughly investigated as sites of astrobiological interest. Recent oceanographic expeditions to the GoC, specifically to the Guaymas Basin ([Teske, 2021](#)) and the Pescadero Basin ([Caress et al., 2023](#); [Schmidt Ocean Institute, 2018](#)), have been conducted to explore the seafloor and study hydrothermal vent systems along with their associated biosphere.

The Guaymas Basin is a dynamic environment where a deep marginal rift basin is characterized by active seafloor spreading and rapid sediment deposition, including organic-rich sediments. Reaches depths of up to 2,500 meters below sea level, providing a unique opportunity to study processes occurring in its thick sediment layer influenced by sills ([Teske, 2021](#)). The interaction of thermal and chemical processes is of particular interest due to their influence on shaping the deep-sea biosphere. The Pescadero Basin, situated at a depth of 3,670 meters, represents the deepest region of the GoC offering an exceptional setting to explore the limits of life on Earth. Recently discovered hydrothermal vent fields in this region have captured attention due to their chemical composition, which includes anhydrite and calcite, and their remarkable microbial diversity ([Goffredi et al., 2017](#); [Speth et al., 2022](#)).

As mentioned previously, developing quantitative habitability models, particularly for Europa, requires analyzing oceanographic datasets to constrain ranges that help determine the conditions under which life can exist ([Glass et al., 2022](#)). Based on the recent exploration of hydrothermal vent systems in the Gulf of California, the habitability model for Europa's subsurface ocean must encompass physical, geochemical, and biological parameters, such as temperature,

pH, and the chemical composition of hydrothermal fluids, along with a biological assessment of diversity and metabolic capabilities. This approach would enable the establishment of comparative benchmarks essential for future space missions, such as the upcoming Europa Clipper mission. ([Roberts et al., 2023](#); [Vance et al., 2023](#))

So far, thanks to these oceanographic expeditions in the GoC, we have obtained measurements of chemical compounds of interest for Europa, such as H₂S and methane, as well as ions like magnesium and calcium. Additionally, there are estimates of temperature and heat flux, along with information on extremophilic organisms thriving in these systems. The metabolic processes proposed for Europa, specifically sulfur reduction and methane oxidation, are indeed characteristic of these hydrothermal fields ([Speth et al., 2022](#); [Teske et al., 2002](#)), thereby establishing the Guaymas and Pescadero Basin as ideal analogue sites for studying Europa's subsurface ocean.

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CAPÍTULO 4

Conclusiones Generales

4.1 Conclusiones

Esta investigación marca un avance significativo en el entendimiento de los sistemas hidrotermales del Golfo de California. Por primera vez, se describe y caracteriza el campo de ventilas hidrotermales de *JaichMaa 'ja 'ag* en la Cuenca Pescadero. A través del análisis de los fluidos hidrotermales, se evaluó la diversidad taxonómica y la estructura poblacional de bacterias termófilas que habitan en los sedimentos de estos campos mediante el uso del gen 16S rRNA. Además, se ha determinado la similitud entre los campos hidrotermales de *Auka* y *JaichMaa 'ja 'ag*, revelando que forman parte de un mismo sistema hidrotermal dentro de la Cuenca Pescadero.

Nuestro estudio ha identificado una amplia diversidad de microorganismos extremófilos capaces de prosperar en los sedimentos de la Cuenca Pescadero. Se realizó una investigación detallada sobre la densidad, frecuencia relativa y patrones de distribución de las familias de las bacterias termófilas del phylum Thermotogota, donde se encontró que múltiples factores bióticos y abióticos controlan su distribución en los sedimentos.

En el ámbito de la astrobiología, se emplearon a las ventilas hidrotermales de la Cuenca de Guaymas y la Cuenca Pescadero del Golfo de California como sitios análogos para estudiar a Europa, la luna congelada de Júpiter. Se propone que la comprensión de los parámetros físicos, geoquímicos y biológicos en las ventilas hidrotermales terrestres proporciona un marco de referencia crucial para evaluar las condiciones de habitabilidad en el océano subsuperficial de este satélite. Este enfoque no solo enriquece nuestro conocimiento sobre la vida en la Tierra, sino que también establece las bases para la búsqueda de vida más allá de nuestro planeta.

APÉNDICE

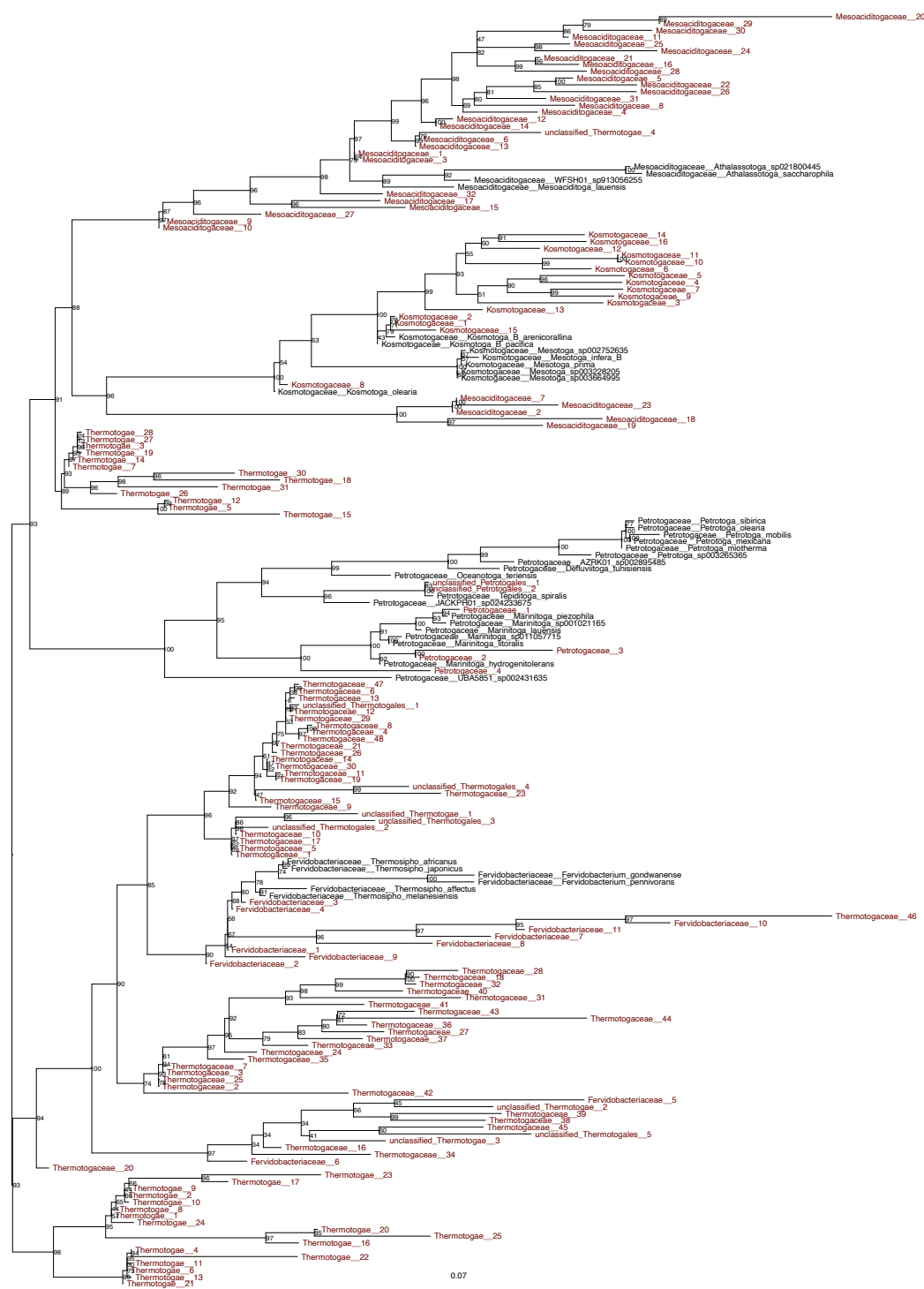


Figure S4. Phylogenetic comparison of Thermotogota ASVs from S. Pescadero Basin with reference 16S rRNA sequences from the Genome Taxonomy Database the tree illustrates the evolutionary relationships between Thermotogota ASV sequences obtained from the study (highlighted in red) and reference sequences.

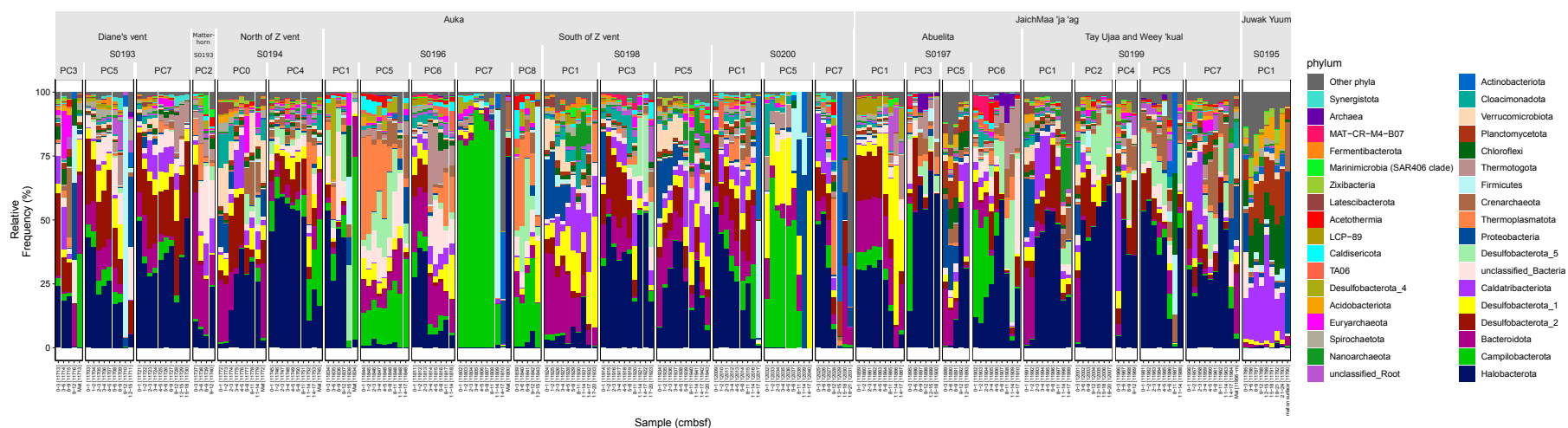


Figure S1. Microbial diversity in the S. Pescadero Basin hydrothermal vent fields. The relative frequencies of phyla derived from the 16S rRNA amplicon sequence variants found in the hydrothermal vent fields of *Auka* and *JaichMaa 'ja 'ag*.

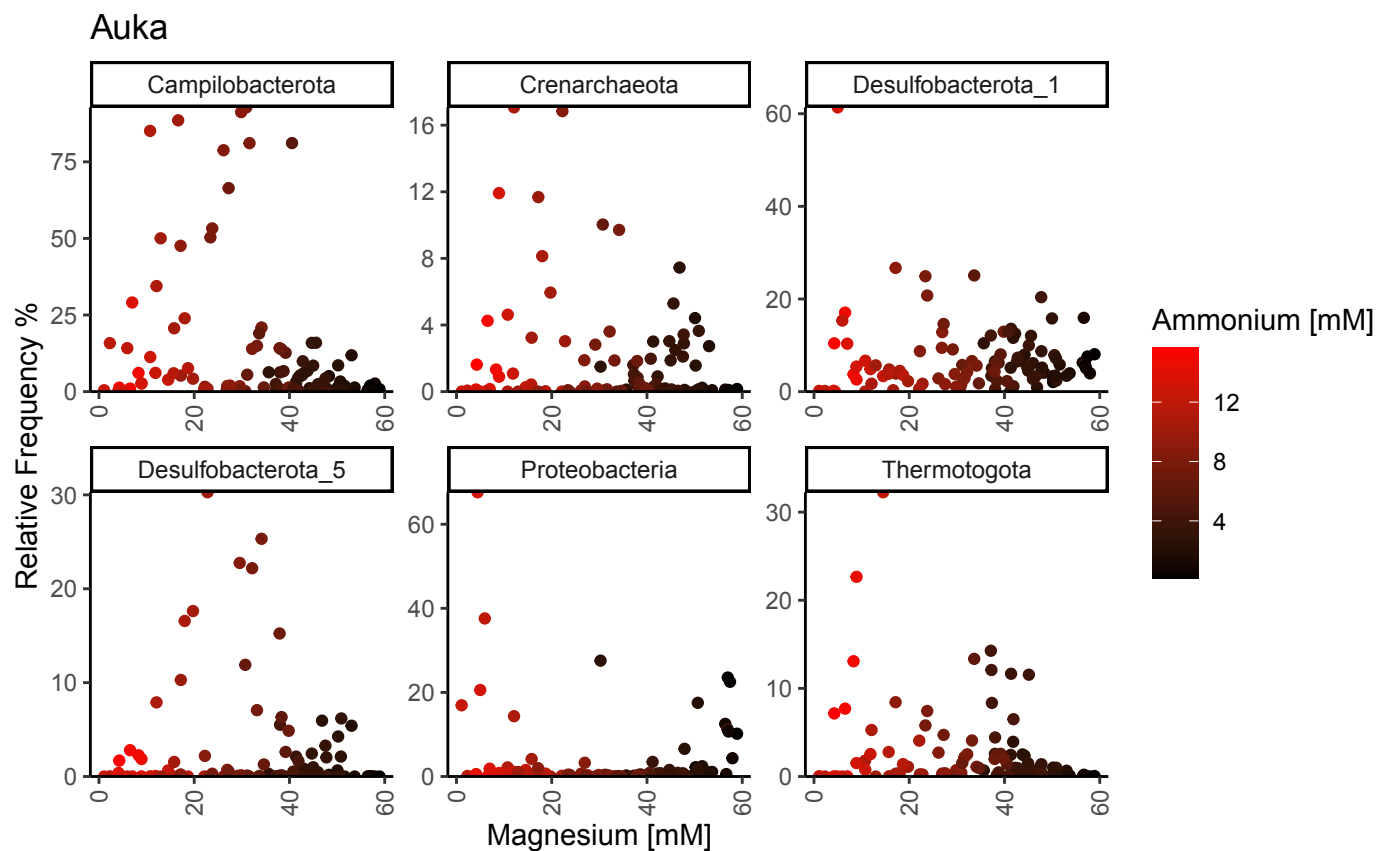
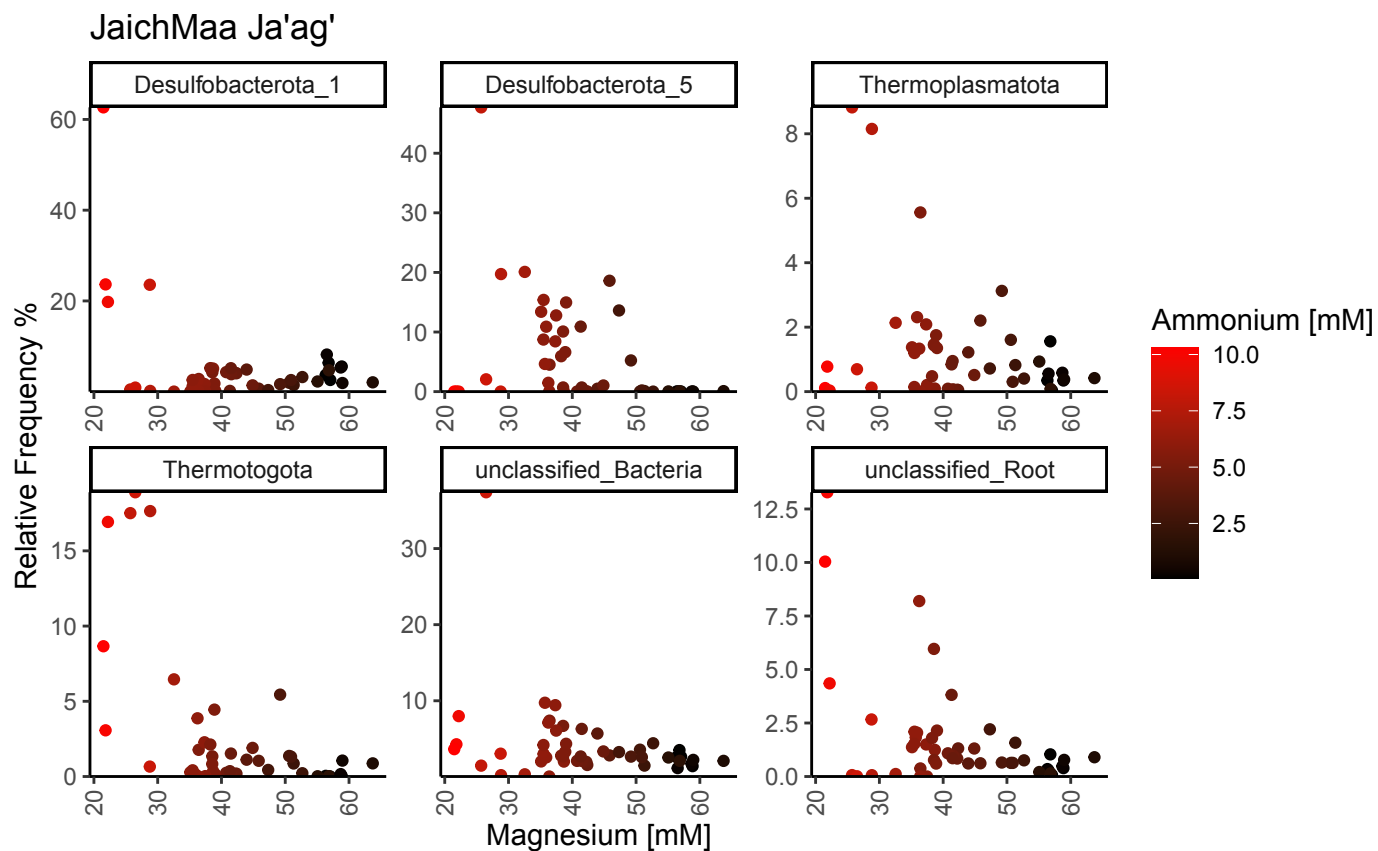
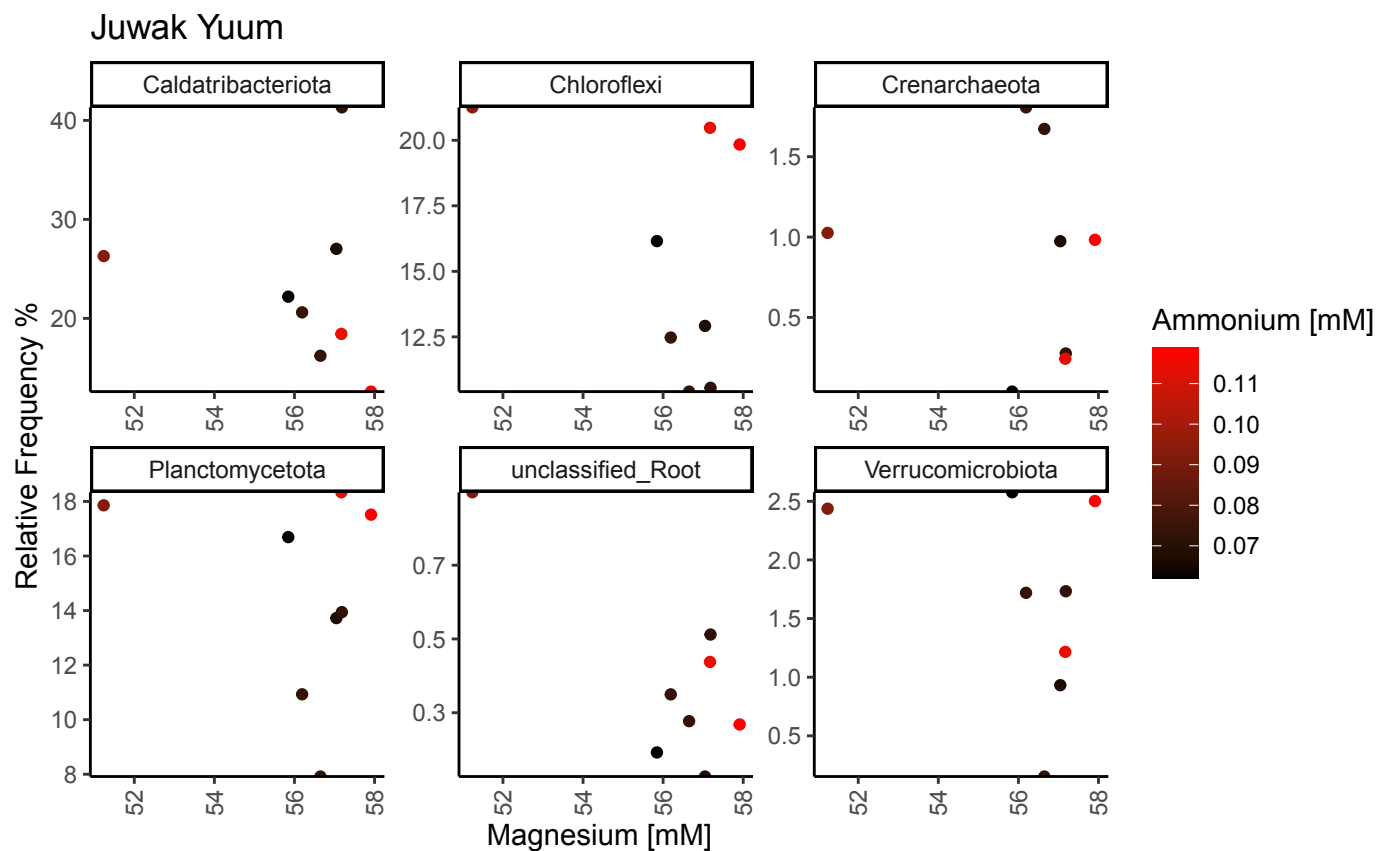


Figure S2. Microbial diversity correlated with hydrothermal fluids beneath the sediments in the Pescadero Basin hydrothermal vent fields. The most abundant Phyla with respect to magnesium [mM] in (A) *Auka*, (B) *JaichMaa 'ja 'ag*, and (C) *Juwak Yuum* with color coding based on ammonium and sulfide [mM]. All taxa correspond to Bacteria except for Crenarchaeota which corresponds to Archaea. The unclassified group could include both domains.



Microbial diversity correlated with hydrothermal fluids beneath the sediments in the Pescadero Basin hydrothermal vent fields. The most abundant Phyla with respect to magnesium [mM] in (A) *Auka*, (B) *JaichMaa 'ja 'ag*, and (C) *Juwak Yuum* with color coding based on ammonium and sulfide [mM]. All taxa correspond to Bacteria except for Crenarchaeota which corresponds to Archaea. The unclassified group could include both domains.



Microbial diversity correlated with hydrothermal fluids beneath the sediments in the Pescadero Basin hydrothermal vent fields. The most abundant Phyla with respect to magnesium [mM] in (A) *Auka*, (B) *JaichMaa 'ja 'ag*, and (C) *Juwak Yuum* with color coding based on ammonium and sulfide [mM]. All taxa correspond to Bacteria except for Crenarchaeota which corresponds to Archaea. The unclassified group could include both domains.

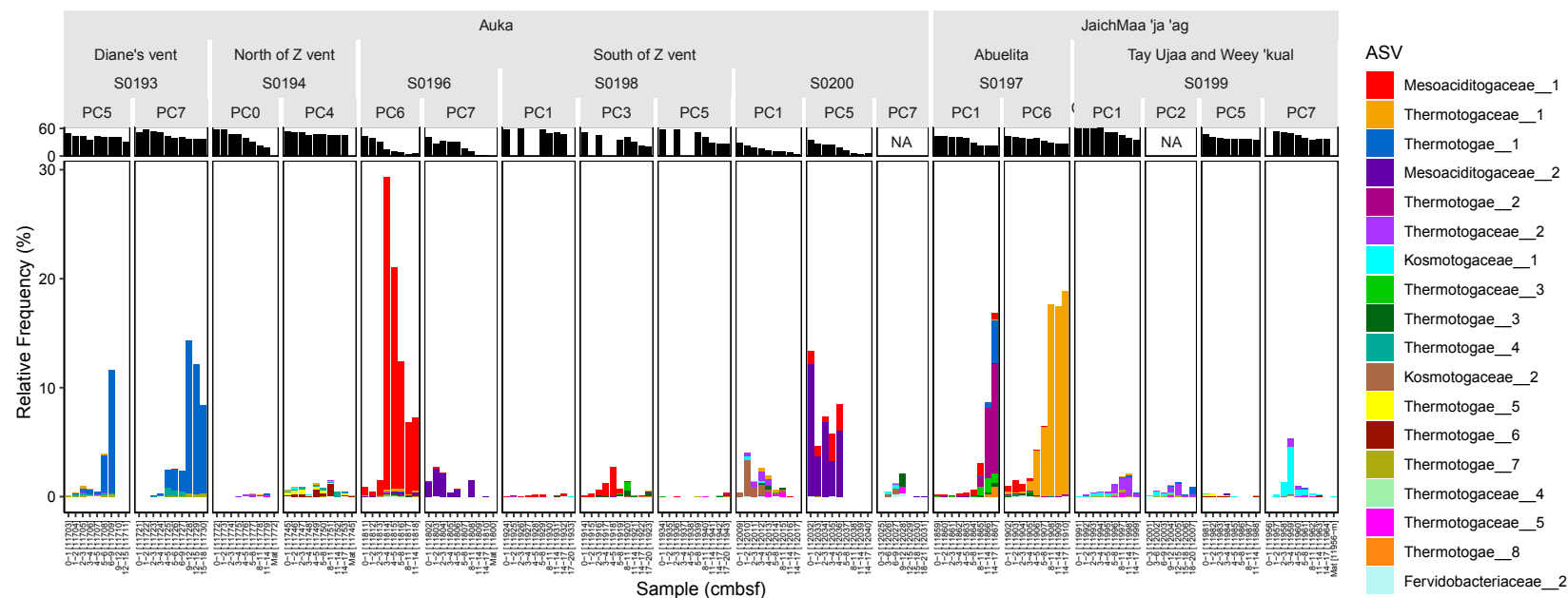


Figure S3. Microbial structure and composition of the phylum Thermotogota in the *Auka* and *JaichMaa 'ja 'ag* hydrothermal vent fields. The relative frequency is no normalized to total Thermotogota abundance.

Table 1. Sample list and physicochemical data obtained from Pescadero Basin during expedition FK181031. Temperature data were measured in situ. Ammonium and magnesium were determined by ion chromatography.

Sample ID	Dive	Core	Location	Site	Depth (mbsl)	Latitude	Longitude	Horizon (cmbsf)	Temp. (°C) 15 cmbsf	Temp. (°C) 30 cmbsf	Ammonium (mM)	Magnesium (mM)
FK181031-11731	S0193	NA	<i>Auka</i>	Matterhorn	3656.39	23 57.23208 N	108 51.78253 W	Mat	NA	10.99	NA	NA
FK181031-11742	S0193	NA	<i>Auka</i>	Matterhorn	3652.8	23 57.23016 N	108 51.7797 W	Mat	NA	NA	NA	NA
FK181031-11743	S0193	NA	<i>Auka</i>	Matterhorn	3650.23	23 57.23394 N	108 51.78091 W	Mat	NA	NA	NA	NA
FK181031-11732	S0193	PC1	<i>Auka</i>	Matterhorn	3657.85	23 57.22692 N	108 51.7723 W	0-3	NA	10.99	NA	NA
FK181031-11735	S0193	PC1	<i>Auka</i>	Matterhorn	3657.85	23 57.22692 N	108 51.7723 W	10-13	NA	10.99	NA	NA
FK181031-11737	S0193	PC2	<i>Auka</i>	Matterhorn	3657.85	23 57.22692 N	108 51.7723 W	0-3	NA	10.99	2.3238	44.2195
FK181031-11738	S0193	PC2	<i>Auka</i>	Matterhorn	3657.85	23 57.22692 N	108 51.7723 W	3-6	NA	10.99	3.8765	45.1196
FK181031-11739	S0193	PC2	<i>Auka</i>	Matterhorn	3657.85	23 57.22692 N	108 51.7723 W	6-9	NA	10.99	4.635	41.8845
FK181031-11740	S0193	PC2	<i>Auka</i>	Matterhorn	3657.85	23 57.22692 N	108 51.7723 W	9-12	NA	10.99	4.5982	38.0263
FK181031-11714	S0193	PC3	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	3-6	NA	NA	NA	NA
FK181031-11715	S0193	PC3	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	6-9	NA	NA	NA	NA
FK181031-11716	S0193	PC3	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	9-12	NA	NA	NA	NA
FK181031-11713	S0193	PC3	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	0-3	NA	NA	NA	NA
FK181031-11713mat	S0193	PC3	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	Mat	NA	NA	NA	NA
FK181031-11710	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	9-12	NA	NA	3.5134	41.1848
FK181031-11711	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	12-5	NA	NA	2.581	30.2564

FK181031-11703	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	0-1	NA	NA	1.4723	48.2874
FK181031-11704	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	1-2	NA	NA	2.6566	43.0137
FK181031-11705	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	2-3	NA	NA	3.0836	42.234
FK181031-11706	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	3-4	NA	NA	2.6713	35.6576
FK181031-11707	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	4-5	NA	NA	3.12	42.6345
FK181031-11708	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	5-6	NA	NA	2.5289	41.8211
FK181031-11709	S0193	PC5	<i>Auka</i>	Diane's vent	3656.64	23 57.28961 N	108 51.78176 W	6-9	NA	NA	3.539	41.381
FK181031-11721	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	0-1	NA	NA	0.4534	50.203
FK181031-11722	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	1-2	NA	NA	0.756	57.9441
FK181031-11723	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	2-3	NA	NA	1.2917	53.677
FK181031-11724	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	3-4	NA	NA	1.7577	51.5911
FK181031-11725	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	4-5	NA	NA	2.6146	43.7716
FK181031-11726	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	5-6	NA	NA	3.7169	37.9884
FK181031-11727	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	6-9	NA	NA	2.873	41.3041
FK181031-11728	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	9-12	NA	NA	4.2429	37.1396
FK181031-11729	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	12-15	NA	NA	4.1996	37.2565
FK181031-11730	S0193	PC7	<i>Auka</i>	Diane's vent	3656.7	23 57.29105 N	108 51.78176 W	15-18	NA	NA	4.2224	37.3546
FK181031-11772	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	0-1	NA	NA	0.8762	56.4273
FK181031-11773	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	1-2	NA	NA	3.1127	56.8865
FK181031-11774	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	2-3	NA	NA	2.1942	47.888

FK181031-11775	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	3-4	NA	NA	3.8498	46.4467
FK181031-11776	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	4-5	NA	NA	5.0597	38.3971
FK181031-11777	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	5-8	NA	NA	6.5252	30.7198
FK181031-11778	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	8-11	NA	NA	8.5878	22.2461
FK181031-11779	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	11-14	NA	NA	9.7592	17.1903
FK181031-11772mat	S0194	PC0	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	Mat	NA	NA	NA	NA
FK181031-11770	S0194	PC1	<i>Auka</i>	Diane's vent	3659.14	23 57.27891 N	108 51.7946 W	0-3	54.78	112.2	1.4611	50.0851
FK181031-11771	S0194	PC1	<i>Auka</i>	Diane's vent	3659.14	23 57.27891 N	108 51.7946 W	3-6	54.78	112.2	2.3595	46.8343
FK181031-11780	S0194	PC2	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	0-3	NA	NA	NA	NA
FK181031-11783	S0194	PC2	<i>Auka</i>	North of Z vent	3685.44	23 57.42174 N	108 51.7309 W	9-12	NA	NA	NA	NA
FK181031-11760	S0194	PC3	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	0-3	NA	NA	NA	NA
FK181031-11763	S0194	PC3	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	9-12	NA	NA	NA	NA
FK181031-11750	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	5-8	NA	NA	3.333	47.5503
FK181031-11752	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	11-14	NA	NA	3.2083	45.5676
FK181031-11745	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	0-1	NA	NA	1.8261	53.0332
FK181031-11746	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	1-2	NA	NA	2.3603	50.2191
FK181031-11747	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	2-3	NA	NA	2.9229	50.8802
FK181031-11748	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	3-4	NA	NA	3.004	45.9738
FK181031-11749	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	4-5	NA	NA	3.1282	47.7527
FK181031-11751	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	8-11	NA	NA	2.9662	44.9723

FK181031-11753	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	14-17	NA	NA	3.1821	44.6916
FK181031-11745mat	S0194	PC4	<i>Auka</i>	North of Z vent	3677.99	23 57.41007 N	108 51.76061 W	Mat	NA	NA	NA	NA
FK181031-11835	S0196	PC1	<i>Auka</i>	South of Z vent	3687.52	23 57.36971 N	108 51.71488 W	3-6	NA	NA	NA	NA
FK181031-11836	S0196	PC1	<i>Auka</i>	South of Z vent	3687.52	23 57.36971 N	108 51.71488 W	6-9	NA	NA	NA	NA
FK181031-11837	S0196	PC1	<i>Auka</i>	South of Z vent	3687.52	23 57.36971 N	108 51.71488 W	9-12	NA	NA	NA	NA
FK181031-11838	S0196	PC1	<i>Auka</i>	South of Z vent	3687.52	23 57.36971 N	108 51.71488 W	12-15	NA	NA	NA	NA
FK181031-11834	S0196	PC1	<i>Auka</i>	South of Z vent	3687.52	23 57.36971 N	108 51.71488 W	0-3	NA	NA	NA	NA
FK181031-11834mat	S0196	PC1	<i>Auka</i>	South of Z vent	3687.52	23 57.36971 N	108 51.71488 W	Mat	NA	NA	NA	NA
FK181031-11854	S0196	PC3	<i>Auka</i>	South of Z vent	3687.68	23 57.37023 N	108 51.715 W	0-3	NA	NA	NA	NA
FK181031-11857	S0196	PC3	<i>Auka</i>	South of Z vent	3687.68	23 57.37023 N	108 51.715 W	9-12	NA	NA	NA	NA
FK181031-11851	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	11-14	50	93	10.3447	15.7879
FK181031-11852	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	14-17	50	93	10.8905	12.0873
FK181031-11849	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	5-8	50	93	7.6707	34.1424
FK181031-11850	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	8-11	50	93	10.7032	18.0026
FK181031-11844	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	0-1	50	93	5.9716	39.1882
FK181031-11845	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	1-2	50	93	6.2443	38.3399
FK181031-11846	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	2-3	50	93	7.4995	33.178
FK181031-11847	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	3-4	50	93	7.9596	32.1619
FK181031-11848	S0196	PC5	<i>Auka</i>	South of Z vent	3687.68	23 57 37005 N	108 51.71369 W	4-5	50	93	6.9597	37.9314
FK181031-11811	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	0-1	19	22.6	3.6546	42.7971

FK181031-11812	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	1-2	19	22.6	4.5173	38.7628
FK181031-11813	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	2-3	19	22.6	6.5867	31.129
FK181031-11814	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	3-4	19	22.6	12.3082	14.5281
FK181031-11815	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	4-5	19	22.6	14.3784	8.9332
FK181031-11816	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	5-8	19	22.6	14.7845	8.3101
FK181031-11817	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	8-11	19	22.6	15.6545	4.2604
FK181031-11818	S0196	PC6	<i>Auka</i>	South of Z vent	3687.76	23 57.37072 N	108 51.71493 W	11-14	19	22.6	15.0011	6.5312
FK181031-11805	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	3-4	103	128	8.2054	30.9389
FK181031-11806	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	4-5	103	128	8.8889	29.855
FK181031-11807	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	5-8	103	128	10.2224	16.6325
FK181031-11808	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	8-11	103	128	11.1329	10.7334
FK181031-11809	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	11-14	103	128	11.7773	2.2881
FK181031-11810	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	14-17	103	128	12.5022	1.0838
FK181031-11802	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	0-1	103	128	5.6337	40.5307
FK181031-11803	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	1-2	103	128	8.4312	26.1534
FK181031-11804	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	2-3	103	128	8.163	31.6062
FK181031-11800	S0196	PC7	<i>Auka</i>	South of Z vent	3687.33	23 57.37 N	108 51.71424 W	Mat	NA	NA	NA	NA
FK181031-11840	S0196	PC8	<i>Auka</i>	South of Z vent	3687.46	23 57.3706 N	108 51.71501 W	3-6	50	93	NA	NA
FK181031-11841	S0196	PC8	<i>Auka</i>	South of Z vent	3687.46	23 57.3706 N	108 51.71501 W	6-9	50	93	NA	NA
FK181031-11842	S0196	PC8	<i>Auka</i>	South of Z vent	3687.46	23 57.3706 N	108 51.71501 W	9-12	50	93	NA	NA

FK181031-11843	S0196	PC8	<i>Auka</i>	South of Z vent	3687.46	23 57.3706 N	108 51.71501 W	12-15	50	93	NA	NA
FK181031-11839	S0196	PC8	<i>Auka</i>	South of Z vent	3687.46	23 57.3706 N	108 51.71501 W	0-3	50	93	NA	NA
FK181031-11948	S0198	NA	<i>Auka</i>	South of Z vent	3666.17	23 57.39595 N	108 51.70841 W	Mat	NA	NA	NA	NA
FK181031-11933	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	17-20	21.4	24.9	NA	NA
FK181031-11924	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	0-1	21.4	24.9	0.1385	56.9682
FK181031-11925	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	1-2	21.4	24.9	NA	NA
FK181031-11926	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	2-3	21.4	24.9	0.1352	58.907
FK181031-11927	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	3-4	21.4	24.9	NA	NA
FK181031-11928	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	4-5	21.4	24.9	NA	NA
FK181031-11929	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	5-8	21.4	24.9	1.1413	56.654
FK181031-11930	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	8-11	21.4	24.9	2.9649	49.9752
FK181031-11931	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	11-14	21.4	24.9	3.2898	50.4854
FK181031-11932	S0198	PC1	<i>Auka</i>	South of Z vent	3690.21	23 57.37079 N	108 51.70725 W	14-17	21.4	24.9	4.0264	47.7039
FK181031-11922	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	14-17	NA	NA	10.0888	22.7952
FK181031-11914	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	0-1	NA	NA	2.0036	50.6721
FK181031-11915	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	1-2	NA	NA	NA	NA
FK181031-11916	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	2-3	NA	NA	3.4538	45.9755
FK181031-11917	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	3-4	NA	NA	NA	NA
FK181031-11918	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	4-5	NA	NA	NA	NA
FK181031-11919	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	5-8	NA	NA	6.5773	34.6274

FK181031-11920	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	8-11	NA	NA	7.0172	39.8369
FK181031-11921	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	11-14	NA	NA	8.6128	29.5539
FK181031-11923	S0198	PC3	<i>Auka</i>	South of Z vent	3689.98	23 57.37054 N	108 51.70713 W	17-20	NA	NA	10.3232	19.743
FK181031-11934	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	0-1	21.4	24.9	0.2612	57.4314
FK181031-11935	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	1-2	21.4	24.9	NA	NA
FK181031-11936	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	2-3	21.4	24.9	0.5914	57.1264
FK181031-11937	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	3-4	21.4	24.9	NA	NA
FK181031-11938	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	4-5	21.4	24.9	NA	NA
FK181031-11939	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	5-8	21.4	24.9	2.5137	50.7974
FK181031-11940	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	8-11	21.4	24.9	4.5266	40.7956
FK181031-11941	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	11-14	21.4	24.9	7.5745	29.1479
FK181031-11942	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	14-17	21.4	24.9	8.3713	26.8493
FK181031-11943	S0198	PC5	<i>Auka</i>	South of Z vent	3690.05	23 57.37097 N	108 51.70713 W	17-20	21.4	24.9	8.7063	26.9408
FK181031-12013	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	4-5	30	46.3	12.6383	11.8639
FK181031-12014	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	5-8	30	46.3	12.807	10.7743
FK181031-12015	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	8-11	30	46.3	13.1089	8.9304
FK181031-12016	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	11-14	30	46.3	13.6106	6.9823
FK181031-12017	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	14-17	30	46.3	14.2131	4.1149
FK181031-12009	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	0-1	30	46.3	8.9946	27.534
FK181031-12010	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	1-2	30	46.3	10.6699	22.1092

FK181031-12011	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	2-3	30	46.3	11.6455	18.6946
FK181031-12012	S0200	PC1	<i>Auka</i>	South of Z vent	3688.8	23 57.36615 N	108 51.71425 W	3-4	30	46.3	11.4881	15.686
FK181031-12043	S0200	PC3	<i>Auka</i>	South of Z vent	3688.19	23 57.36481 N	108 51.71433 W	whole core	NA	NA	NA	NA
FK181031-12033	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	1-2	NA	NA	7.2438	27.2236
FK181031-12034	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	2-3	NA	NA	8.0083	23.7795
FK181031-12035	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	3-4	NA	NA	7.6878	23.3997
FK181031-12036	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	4-5	NA	NA	9.039	17.1407
FK181031-12037	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	5-8	NA	NA	10.1362	12.9539
FK181031-12038	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	8-11	NA	NA	12.0821	5.9492
FK181031-12039	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	11-14	NA	NA	13.0468	4.4327
FK181031-12040	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	14-17	NA	NA	13.0842	4.9889
FK181031-12032	S0200	PC5	<i>Auka</i>	South of Z vent	3688.54	23 57.36714 N	108 51.71438 W	0-1	NA	NA	5.8616	33.6443
FK181031-12026	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	3-6	30	46.3	NA	NA
FK181031-12027	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	6-9	30	46.3	NA	NA
FK181031-12028	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	9-12	30	46.3	NA	NA
FK181031-12029	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	12-15	30	46.3	NA	NA
FK181031-12030	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	15-18	30	46.3	NA	NA
FK181031-12031	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	18-21	30	46.3	NA	NA
FK181031-12025	S0200	PC7	<i>Auka</i>	South of Z vent	3688.82	23 57.36632 N	108 51.7136 W	0-3	30	46.3	NA	NA
FK181031-11785	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	0-3	NA	NA	0.073	56.6484

FK181031-11786	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	3-6	NA	NA	0.0739	56.1911
FK181031-11787	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	6-9	NA	NA	0.067	57.0465
FK181031-11788	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	9-12	NA	NA	0.062	55.8452
FK181031-11789	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	12-15	NA	NA	0.0718	57.1839
FK181031-11790	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	mat on surface	NA	NA	NA	NA
FK181031-11791	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	15-18	NA	NA	0.0926	51.2366
FK181031-11792	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	18-21	NA	NA	0.1188	57.9119
FK181031-11793	S0195	PC1	<i>Juwak Yuum</i>	<i>Juwak Yuum</i>	3712.09	23 56.95389 N	108 51.20008 W	21-24	NA	NA	0.1139	57.171
FK181031-11859	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	0-1	NA	20.8	4.2963	42.3496
FK181031-11860	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	1-2	NA	20.8	4.4464	42.2045
FK181031-11861	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	2-3	NA	20.8	4.6344	41.5421
FK181031-11862	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	3-4	NA	20.8	4.8055	40.7443
FK181031-11863	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	4-5	NA	20.8	5.7464	38.6876
FK181031-11864	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	5-8	NA	20.8	8.291	28.7666
FK181031-11865	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	8-11	NA	20.8	10.0475	21.8305
FK181031-11866	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	11-14	NA	20.8	10.2942	21.491
FK181031-11867	S0197	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.74	23 56.54133 N	108 51.34949 W	14-17	NA	20.8	9.7605	22.1977
FK181031-11889	S0197	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54328 N	108 51.34193 W	0-3	NA	NA	0.075	57.0609
FK181031-11890	S0197	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54328 N	108 51.34193 W	3-6	NA	NA	0.0661	56.3494
FK181031-11891	S0197	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54328 N	108 51.34193 W	6-9	NA	NA	0.1154	56.8057

FK181031-11892	S0197	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54328 N	108 51.34193 W	9-12	NA	NA	0.2633	56.5234
FK181031-11893	S0197	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54328 N	108 51.34193 W	12-15	NA	NA	1.396	55.0728
FK181031-11895	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	0-3	NA	NA	NA	NA
FK181031-11896	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	3-6	NA	NA	NA	NA
FK181031-11897	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	6-9	NA	NA	NA	NA
FK181031-11898	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	9-12	NA	NA	NA	NA
FK181031-11899	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	12-15	NA	NA	NA	NA
FK181031-11900	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	15-18	NA	NA	NA	NA
FK181031-11901	S0197	PC3	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.34	23 56.54178 N	108 51.35008 W	18-21	NA	NA	NA	NA
FK181031-11902	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	0-1	47	83.7	3.8253	43.9454
FK181031-11903	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	1-2	47	83.7	4.3967	41.4823
FK181031-11904	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	2-3	47	83.7	5.0759	38.5645
FK181031-11905	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	3-4	47	83.7	5.3631	36.4296
FK181031-11906	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	4-5	47	83.7	5.3232	38.8964
FK181031-11907	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	5-8	47	83.7	6.8306	32.5536
FK181031-11908	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	8-11	47	83.7	7.4741	28.8253
FK181031-11909	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	11-14	47	83.7	8.0345	25.7129
FK181031-11910	S0197	PC6	<i>JaichMaa 'ja 'ag</i>	<i>Abuelita</i>	3692.42	23 56.54133 N	108 51.35133 W	14-17	47	83.7	8.4242	26.4871
FK181031-11956-mat	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	Mat	38	86	1.6465	56.8501
FK181031-11956	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	0-1	NA	NA	NA	NA

FK181031-11957	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	1-2	38	86	2.5108	52.6799
FK181031-11958	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	2-3	38	86	2.8838	50.6143
FK181031-11959	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	3-4	38	86	3.2249	49.2005
FK181031-11960	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	4-5	38	86	3.8732	45.8388
FK181031-11961	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	5-8	38	86	5.3464	38.5537
FK181031-11962	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	8-11	38	86	6.06	35.1189
FK181031-11963	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	11-14	38	86	6.0186	35.9127
FK181031-11964	S0199	PC7	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46168 N	108 51.34399 W	14-17	38	86	6.116	35.71
FK181031-11966	S0199	PC4	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46304 N	108 51.34308 W	0-3	NA	NA	NA	NA
FK181031-11967	S0199	PC4	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46304 N	108 51.34308 W	3-6	NA	NA	NA	NA
FK181031-11968	S0199	PC4	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46304 N	108 51.34308 W	6-9	NA	NA	NA	NA
FK181031-11969	S0199	PC4	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.71	23 56.46304 N	108 51.34308 W	9-12	NA	NA	NA	NA
FK181031-11981	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	0-1	63.3	79.3	2.8047	47.3266
FK181031-11982	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	1-2	63.3	79.3	4.4289	41.3215
FK181031-11983	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	2-3	63.3	79.3	5.3573	39.0319
FK181031-11984	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	3-4	63.3	79.3	5.9596	37.3381
FK181031-11985	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	4-5	63.3	79.3	5.8511	37.4721
FK181031-11986	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	5-8	63.3	79.3	6.0799	36.247
FK181031-11987	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	8-11	63.3	79.3	6.0086	36.3943
FK181031-11988	S0199	PC5	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3685.86	23 56.46009 N	108 51.34167 W	11-14	63.3	79.3	6.0729	35.5012

FK181031-11991	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	0-1	28.1	53	0.103	58.8598
FK181031-11992	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	1-2	28.1	53	0.2695	58.6971
FK181031-11993	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	2-3	28.1	53	0.4433	58.9689
FK181031-11994	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	3-4	28.1	53	0.9665	63.7231
FK181031-11995	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	4-5	28.1	53	2.4118	51.3183
FK181031-11996	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	5-8	28.1	53	3.0318	50.9073
FK181031-11997	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	8-11	28.1	53	4.5529	44.8807
FK181031-11998	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	11-14	28.1	53	5.3261	38.2548
FK181031-11999	S0199	PC1	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.52	23 56.46498 N	108 51.34608 W	14-17	28.1	53	5.8813	35.4803
FK181031-12001	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	0-3	28.1	53	NA	NA
FK181031-12002	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	3-6	28.1	53	NA	NA
FK181031-12003	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	6-9	28.1	53	NA	NA
FK181031-12004	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	9-12	28.1	53	NA	NA
FK181031-12005	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	12-15	28.1	53	NA	NA
FK181031-12006	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	15-18	28.1	53	NA	NA
FK181031-12007	S0199	PC2	<i>JaichMaa 'ja 'ag</i>	<i>Tay Ujaa and Weey 'kual</i>	3686.64	23 56.4574 N	108 51.33828 W	18-20	28.1	53	NA	NA