

SUPPORTING INFORMATION APPENDIX 1A: Extended Figures

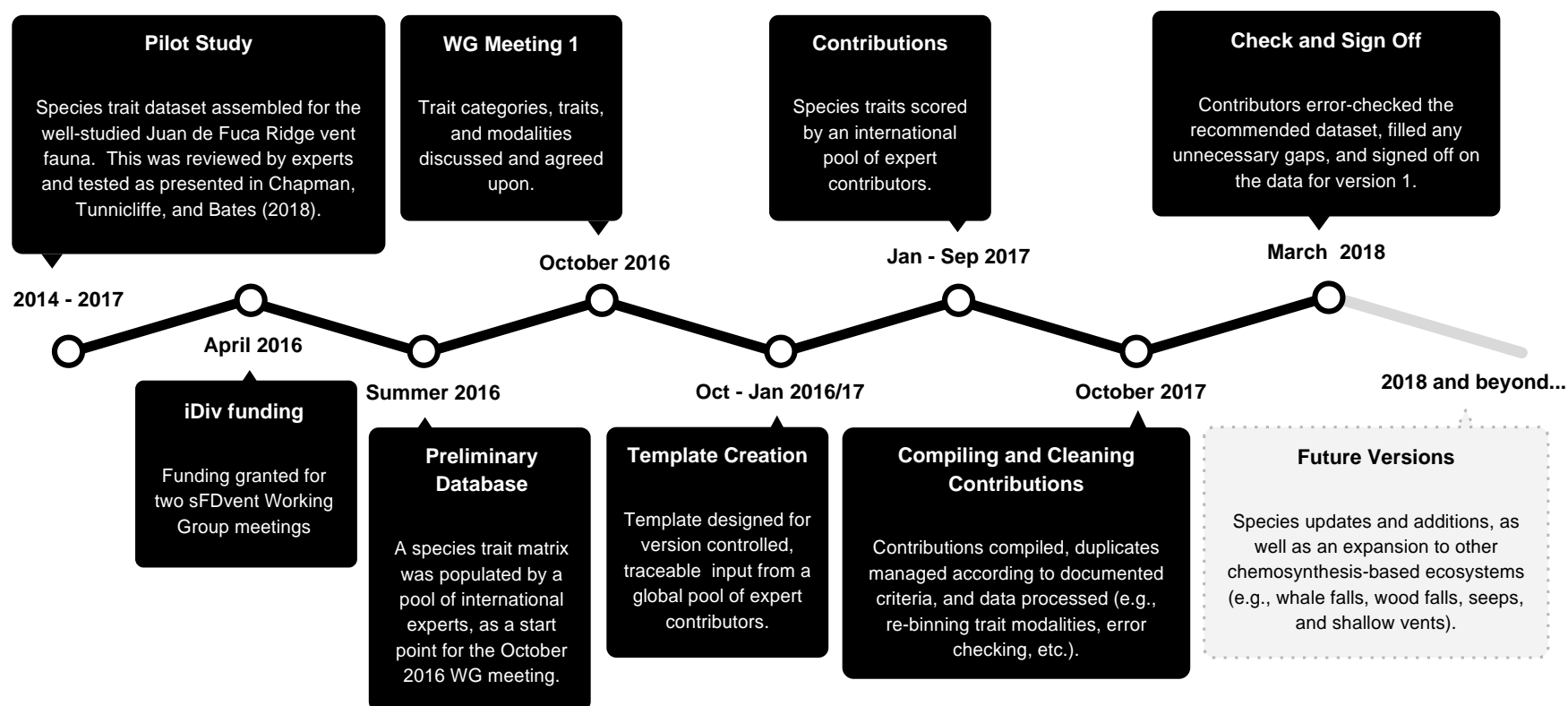


Figure S1A.1: Overview of the workflow undertaken to build the sFDvent database. The sFDvent working group (WG) was funded by the German Centre for Integrative Biodiversity Research (iDiv) under the Synthesis Centre for Biodiversity Studies (sDiv) (<https://www.idiv.de/sdiv.html>). The database – ‘sFDvent’ – is therefore named with an ‘s’ to highlight that it is a product of sDiv. ‘FDvent’ is an abbreviation of ‘functional diversity of vents’, which the sFDvent database can be used to study. This name may be updated for future versions, when other chemosynthesis-based ecosystems are added.

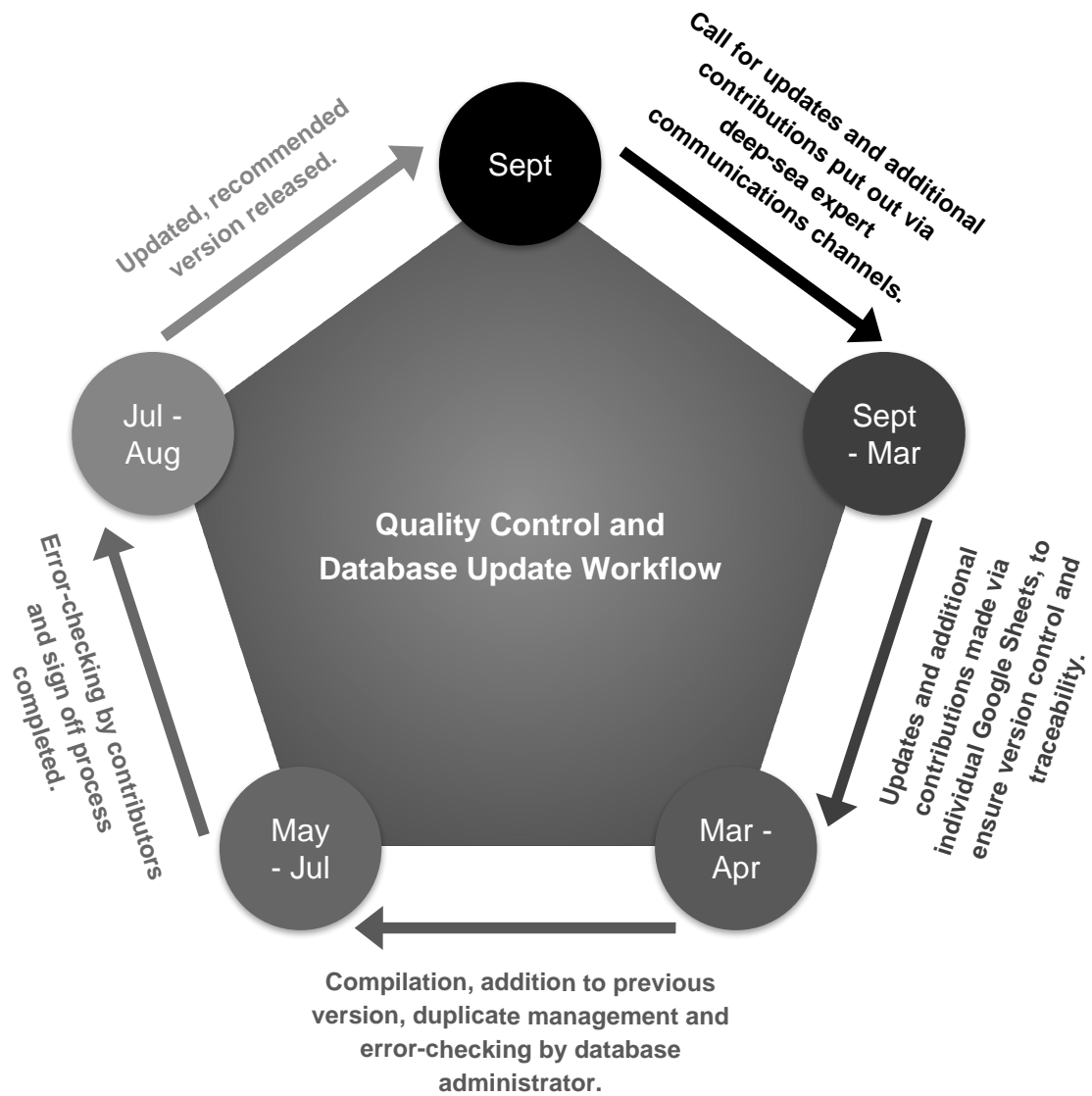
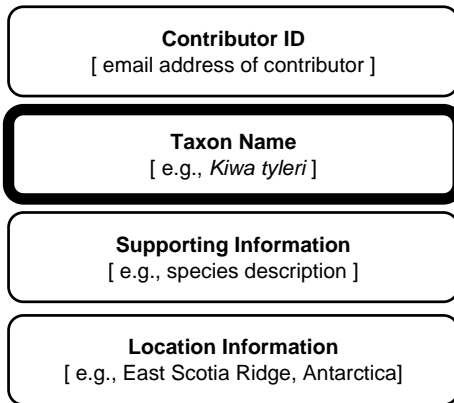
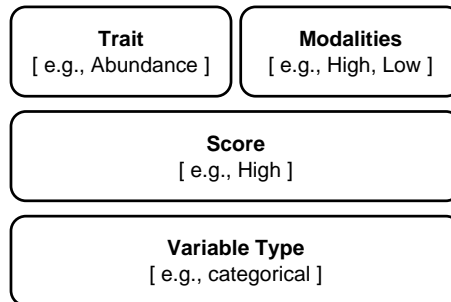


Figure S1A.2: Proposed quality control and update release workflow for future versions of the sFDvent database. The cycle would begin every 4 years to enable a new version to be released every 5 years. This cycle illustrates the process that would take place over the course of the year. The process could begin to include species from other chemosynthesis-based ecosystems from version 2 onwards, though it is recommended that species would then be given an associated record to highlight the ecosystem(s) they are found in, to ensure that those wanting to focus on a specific ecosystem could filter the database. Further information on how to contribute to future versions of the sFDvent database is provided in Appendix S5.

a) METADATA



b) TRAIT DATA



c) LINKING TO OTHER DATASETS

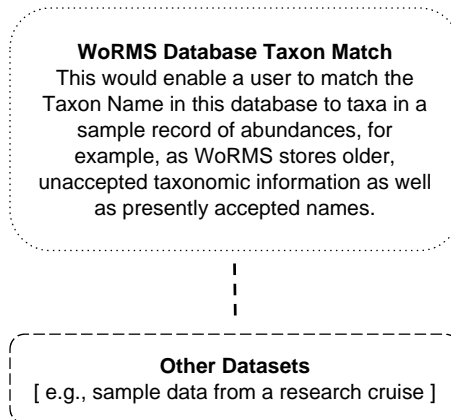


Figure S1A.3: Overview of the sFDvent database design. Example information is given in square brackets beneath each database component. Taxon Name is shown with a darker outline because it is the component used to link datasets (as highlighted by the dashed line connectors). WoRMS Database Taxon Match has a dotted outline because it is a process a user could undertake to join the sFDvent database information with other datasets (for example, presence-absence data, abundances, and cruise report sample logs). Other Datasets has a dashed outline because these data are external to the sFDvent database.

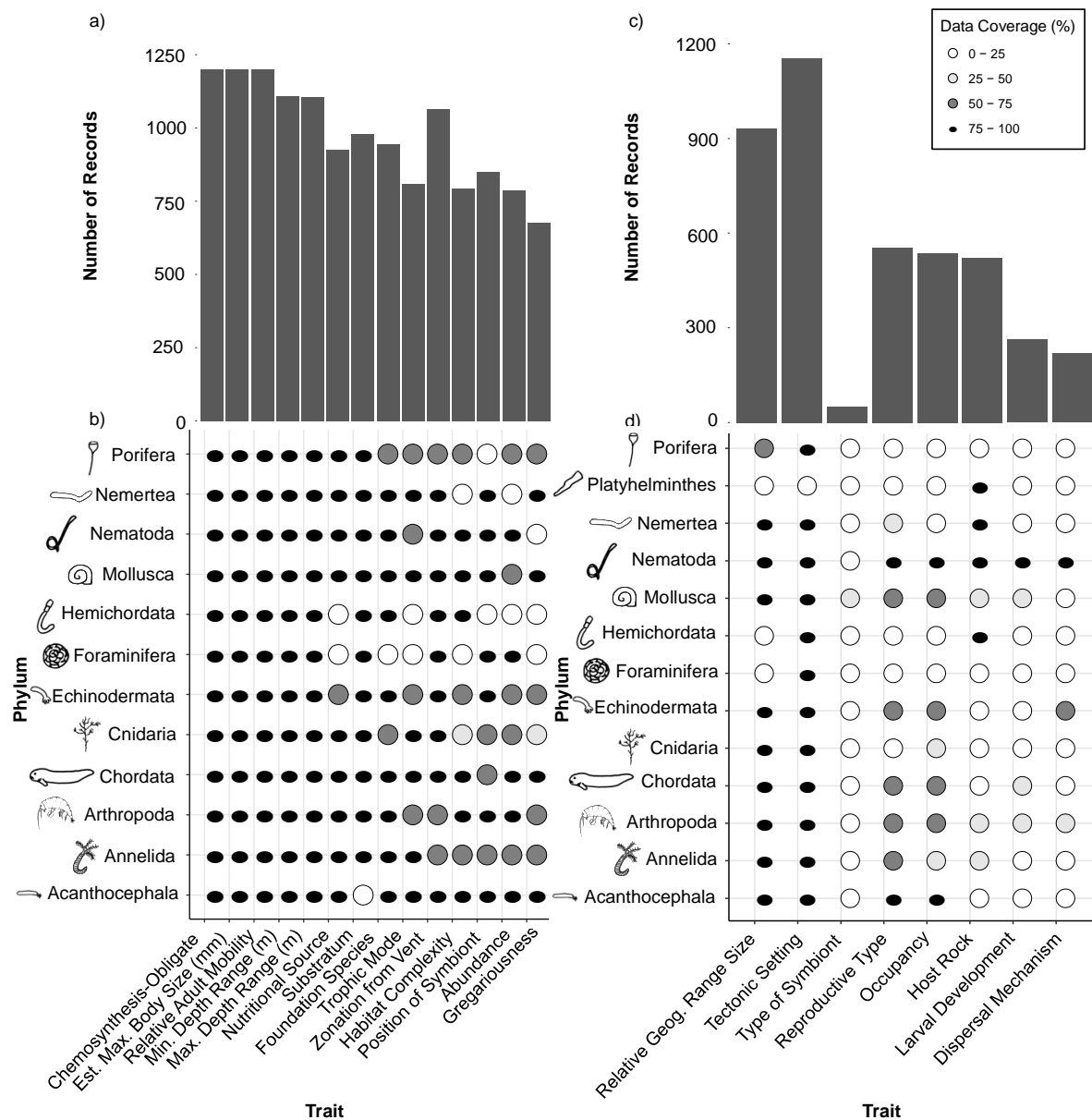


Figure S1A.4: Data coverage with respect to trait (a, c) and phylum (b, d). The figure concept was developed from Brun et al. (2017) to depict the relative coverage per phylum for each trait using a dotplot (b, d) and to give an overview of the number of records per trait in a bar chart (a, c). This figure is therefore split into panels according to dataset ('Recommended', Table S4.2, vs. 'Clean Binned', Table S4.4) and measure (trait records vs. taxonomic records). Note that the 'Data Coverage' legend applies to panels (b) and (d). Panels (a) and (b) represent the coverage for the recommended dataset. Panels (c) and (d) include data from the 'Clean Binned' file described in Table S4.5 and therefore include data that may need further cleaning, but demonstrate which traits removed from the recommended dataset have relatively high coverage for a given phylum. Some traits have been abbreviated for display purposes as follows: 'Est. Max. Body Size (mm)' – Estimated Maximum Body Size (millimetres); 'Min. Depth Range (m)' – Minimum Depth Range (metres); 'Max. Depth Range (m)' – Maximum Depth Range (metres); and 'Relative Geog. Range Size' – Relative Geographic Range Size.

SUPPORTING INFORMATION APPENDIX 2: Scopus Search Information

i) Scopus search referenced in the Introduction:

Scopus search: 'trait' AND 'database' in agricultural, biological, environmental, and earth sciences.

Results: 53 titles published since 2000, which were then manually filtered for relevance, to ensure they were describing trait databases being released, resulting in 25 records, 6 of which were published in 2017.

An Excel file (Table S2.1) containing the exported records is provided for reference.

ii) Scopus search referenced in the Discussion:

Scopus search 1: 'hydrothermal vent' AND 'annelid' OR 'worm' OR 'polychaete'

Search 1 results: 602 records

Scopus search 2: 'hydrothermal vent' AND 'mollusc' OR 'mollusk' OR 'snail' OR 'gastropod' OR 'bivalve' OR 'clam' OR 'mussel' OR 'limpet' OR 'whelk'.

Search 2 results: 900 records

Scopus search 3: 'hydrothermal vent' AND 'arthropod' OR 'amphipod' OR 'decapod' OR 'shrimp' OR 'copepod'.

Search 3 results: 369 records

Scopus search 4: 'hydrothermal vent' AND 'Pacific'.

Search 4 results: 1947 records

Scopus search 5: 'hydrothermal vent' AND 'Atlantic'.

Search 5 results: 1103 records

Scopus search 6: 'hydrothermal vent' AND 'Indian Ocean'

Search 6 results: 202 records

Scopus search 7: 'hydrothermal vent' AND 'East Pacific'

Search 7 results: 855 records

Scopus search 8: 'hydrothermal vent' AND 'West Pacific'

Search 8 results: 119 records

SUPPORTING INFORMATION APPENDIX 3: Summary of Decisions Made by the sFDvent Working Group During Database Design and Testing

Defining 'trait':

Our working group decided to focus on species traits (e.g., trophic level, maximum body size, etc.), rather than individual traits capturing variation within species and populations, given the availability of information regarding populations of vent species.

Trait selection:

Looking to existing databases to ensure cross-ecosystem compatibility with sFDvent, we suggested the following traits (within categories, as underlined), before reducing these in number to those which could be scored for many of the species across the globe, given the current state of knowledge for vent species:

Ecosystem Engineer:

- Foundation species (note that the group deemed this to be a binary – yes or no – trait scored according to whether a species provided a physical structure from which other species could benefit).
- Early coloniser (i.e., whether a species is present at an early successional stage)
- Habitat builder (capturing habitat complexity as a shape descriptor)
- Host / guest (in terms of symbiosis)
- Body form

Species Associations / Interaction Strengths:

- Using other organisms as a substratum (yes or no)
- Strong species dependency? (yes/no with host/guest also described)

Biogeography / Geographic Distribution:

- Geographic range size (latitudes and longitudes)
- Patchiness or occupancy
- Depth (e.g., vertical range size)

Generalist / Specialist:

- Basalt or sulfide (rock type most commonly occupied)

Habitat Use:

- Gregariousness (or 'aggregated' with yes or no)
- Substratum (soft or hard, basalt or sulphide)
- Zonation (e.g., at and/or from a vent chimney)

Adult Mobility:

- Mobility, captured as per Faulwetter et al. (2017): sessile/mobile, crawler, burrower, swimmer, non-motile or semi-motile, zoochory

Trophic Structure:

- Trophic level
- Feeding mode (capturing the 'messiness' of feeding and, thus, whether a species enables access to food by other organisms)
- Food source / nutritional supply (origin of the food – e.g., water column and therefore possibly the sea surface, or at depth)

Morphology:

- Maximum body size
- Maximum possible abundance / biomass / dominance achieved (or an estimator of the relative abundance curve for a species)

Life History:

- Life span (1, 10, 100)
- r- or K- selected ("weediness")
- Larval dispersal and other reproductive traits

Energy / Holobiont:

- Type of symbiont
- Source
- Location of symbiont
- Type of bacteria
- Transmission

Physiology:

- Fundamental temperature range

Parasite Host:

- Parasite host (yes or no)

Refinements after testing:

Our working group tested the trait database design to determine whether the traits, modalities, and setup worked well when scoring using Google Sheets (selected to facilitate population by collaborators from institutes across the globe). We deem the following features important for the user-friendly setup of a trait database, to encourage scoring:

- Column order (i.e. a database should be set up with the traits that are easiest to score to the left, progressing to the hardest on the right, to encourage contributions).
- Ranges should be given as numbers (e.g., for relative adult mobility, scores ranged from 1 for sessile to 4 for the most mobile).
- References should be required for each score, to ensure that every score has a traceable origin (even if the origin is 'expert opinion'). Ideally, these should be provided in a consistent format (e.g., entered into a spreadsheet like that provided in Table S1.1 and then cross-referenced using an identifier).
- Fixed, drop-down options should be given to ensure quality and consistency of entries.
- The taxon names should be 'frozen', to enable the user to view the taxon at all times when scoring.
- A certainty score of '0' should be allowed, to ensure that lack of knowledge is captured in these cells, as blank cells could otherwise represent: i) lack of knowledge, or ii) a missed entry.

SUPPORTING INFORMATION APPENDIX 4: sFDvent Data Files

Appendix S4 describes Supporting Tables S4.1, S4.2, S4.3, S4.4, and S4.5, which are separate Excel files which will be accessible via Digital Object Identifiers (DOIs). A tutorial video (Supporting Video S4.1) is also described here but provided as a separate .mov file. References cited in all files are provided in Appendix S1 and Table S1.1.

Video S4.1 is a copy of a narrated tutorial sent to all contributors as part of the online, personalised Google Sheets populated to create Table S4.3. This video could be used as a guide by future contributors to the database. It is accessible via 10.5061/dryad.cn2rv96.

Table S4.2 is the processed, 'ready-to-use' dataset that we recommend for use and refer to for coverage and certainty values, etc. in the main manuscript. It is accessible via 10.5061/dryad.cn2rv96. We would recommend that users always check the data are processed in line with criteria and thresholds appropriate for their research question and/or analytical approach and make adjustments where required, as no dataset will be fit for all purposes. Nevertheless, to ensure the recommended dataset is as user-friendly and 'ready-to-use' as possible, we only include traits in this version of the dataset that meet thresholds for certainty and coverage, with more than 50% of species scored and/or an average certainty score of more than 2.3. References have been assigned numeric identifiers, which can be matched to the references provided in Table S1.1. If more than one reference is provided to support a score, the reference identifiers are separated by a semi-colon (;). 'Taxon' refers to the taxonomic identity assigned by contributors, while 'UniqueID' is an identifier created using letters from the taxon and the entry number, to make it easier to work with the data and reference a taxon. A glossary to support the traits and modalities given in Table S4.2 is provided in Table S4.1 (10.5061/dryad.cn2rv96).

Table S4.3 is a copy of raw data contributions, compiled from the personalised files sent to each sFDvent contributor. This version of the dataset will be provided for transparency and as metadata for users wanting to refer to raw contributions and/or data provided by specific contributors via 10.5061/dryad.cn2rv96. This dataset includes traits that were removed from the error-checked, quality-controlled dataset due to lack of coverage and would require appropriate processing for each user's research question before it could be used in an analysis. A glossary to support the traits and modalities given in Table S4.3 is provided in Table S4.1 (10.5061/dryad.cn2rv96).

Table S4.4 is a cleaned version of Table S4.3, processed according to the decision rules documented in **Table S4.5** (10.5061/dryad.cn2rv96). This version of the dataset will, again, be provided for transparency and additional supporting metadata via 10.5061/dryad.cn2rv96. It would likely need further processing before use in an analysis. Table S4.5 also outlines the processing steps undertaken to take the raw data file (Table S4.3) to the file that was sent to all contributors to conduct final error-checks on. Here, we provide a summary of the level of processing associated with each file:

1. First, individual contributor sheets were joined together manually, as the number of columns per trait differed in each sheet because contributors could provide more than one score per trait per species. These data form the **raw database (Table S4.3; 10.5061/dryad.cn2rv96)**.

2. Next, empty columns, NAs, and other missing data descriptors (e.g., -) were removed, before duplicates were identified and managed as documented in Table S4.5. The names of taxa were then checked using the 'Match taxa' WoRMS database tool (Horton et al., 2017). Any taxa that were not identified to species level and could not be traced to a taxonomist by observed location or literary source were then removed, to avoid artificial inflation of diversity in analyses conducted using the database. The average certainty score and percentage of scored species were then calculated for each trait. Traits with fewer than 50% of species scored and/or an average certainty score below 2.3 were removed. These data form the **clean binned dataset (Table S4.4; 10.5061/dryad.cn2rv96)**.
3. Consequently, these data were copied into a Google Sheet document shared with all contributors for error-checking and final gap filling. These clean, checked data form the **recommended dataset in Table S4.2** (10.5061/dryad.cn2rv96) and thus represent data approved by expert deep-sea researchers and the state of knowledge on vent species traits across the globe. Table 1 summarises traits, modalities (or scoring options), and associated rationale.
4. This dataset can be linked with location information (also provided by deep-sea expert contributors) and other, well-known databases as shown in Figure S1A.3. Location Information provided with Table S4.2 contains symbols and will therefore need to be further processed by those wanting to use these data as part of analyses (see further details below). Alternatively, users can remove this column and use the remaining data in their presented form.

Tables S4.2 and S4.4 also contain **location information** for the species in the sFDvent database. This was collected as ancillary data; it therefore has not been standardised and may not represent the full extent of current knowledge. It requires further processing before it can be used in an analysis. However, there has not yet been a single repository for data on vent species distributions. Instead, there are separate sources of information, such as: ChEssBase – geo- and literary-referenced species lists for fauna from chemosynthesis-based ecosystems, now accessible using OBIS – the Ocean Biogeographic Information System (Baker, Ramirez-Llodra, & Perry, 2010; OBIS, 2017); the InterRidge Vents Database, comprising a list of hydrothermal vent field locations and ancillary data (Beaulieu, 2015); species presence data available in the Supplementary Data supporting Bachraty, Legendre, & Desbruyères (2009); and information published in the renowned Handbook on Deep-sea Hydrothermal Vent Fauna produced by Desbruyères, Segonzac, & Bright (2006) (though note that this book also includes non-vent fauna observed in the periphery of vent fields). To begin to resolve this, location information was compiled to meet a wider sFDvent working group aim using Desbruyères, Segonzac, & Bright (2006) and expert knowledge. It can be linked to each taxon using the 'Taxon' column and any name updates that can be traced using the AphiaID for the taxon. The location information, however, varies in spatial scale due to disparities in data availability on species observations across the globe. Hence, for the spatial coverage data presented in this paper, we re-classified location information into i) ocean, and ii) region, controlled vocabularies as per the InterRidge Vents Database (Beaulieu, 2015; e.g., Figure 1). In addition, the taxa presented in sFDvent have been checked using the WoRMS 'Match Taxa' function (Horton et al., 2017), to ensure sFDvent taxonomy is up-to-date (and associated 'AphiaIDs' are provided in Table S4.2 for the highest taxonomic level possible). As we are launching sFDvent more than eight years after version 3 of ChEssBase was released (Baker et al., 2010), the updated species list provided as part

of the database can be considered complementary to ChEssBase for taxonomic and geographic information on vent species.

SUPPORTING INFORMATION APPENDIX 5: Usage Notes

Version 1 of the sFDvent database is comprised of two parts:

1. A data file comprising the processed, cleaned, 'ready-to-analyse' dataset that has been approved and recommended for use (Table S4.2), hosted at 10.5061/dryad.cn2rv96. References associated with the scores in this dataset are provided in Appendix S1 and Table S1.1. While traits have been binned in this dataset to improve accessibility and reduce bias, we recommend that each user bins traits and/or processes the dataset as appropriate for the study being conducted.
2. A data file containing all raw data contributions as a static release (Table S4.3) will be hosted at 10.5061/dryad.cn2rv96. References associated with raw data entries can also be found in the full reference list provided in Appendix S1. These raw data would need to be processed before use and we recommend: i) checking for collinearity among traits when selecting from these traits for a given study; ii) conducting error checks using the recommended dataset and/or literary sources; and iii) weighting or processing data according to given certainty scores (giving particular attention to certainty scores of '0', which have been given to show that the trait score should be removed and was randomly filled to demonstrate a lack of knowledge rather than an otherwise empty cell).

We also provide a metadata file for use in conjunction with trait data to determine which traits, species, and/or data files are most appropriate for a given research question. We do not recommend using the location metadata in isolation, as they were collected as ancillary data with the trait database, so may not represent the full extent of current knowledge.

Please note that references to 'Handbook', or the 'Handbook of Hydrothermal Vent Fauna', or similar, refer to Desbruyères et al. (2006). Any references that are unclear can be sought from the contributor, though are provided in full in Appendix S1 and Table S1.1. It is also worth noting when using the sFDvent trait database that a score with reference 'expert opinion' (or 66 in Table S4.2) may be more accurate or higher quality than some older, literary sources and it should not always be assumed that an expert opinion is an estimate or less accurate than a literary source. For vent species, the current state of knowledge is not always otherwise captured in publications or cruise reports, given the observational nature of work conducted using remotely operated vehicles (ROVs). For instance, an expert can learn a considerable amount about a species through hours of observation during a ROV dive that is not officially documented or further investigated (as sample numbers are governed by ROV storage capacity) but could form the basis for a trait score; sFDvent captures this knowledge, of particular importance for rare or less well-studied species.

Citation:

We ask that the sFDvent database is cited in all outputs using and/or developing the data, giving: i) the recommended citation for this paper, and ii) the sFDvent database DOI (10.5061/dryad.cn2rv96). When an accompanying website is released for updated database versions at a later date, this should be referred to for up-to-date recommended citations, so we ask all users to search 'sFDvent' online before citing.

We also ask all users of the sFDvent database to provide a copy of the data used for the analyses initiated with sFDvent data (i.e. including any modifications or corrections made) to abbiesachapman@gmail.com and abates@mun.ca, so the sFDvent database can be updated and improved accordingly and, thus, best represent the current state of knowledge of the species traits of deep-sea chemosynthetic fauna.

We propose that future versions of sFDvent should be released on a five-year cycle, to ensure that each version captures a substantial contribution to the state of knowledge of trait data for deep-sea vent species, given typical research cruise timeframes. A workflow for the cycle is proposed and illustrated in Figure S1A.2. During this process, the database may expand to include other chemosynthesis-based ecosystems, such as whale falls, wood falls, and cold seeps, and, eventually, individual-level (intraspecific) traits. We would also recommend, for the maintenance of this regular workflow of sFDvent, that any issues or updates are flagged and provided by users by completing the table below and returning it to: abbiesachapman@gmail.com and abates@mun.ca.

Contributor Name	Taxon ID No.	Genus	Species	Trait / Column	Current Score	Proposed Change	Rationale / Support for Change	Other Comments

We also propose that any future cruise log designers should consider storing behavioural observations with geo-referenced trait ‘tags’, to facilitate inclusion in databases such as sFDvent. This would ensure that key ecological observations are not lost in modern-day, deep-sea equivalents of personal, hand-written field notebooks.

SUPPORTING INFORMATION APPENDIX 6: Extended Results - Trait-by-trait

Trait-specific descriptions

Relative adult mobility: Relative adult mobility ranges from 1 to 4, with the majority of taxa scoring 3. Taxa in the Arthropoda and Chordata phyla have the highest mobility scores (with mean scores of 3.3 and 3.9, respectively) and the lowest scores are assigned to taxa in the Cnidaria and Porifera (with respective mean scores of 1.1 and 1). Average mobility is similar (3) across all oceans except the Arctic, Southern, and Mediterranean oceans, which have a mean relative adult mobility of 2.

Depth range: Depth ranges vary in the sFDvent database from 0 to 500 metres to > 5000 metres, with the most common depth records ranging from 2000 to 3000 metres. *Sirsoe hessleri*, *Acharax johnsoni*, *Coryphaenoides armatus*, and *Abyssorhynchomene distinctus* species have the deepest recorded ranges (> 5000 m) and 7 taxa have only the shallowest range (0 - 500 m: 4 molluscs and 3 arthropods).

Maximum body size: Estimated maximum body size ranges from 1 mm to 1000 mm, with 100 mm the most common body size class in the database (41% of taxa scored for body size) and 10 mm also common (40% of taxa with body size scores). More species had a score of 1000 mm as an estimated maximum body size (10%) than 1 mm (8%). The phylum Chordata hosts the largest species on average (mean estimated maximum body size 700 mm) and Acanthocephala, Foraminifera, and Nematoda the smallest (mean estimated maximum body size 1 mm). The Mediterranean has the highest mean estimated maximum body size (505), while the Arctic Ocean has the lowest (49).

Substratum preference: The majority of species are found on hard substrata (81% of species scored for this trait), while the fewest are associated with the water column (6% of species with a substratum preference score). Hard substrata are most often associated with arthropods (146 taxa) and soft substrata with molluscs (27 taxa).

Foundation species: Species are not commonly foundation species (84% scored 'No' and 16% 'Yes' for this trait).

Abundance: Overall, 'High' and 'Low' abundance scores were relatively evenly split across all taxa and oceans.

Gregariousness: Gregariousness is most often scored as 'Solitary' (44% of species with a Gregariousness score) and least often 'Always' (26% of species scored for this trait) but Arctic Ocean, Indian Ocean, and Southern Ocean taxa are more gregarious than taxa in other ocean basins.

Habitat Complexity: Habitat Complexity has scoring options: 'dense bush forming', 'open bush forming', 'bed forming (> 10 cm)', 'mat forming (< 10 cm)', 'burrow forming', and 'does not add'. The majority of species in the sFDvent database do not add habitat complexity (77% of taxa scored for Habitat Complexity), while 'dense bush forming' is the least common score for this trait (2% of species scored for the Habitat Complexity trait - all annelids).

Trophic mode: The most common trophic mode is 'Bacterivore' (39% of species scored with a Trophic Mode) and the least common (excluding 'Omnivore', only assigned to one species) is 'Carnivore - scavenger' (8% of species scored), despite 'Carnivore - other' being the second most common mode (29% of scored species). Scavenging carnivores are mostly from the Arthropoda phylum, while other carnivores were most commonly annelids and bacterivores and/or detritivores most commonly molluscs.

Nutritional source: Nutritional source is most commonly 'Sediment or rock surface' (41% of species scored for this trait), and least often 'Water column' (8% of scored species), with arthropods more often dependent on fauna and/or the water column and molluscs more often dependent on sediment or rock surfaces and/or symbionts.

Chemosynthesis-obligate: 'Chemosynthesis-obligate' is a trait specific to chemosynthesis-based ecosystems (CBEs), with scoring options of 'Vent', 'Other CBE', and 'No' used to represent the least restricted score for the species (e.g., a species found at vents but also in non-chemosynthetic ecosystems is given a score of 'No', as this score best demonstrates that this species is not tied to vents or chemosynthesis-based ecosystems). The most common score in the database is 'Vent' (74% of taxa, though we note that this might change in future versions of the database as more meiofauna, of less than 1 mm body size, are included) and the least common is 'Other CBE' (10%). The Arthropoda are predominantly vent-obligate (though also the phylum most often scored 'No'), while molluscs are most often also found in other CBEs, and the Chordata are mostly also found in non-vent environments.

Zonation from vent: 'Zonation from a vent' is a vent-specific trait with three modalities - 'High', 'Medium', and 'Low' - and the majority of taxa in the database are found in the 'Medium' zone (49% of species scored for this trait).

Position of symbiont: Position of symbiont has three modalities: 'Endosymbiont', 'Episymbiont', and 'None'. Of these modalities, most taxa do not have symbionts (80% of the species scored for this trait score 'None'), while 16% have endosymbionts and 4% have episymbionts, according to trait scores. Arthropods, molluscs, and annelids are the only taxonomic groups containing taxa with episymbionts and endosymbionts, though many taxa within these phyla do not have symbionts. All ocean basins host taxa with and without symbionts and there is a relatively consistent split in the proportion of taxa with each symbiont position (~75% without symbionts, ~19% with endosymbionts, and ~7% with epibionts, when the Mediterranean is excluded, given it only has two taxonomic records). The Southern Ocean has an above average proportion of symbiont-hosting species (44% have endosymbionts, 11% have episymbionts, and 44% are without symbionts, though we note that there is a low total number of taxa).

SUPPORTING INFORMATION APPENDIX 7: Comparative Review of Faunal Trait Databases

The Excel file Table S7.1 is provided to support Table 4. It comprises information collated during a comparative review of animal trait databases, seeking to identify a 'common terminology' for traits across ecosystems and taxa.

SUPPORTING INFORMATION - References

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