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The development of an indicator of the condition of sublittoral rock communities (Phase 2): Spatial correlation between environmental conditions and biological data

Anita Franco, Krysia Mazik, Shona Thomson, Stephen Duncombe-Smith and Gemma Singleton

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For further information on JNCC's report series please contact:
Joint Nature Conservation Committee
Quay House,
2 East Station Road,
Fletton Quays,
Peterborough, PE2 8YY
https://jncc.gov.uk/
Communications@jncc.gov.uk

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Author affiliation:
1. University of Hull, Cottingham Rd, Hull HU6 7RX
2. JNCC, Peterborough.

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Please note that this report was written in 2018, prior to the UK's exit from the European Union.

Summary

This report is capturing the continuation of Phase 1 and Phase 2 work on the development of the sublittoral rock indicator, reflecting the work which took place between 2017 and 2018.

Phase 1 (Strong & Johnson 2023) identified potential species that show strong correlations in abundance (increasing or decreasing) with a pressure gradient. Phase 2 aimed to improve the method developed, this included exploring additional data, most notably from inshore sites (Seasearch).

Threshold Indicator Taxa ANalysis (TITAN, R package) was used to analyse biological data. The analysis aims to detect the change in abundance of multiple indicator species/groups for sublittoral rock communities across a gradient of anthropogenic pressure (resuspension of sediment caused by mobile bottom-contact fishing gear).

New data were obtained from seven Seasearch surveys with the aim to expand the Phase 1 dataset. Integration of Seasearch data with previous Phase 1 biological and environmental data was explored and the combination of digital still images and diver survey records evaluated. Pre-selection criteria applied to Seasearch data resulted in 33 of the 82 records being taken forward for analysis, however these were ultimately not included following data stratification analysis.

Biological data processing was revised in Phase 2. Taxa recorded in multiple forms or in very low occurrence were merged where possible. Sponge morphologies were aligned with the standardised classification adopted by JNCC (2013; after Bell *et al.* 2006), reducing morphotypes from 15 to 10. The resulting taxa/forms dataset was further processed to create a conspicuous dataset of high confidence records (188 taxa/forms) and an aggregated taxa dataset with multiple species records from a genus merged (177 taxa/forms). The revised approach gave two biological datasets with significantly more taxa/forms used in the analysis compared with Phase 1 (62 taxa/forms).

Habitat maps and bathymetric data were updated from Phase 1 with UK SeaMap (2016) replacing EUSeaMap (2010), and Astrium (2016) replacing Astrium (2015). These datasets providing high resolution data for biotopes, environmental variables, and sediment categories were used to calculate sediment resuspension. Data were stratified where possible to reduce the expected variance in biological data from communities recorded from varying sublittoral rock habitats. Principal Components Analysis (PCA) of environmental variables was used to explore the most suitable stratification of data. Environmental variable gradients identified by PCA (North & South, biozone/depth, energy, turbidity, and rock type) were validated using ANOSIM of biological data and consideration was given to dataset size and pressure range. Final data were stratified into five subgroups:

- Northern, shallow (deep circalittoral), low energy.
- Northern, shallow (shallow-deep circalittoral), moderate energy.
- Southern, bedrock, low turbidity, low energy.
- Southern, boulders, low energy.
- Southern, cobble, low energy.

Observations with zero pressure values were included in Phase 2 analysis. Previously in the Phase 1 analysis, these had been excluded.

A stricter selection of indicators from the TITAN results were used in Phase 2, taxa/forms in the top ten ‘indicator quality’ score results were not included unless they met purity and reliability criteria. Similar to Phase 1 analysis, negative responding taxa showed a

corresponding change in abundance at lower pressure values than those positively correlating with increased pressure values. Negative change points were the lowest in the two Northern area datasets (SA0 less than = 0.07) and the Southern cobble dataset (SA0 less than = 0.1), Southern bedrock and Southern boulder datasets had a slightly higher change point (SA0 less than = 0.45). Confidence in negative change points identified were also higher than positive change points. The results indicated a high level of accuracy when validated against randomly selected subsets (greater than 79%, often greater than or equal to 90%), with higher validation accuracy from the larger datasets. Validation results should be interpreted with caution. This is due to the randomised datasets used for the validation not being independent from the data used to generate the benchmark values.

Indicator taxa identified with the adapted Phase 2 approach showed a more consistent response to pressure across the different datasets. Sertulariidae, Ophiuroidea, Brachiopoda, and *Swiftia pallida* were frequently selected as indicator taxa showing a negative response. While some taxa were shown to be positively responding indicator taxa (e.g. Actiniaria, encrusting sponges, *Munida*, Paguroidea), there were fewer consistent positive responding indicators compared with the negative responding indicators. Some indicator taxa identified by the analysis showed a mixed response between datasets (e.g. *Porania pulvillus*, Hydrozoa, *Parazoanthus*). For most datasets, the same indicator taxa were identified using either the conspicuous or aggregated taxa/forms list; neither the conspicuous nor aggregated list consistently identified a greater number of indicators. The most indicators were identified in the two largest datasets. The Northern, moderate energy, variable rock type dataset (N2) not only identified the most indicators but showed a higher proportion of positive response indicators to negative response indicators. All other datasets identified more negative response indicators than positive response indicators.

Due to the stratification and data requirements needed for analysis in the Phase 2 method, dataset size was not increased from that used in Phase 1. Despite this, and despite the more restrictive criteria used in the present study for the selection of indicator taxa (based only on purity and reliability), a general improvement in the predictive accuracy and in the number of selected indicator taxa was obtained in Phase 2. This suggests a more systematic approach to data stratification and indicator choice were critical in affecting the results.

Further development and validation of the sublittoral rock indicator would benefit from data covering the wider environmental variables around the UK, increased detail of the anthropogenic pressure, and standardised data recording. Confidence in the indicator can be improved with larger datasets that allow for data excluded from analysis to be used for validation of results.

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1 Introduction

Under the obligations set by the Marine Strategy Framework Directive (MSFD) (2008/56/EC) to Member States, and in line with the subsequent Commission Decision (2010/477/EC) and the resulting UK Marine Strategy (Part one; Defra 2012), JNCC is developing an indicator of condition for sublittoral rock habitats. This will contribute to the assessment of the Good Environmental Status (GES). See Strong and Johnson (2023) for a full background on the policy context and rationale behind this project.

A first stage of this work (Phase 1) has been undertaken, in collaboration with the Institute of Estuarine and Coastal Studies (IECS, University of Hull) in 2016/17 (Strong & Johnson 2023). Eight datasets were analysed, and an analytical approach was refined by using Threshold Indicator Taxa ANalysis (TITAN; Baker & King 2010), to facilitate the detection of community change along a gradient of anthropogenic pressure relating to fishing activities. TITAN only works with a single environmental gradient against which the species response is assessed. In Phase 1 the specific gradient of anthropogenic pressure used was sediment resuspension originating from fishing-related surface abrasion. Additional sources of environmental variability were explored, including spatial variability (latitude, longitude), depth, rock type and quantity, turbidity, and sea temperature. Indicators of ecological and environmental status should be able to respond to the signal associated with anthropogenic pressure over the background noise given by the natural environmental variability. In order to maximise the signal-to-noise ratio, hence the response to the pressure gradient, the datasets were combined and stratified according to natural variability, based on rock type, rock quantity, biozone and turbidity (backscatter). Semi-quantitative data (SACFOR, based on counts or cover) were used, with the biological components of the community being identified using morphological (for sponges) or taxonomical identifiers. A protocol was developed for data processing (i.e. conversion of SACFOR data into quantitative information) and pre-selection (e.g. removal of very rare species) before the TITAN analysis was undertaken (Strong & Johnson 2023).

The TITAN analysis allowed successful identification of indicator species/groups as positive or negative responders to the gradient of anthropogenic resuspension separately for low turbidity bedrock, boulder, cobble and high turbidity mixed rock habitats (Strong & Johnson 2023). Indicator species/groups appeared to be sensitive to the analysed anthropogenic pressure, particularly in bedrock habitats (a community change was detected at relatively low levels of anthropogenic resuspension). Validation of the method showed high levels of predictive accuracy. The number of indicator species/groups identified by the analysis appeared to be influenced by the size of the dataset for the specific stratum defined based on habitat characteristics, resulting in a smaller number of indicators identified for the smaller datasets for boulder and cobble, compared to the larger datasets for bedrock and high turbidity. Furthermore, the exploration of environmental gradients in the available datasets highlighted that only a small proportion of the biological variability could be explained by the environmental (natural and anthropogenic) variables, and the anthropogenic resuspension was less important compared to other natural variability (e.g. latitude and longitude, depth, substratum).

The results obtained in Phase 1 are likely to have been highly affected by the nature of the data (semi-quantitative), dataset sizes and choices made in the data processing and analysis (e.g. thresholds or criteria for species grouping, inclusion or exclusion). Therefore, JNCC commissioned the present study (Phase 2).

1.1 Aims and objectives

The Phase 2 study aimed to test and revise the methodological approach developed in Phase 1, in order to improve the performance of the method and therefore the validity of the sublittoral rock indicator. Phase 1 recommended including additional data to improve the method, therefore another aim of Phase 2 was to test the applicability of additional data alongside the Phase 1 dataset. While the additional data was ultimately deemed unsuitable for testing with the TITAN analysis, the overarching aim of this Phase to refine the method where appropriate to better define the condition of sublittoral rock at regional and local scales considering prevailing environmental conditions was achieved. The specific objectives of Phase 2 were:

- To explore and test the assessment method from Phase 1, and explore avenues to reduce the unexplained variance, including exploring the applicability of some additional data.
- To develop a set of recommendations to improve information on survey methods and data collection for the validation of the indicator.

2 Methods

As Phase 2 is largely based on the methodological approach and techniques developed and applied in Phase 1 (as a starting point), we refer to the Phase 1 report (Strong & Johnson 2023) for the details on the methods used there. Additional or alternative methods applied in Phase 2 (including new or modified approaches and techniques used) are described in sections 2.1 to 2.10.

In order to better represent the methodological protocol required to prepare the survey data for the TITAN analysis, the methods below are given as a step-by-step description of the process that was used to prepare, integrate and analyse the data in this phase of the project.

2.1 Step 1 – Data check and screening

The new data provided by JNCC for Phase 2 were obtained from seven Seasearch surveys undertaken between 2006 and 2016 which included data for 82 samples (a total of 1,943 species-by-sample entries, as available from Marine Recorder):

- 2006 Seasearch survey of Skomer Marine Nature Reserve (survey coded as SK 2006)
- 2009 Seasearch Skomer Marine Nature Reserve (SK 2009)
- 2016 Seasearch Survey of Skomer Marine Conservation Zone, Pembrokeshire, West Wales (SK 2016)
- 2012 Seasearch Survey of South Pembrokeshire, Wales (SP 2012)
- 2016 Seasearch Survey of the Smalls, Pembrokeshire, West Wales (TS 2016)
- 2011 Seasearch Scotland Shetland Fair Isle Survey (SFI 2011)
- 2011 Seasearch Scotland Shetland Survey (SS 2011)

Seasearch is a project that makes use of volunteer recreational divers to gather information on seabed habitats and associated marine wildlife in Britain and Ireland. The recording of data is based on an established guidance (Seasearch Survey Form Guidance Notes), with basic training given to divers.

The Seasearch survey data provided for Phase 2 were mostly located on rock habitats (bedrock, boulder, cobble and pebble) on the SW coast and NE coast of the UK (Figure 1). The new survey data were collected in areas near those covered by the data in Phase 1, albeit at more inshore locations, given the nature of the Seasearch surveys.

The Seasearch data (as obtained by JNCC from Marine Recorder) included sample records of taxonomic abundance of epibiota measured on a simplified SACFOR scale (Table 1). As with Phase 1 data, no information was given on whether the SACFOR class reported in the Seasearch datasets was allocated based on observation of coverage or count (densities), nor on the size of the organisms counted.

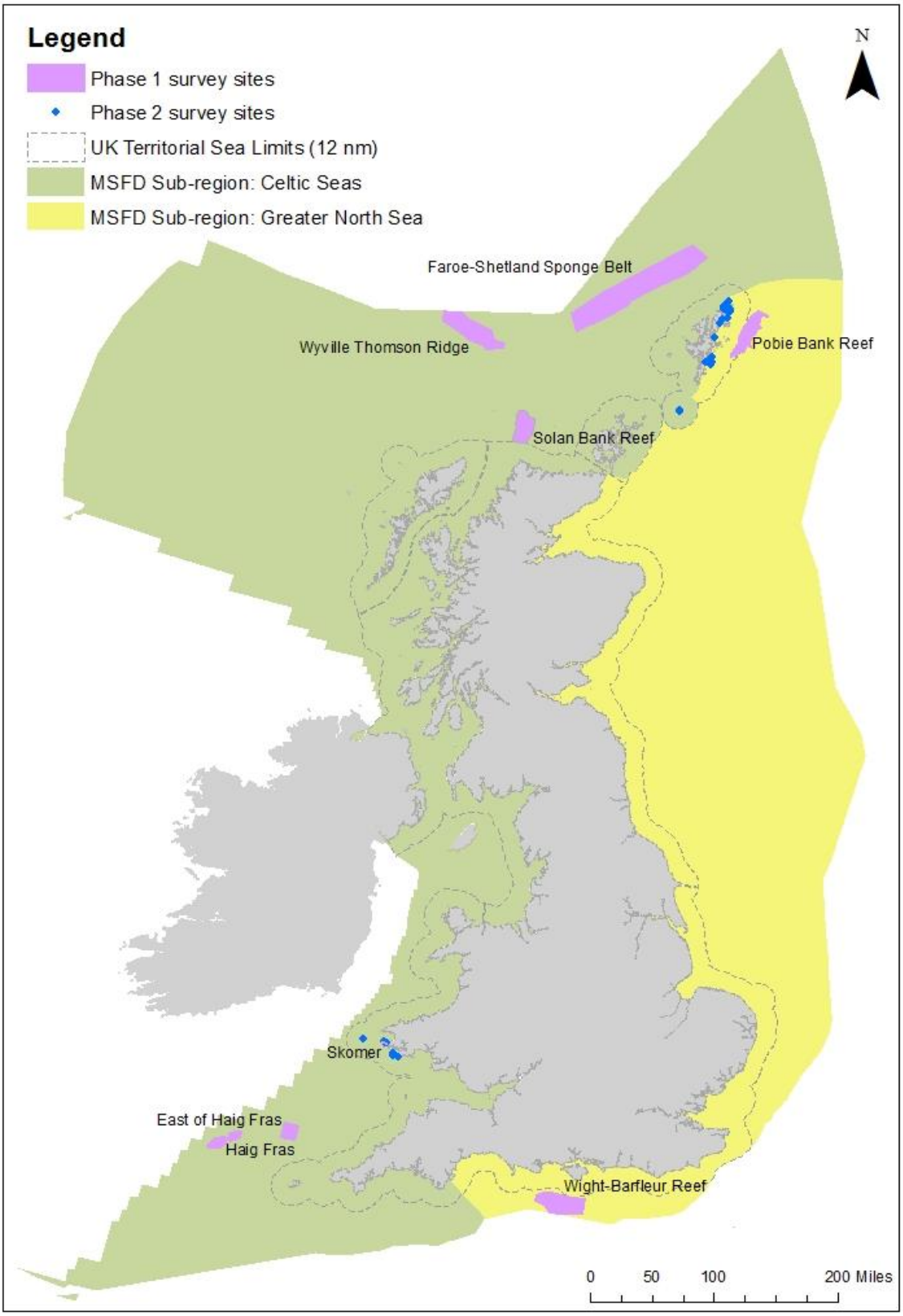

Figure 1. Location of the survey sites from Phase 1 and Phase 2.

Table 1. Simplified SACFOR scale used in Seasearch surveys.

Abundance	Encrusting and turf species (e.g. encrusting algae/sponge, jewel anemones, hydroids, barnacles, mussels, seaweeds)	Small plants and animals (1 to 5 cm) (e.g. worms, small sponges, anemones, cup-corals, shells, solitary sea squirts}	Large plants and animals (> 5 cm) (e.g. large sponges, sea fans and pens, large anemones, crabs and lobsters, starfish, fish)
Superabundant	80–100% cover	10,000 per m^2	100 per m^2
Abundant	40–80% cover	1,000 per m^2	10 per m^2
Common	20–40% cover	100 per m^2	1 per m^2
Frequent	10–20% cover	10 per m^2	1 per 10 m^2
Occasional	5–10% cover	1 per m^2	1 per 100 m^2
Rare	< 5% cover	< 1 per m^2	1 per 1,000 m^2

Survey observations were supplied with qualifying attributes including:

- Survey metadata (date, survey name, site name and sample reference ID, etc.).
- An estimate of confidence in the sample data (RepQuality) that reflects the degree of training of the surveyor ('Adequate' for surveyor trained at higher-level, hence higher confidence in the data; 'Incomplete' for surveyor with observer-level basic training, hence lower confidence in the data).
- Latitude and longitude.
- Substratum composition (as percentage coverage by different types of substrata, for example bedrock, boulder, cobble, pebble, sand, mud, artificial substrata, biogenic substrata, maerl, etc.).
- EUNIS habitat code (not used in the analysis).
- Water depth and salinity classes (not used in the analysis).
- Underwater visibility (in metres (m)).

2.2 Step 2 – Sample data pre-selection

The sample data obtained from different Seasearch surveys were combined into two separate matrices. Both included all samples from the surveys as rows, and either the associated survey/environmental attributes or the species abundance records as columns. These two matrices are identified respectively as Phase 2 ENV dataset and Phase 2 BIO dataset, and collectively as Phase 2 dataset. The matrices were initially explored and processed separately (albeit in parallel) to allow preliminary sample selection (based on different attributes).

A preliminary exploration and sample selection in the Phase 2 dataset was undertaken to ensure the scope and aims of the project could be met with suitable data of suitable quality. This led to the following exclusions which are explained in detail below: samples with kelp habitat, low underwater visibility, absence of sublittoral rock habitat and surveys undertaken before 2009. These exclusions resulted in a reduction of the initial Phase 2 dataset (both ENV and BIO datasets) from 82 samples to 33 samples (Table 2).

Table 2a. Summary of the overall number of samples selected for the analysis in this study.

Phase	Survey name	MSFD Subregion (zone)	Site code	Year	Number of samples
1	2013 Pobie Bank Reef cSAC/SCI	Greater North Sea (North)	PB	2013	345
	2013 Wight-Barfleur Extension MCZ	Greater North Sea (South)	WB	2013	2,063
	2012 Faroe-Shetland Sponge Belt Scottish NCMPA	Celtic Seas (North)	FSSB	2012	200
	2014 Solan Bank Reef cSAC/SCI	Celtic Seas (North)	SB	2014	1,053
	2012 Wyville Thomson Ridge cSAC/SCI	Celtic Seas (North)	WTR	2012	373
	2015 East of Haig Fras	Celtic Seas (South)	EHF	2015	939
	2015 Haig Fras SAC	Celtic Seas (South)	HF	2015	1,824
	2012 Haig Fras cSAC/SCI "Infill"	Celtic Seas (South)	HFI	2012	55
2	2011 Seasearch Scotland Shetland Survey	Greater North Sea (North)	SS	2011	2
	2011 Seasearch Scotland Fair Isle Survey	Celtic Seas (North)	SFI	2011	5
	2009 Seasearch Survey of Skomer Marine Nature Reserve	Celtic Seas (South)	SK	2009	7
	2016 Seasearch Survey of Skomer MCZ, Pembrokeshire, West Wales	Celtic Seas (South)	SK	2016	6
	2012 Seasearch Survey of South Pembrokeshire, Wales	Celtic Seas (South)	SP	2012	7
	2016 Seasearch Survey of The Smalls, Pembrokeshire, West Wales	Celtic Seas (South)	TS	2016	6

Table 2b. Collated Summary of the overall number of samples selected for the analysis in this study.

	Total
Total no. samples, Phase 1	6,852
Total no. samples, Phase 2	33
Total no. samples, Celtic Seas (North)	1,631
Total no. samples, Celtic Seas (South)	2,844
Total no. samples, Greater North Sea (North)	347
Total no. samples, Greater North Sea (South)	2,063

2.2.1 Kelp habitat

Sample sites with kelp habitat were excluded to avoid overlap with a specific indicator for these habitats (currently under development). As kelp habitats only occur in infralittoral areas, this issue only concerned Phase 2 (Seasearch) data.

Kelp habitat was identified where biotopes that have kelp as characterising species occur (genera *Laminaria, Laminariales, Alaria, Saccharina, Sacchorhiza*), such as biotopes IR.HIR.KFaR.AlaAnCrSp, IR.HIR.KSed.LsacSac, IR.MR.KR.Ldig, IR.MIR.KT.LdigT, IR.LIR.K.LhypLoch (JNCC, 2015). In these biotopes, kelp abundance is recorded as 'frequent' or above on the SACFOR scale and were excluded from Phase 2 sample data. This resulted in a reduction of the dataset size by 46% (from 82 to 44 samples; Table 3). Data from all surveys in Phase 2 were affected by this reduction, in particular SFI 2011 (10 out of 15 samples excluded, 67%), SP 2012 (12 out of 20 samples excluded, 60%), and SK 2006 (three out of six samples excluded, 50%).

Table 3. Sample counts by survey for total, causes of reduction in dataset (as a count and proportion of available totals) and combined proportion of samples removed from the Phase 2 dataset. Site Codes: SFI – Scotland Fair Isle; SK – Skomer, Pembrokeshire; SP – South Pembrokeshire; SS – Shetlands, Scotland TS – The Smalls, Pembrokeshire.

Site Code	Year	Total samples available	Source of Sample Reduction				Combined percentage reduction in available samples
			Kelp habitat	Poor underwater visibility	No Sublittoral rock	No pressure data	
SFI	2011	15	10 (67%)	0	0	0	67%
SK	2006	6	3 (50%)	0	0	6 (100%)	100%*
	2009	9	2 (22%)	0	0	0	22%
	2016	14	6 (43%)	0	2 (14%)	0	57%
SP	2012	20	12 (60%)	3 (15%)	1 (5%)	0	65%*
SS	2011	8	1 (13%)	0	5 (63%)	0	75%
TS	2016	10	4 (40%)	0	0	0	40%
Total Phase 2 samples		**82**	**38 (46%)**	**3 (8%)**	**8 (10%)**	**6 (7%)**	**33* 40%***

** Note: Cumulative sample reduction from all sources is less than actual sample reduction due to some individual samples being removed for more than one reason.*

2.2.2 Fishing abrasion pressure

The purpose of this study was to analyse rock habitat survey data in relation to a pressure gradient to identify indicator taxa. The pressure measures used here were derived from abrasion pressure data layers, in accordance with the method defined in Phase 1 (Strong & Johnson 2023; see also Step 6). As abrasion pressure data layers are only available from 2009, any survey data collected before 2009 could not be included in the analysis. As such, data for the 2006 Seasearch survey of Skomer Marine Nature Reserve (six samples, three of which were also recorded on kelp habitat) were excluded (Table 3).

2.2.3 Underwater visibility

Underwater visibility was recorded during Seasearch surveys, with records ranging from 0.5 m to 20 m. This was used as an indicator of the confidence in the survey observations, with lower confidence being associated with lower underwater visibility, as this likely influenced the

surveyor's ability to see seabed features and taxa in the area explored. In the absence of a clear survey protocol defining the survey method (e.g. line transect versus fixed point survey) and the extent of the area assessed by the surveyor, a decision was made to exclude samples with visibility less than 1 m. Only three samples (all from SP 2012, and two of which were recorded on kelp habitat) met these conditions and were therefore excluded (Table 3).

2.2.4 Sublittoral rock substratum

The Phase 2 survey samples were classified according to their dominant sublittoral rock substratum type (bedrock, boulder, cobble or pebble) and the total % area of sublittoral rock was calculated as in Phase 1 (Strong & Johnson 2023). The characterisation of the substratum as 'sublittoral rock' (as opposed to 'sediment') followed the method used to define substratum categories for level 2 in the EUNIS/JNCC classification, as described in Parry (2015) and used in Phase 1 of this project. In order to apply this method, the epibenthic taxa present in the samples were classified as either 'fragile', 'robust erect' or 'other', and the quantity (percentage (%) area) of sublittoral rock calculated as cumulative percentage area by combining the percentage area of bedrock, boulder, cobble and pebble substrata occurring in the survey site from survey records (in accordance with Parry 2015). This information is available in Seasearch survey data, as in data used in Phase 1, based on the same substratum categories, with percentage coverage by category being given.

According to these calculations, eight samples in the Phase 2 dataset were classified as having no sublittoral rock, and therefore were excluded. These samples included six samples where the substratum was 100% artificial (metal) (five samples in SS 2011 and one in SP 2012, the latter also having visibility less than 1 m), and two samples (from SK 2016) with the only hard substratum present being pebbles but where no fragile epibiota occurred (Table 3).

2.2.5 Data quality (RepQuality)

Within the initial datasets provided, 74% of the data were classed as 'adequate', whereas 26% were 'incomplete'. The incidence of lower confidence data was unevenly distributed between the surveys (100% of the data in SK 2006 and SK 2009; 9% in SP 2012; 3% in SK 2016; zero in the other surveys). In this instance, due to the paucity of new data available for Phase 2 compared to those available for Phase 1 (82 versus 6,852 samples, respectively), the choice was made to include all data (adequate and incomplete). As a result, the final data selection included 25 samples classed as 'adequate' and eight samples as 'incomplete'.

2.3 Step 3 – SACFOR conversion

SACFOR scale entries in Phase 2 BIO dataset were converted into numerical data following the methodology described in the Phase 1 report (Strong & Johnson 2023). However, some adjustments to the method were necessary to cope with differences in survey standards between Seasearch surveys and Phase 1 surveys.

The SACFOR scale used in Seasearch surveys (Table 1) is a simplified version of the MNCR SACFOR scale used by JNCC (see Table 2 in Strong & Johnson 2023), in that no differentiation between growth forms is made in the classification of biota based on coverage observations. Instead Seasearch uses a simplified differentiation according to individual or colony size (two levels compared with the four levels in the MNCR SACFOR classification) for biota classified based on count (density) observations. Despite these differences, both scales share similar count and coverage classes, and these were used to establish the correspondence between the SACFOR records in Phase 1 and Phase 2 datasets (Table 4).

The SACFOR transformation approach applied in Phase 1 relies on the ability to establish a clear link between a SACFOR category and the originating count or coverage class range as established by the SACFOR scale tables (Table 4). The knowledge of the type of observation (count or coverage) used to allocate the SACFOR class to a taxon, and the growth form (for coverage-based records in the MNCR SACFOR scale) or the size of the individuals or colony (for count-based records in both SACFOR scales), are the basic/minimum data requirements to allow this link to be understood, hence needed for the SACFOR data to be transformed into numerical values. The type of record and growth form or size was not recorded in the Phase 2 datasets and consequently was inferred by comparison with Phase 1 data.

Table 4. Correspondence between MNCR (JNCC) and Seasearch SACFOR categorisation of abundance data based on: (a) coverage observations; or (b) count (density) observations. Resulting log-transformed numerical values associated with each SACFOR class are also indicated (Log) as obtained by applying the transformation approach used in Phase 1 (Strong & Johnson 2023). S – Superabundant, A – Abundant, C – Common, F – Frequent, O – Occasional, R = Rare.

(a) **Coverage**	**JNCC SACFOR**				**Seasearch SACFOR**	
	Crust/Meadow		**Massive/Turf**		**Any form**	
	SACFOR	**Log_2**	**SACFOR**	**Log_2**	**SACFOR**	**Log_2**
> 80%	S	6.49			S	6.49
40–79%	A	5.91	S	5.91	A	5.91
20–39%	C	4.91	A	4.91	C	4.91
10–19%	F	3.91	C	3.91	F	3.91
5–9%	O	2.91	F	2.91	O	2.91
1–5%	R	1.91	O	1.91	R	1.91
< 1%			R	0.91		

(b) **Count**	**JNCC SACFOR**								**Seasearch SACFOR**			
	Size < 1 cm		**Size 1–3 cm**		**Size 3–15 cm**		**Size > 15 cm**		**Size 1–5 cm**		**Size > 5 cm**	
	SACFOR	**Log_{10}**	**SACFOR**	**Log_{10}**	**SACFOR**	**Log_{10}**	**SACFOR**	**Log_{10}**	**SACFOR**	**Log_{10}**	**SACFOR**	**Log_{10}**
> 10,000 / m^2	S	8.88							S	8.88		
1,000–9,999 / m^2	A	7.88	S	7.88					A	7.88		
100–999 / m^2	C	6.88	A	6.88	S	6.88			C	6.88	S	6.88
10–99 / m^2	F	5.88	C	5.88	A	5.88	S	5.88	F	5.88	A	5.88
1–9 / m^2	O	4.88	F	4.88	C	4.88	A	4.88	O	4.88	C	4.88
1–9 / 10m^2	R	3.88	O	3.88	F	3.88	C	3.88	R	3.88	F	3.88
1 9 / 100 m^2			R	2.88	O	2.88	F	2.88			O	2.88
1–9 / 1,000 m^2					R	1.88	O	1.88			R	1.88
< 1/1,000 m^2							R	0.88				

The overall species list from the Phase 2 dataset was matched with that from Phase 1. Where there was no exact matching in the taxon name, the match was established with the closest taxon or form from Phase 1 (e.g. taxa recorded as *Aglaophenia*, *Aglaophenia kirchenpaueri* and *Aglaophenia pluma* in Phase 2 dataset were all matched with *Aglaophenia* from Phase 1 dataset; taxa recorded as *Raspailia (Clathriodendron) hispida* and *Raspailia (Raspailia) ramosa* in Phase 2 dataset were all matched with Raspailiidae (Porifera arborescent form) from Phase 1 dataset). Possible misspellings and taxonomic synonyms were taken into account in the comparison between the two lists.

Due to the approach described above, combined with the difference in size classes used in the MNCR and Seasearch SACFOR scales (four and two size classes respectively, with different range boundaries; Table 4), a conversion criterion had to be established to match the size classes derived from Phase 1 data (MNCR SACFOR scale) with those needed to convert SACFOR classes in Phase 2 dataset according to the Seasearch scale (Table 5). Individuals of the intermediate size class (3 cm to 15 cm, MNCR SACFOR scale) were those for which the conversion into Seasearch size classes was most uncertain, as smaller individuals within this class (3 cm to 5 cm) could fit in the smallest size class used by Seasearch (1 cm to 5 cm) whereas larger individuals within the MNCR class (5 cm to 15 cm) could fit in the largest size class used by Seasearch (greater than 5 cm). The decision was made to allocate individuals of the class 3 cm to 15 cm (MNCR) to the largest class greater than 5 cm (Seasearch) for Phase 2. Very small individuals (less than 1 cm, MNCR), were not considered in the Seasearch SACFOR scale, most likely due to the lower detectability and higher identification uncertainty associated with these very small sizes. Therefore, a direct correspondence between the two SACFOR scales for this size class was not required. However, this did not affect the dataset analysed in this project, as such small size class was not recorded in the analysed Phase 1 dataset.

Table 5. Correspondence established between the size classes used in the MNCR (JNCC) and Seasearch SACFOR scales for the purpose of SACFOR transformation of Seasearch data.

Size classes in SACFOR scales	
JNCC	**Seasearch**
< 1 cm	n/a
1–3 cm	1–5 cm
3–15 cm	> 5 cm
> 15 cm	> 5 cm

2.4 Step 4 – Taxa harmonisation and preliminary selection

The Phase 1 BIO and Phase 2 BIO datasets were combined into a single matrix and the taxonomic identities were standardised using the online WoRMS database (World Register of Marine Species http://www.marinespecies.org/). A list of updated taxa names is given in Appendix 1.

Sponge taxa in the Phase 2 BIO dataset were qualified and merged according to their morphologies, as was done in Phase 1. Where the sponge morphology was recorded in the survey data (on its own or in addition to a taxonomic identification), this was used as a morphological qualifier. In most cases (32 of the 35 sponge taxa identified in Phase 2

surveys) sponges were only recorded as taxa (e.g. species, families) with no additional information on the observed morphology given. In these instances, a morphotype was allocated to each taxon using expert judgement informed by the morphologies allocated to matching taxa from Phase 1 (as identified on the previous step of the procedure) and online descriptions and photos (e.g. MarLIN [https://www.marlin.ac.uk/], Encyclopedia of Marine Life of Britain and Ireland [http://www.habitas.org.uk/marinelife/]). The classification used in Phase 1 included sixteen possible morphotypes, likely due to combining multiple classifications (e.g. Boury-Esnault & Rützler 1997), with over 30 morphotypes; Bell *et al*. (2006) and Berman *et al*. (2013), with 8 to 10 morphotypes). The sponge morphologies in both Phase 1 BIO and Phase 2 BIO datasets were revised and harmonised with the classification in Berman *et al*. (2013 after Bell *et al.* 2006; Figure 2) which is the standardised sponge morphological classification adopted by the JNCC.

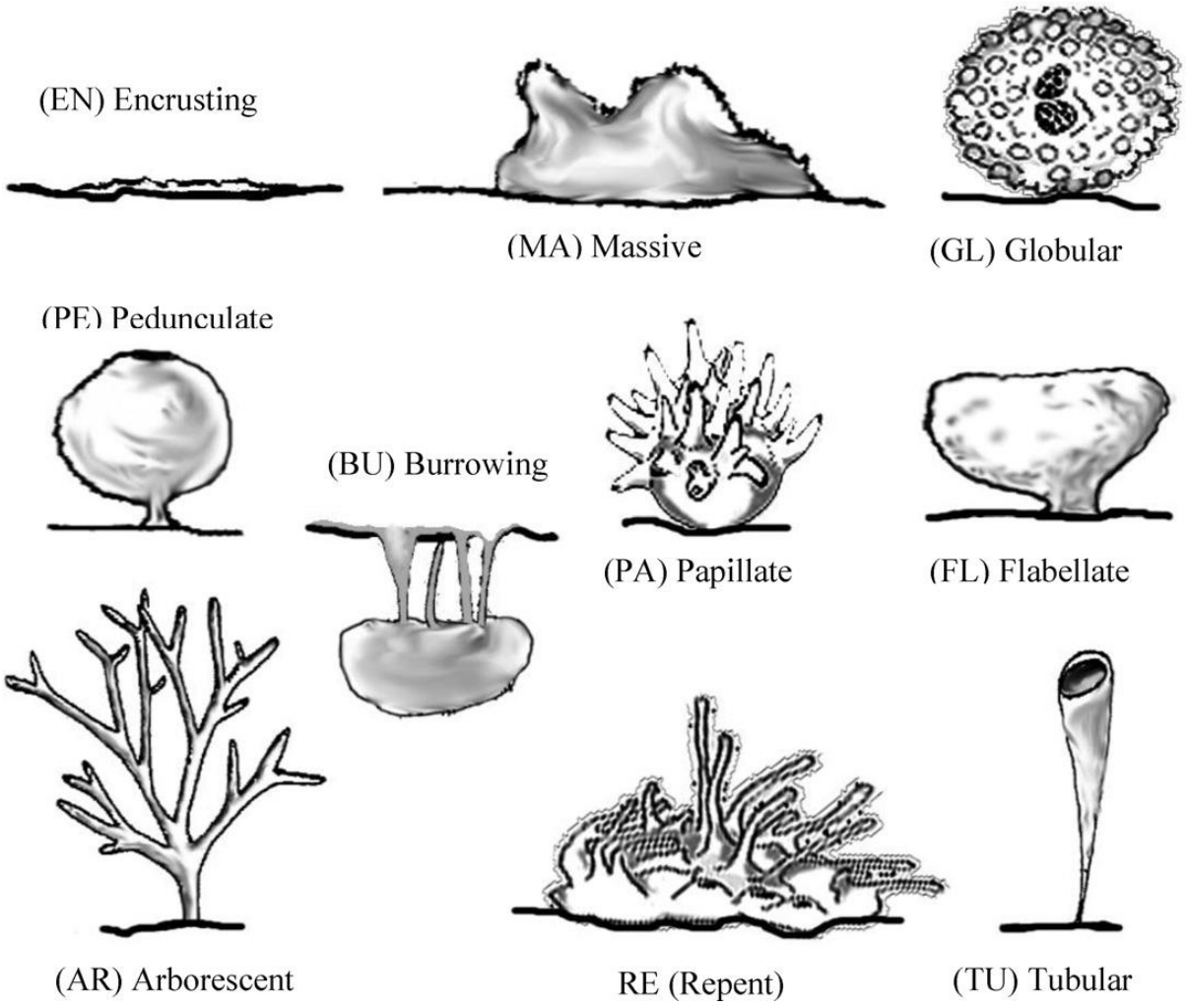

Figure 2. Sponge morphological types (Berman *et al.* 2013; after Bell *et al.* 2006).

Preliminary exclusions and aggregations of taxa were undertaken based on the following criteria:

- Taxa with high mobility or lower association with the seabed (fish and other mobile, swimming, or pelagic species, such as mysids, prawns, large crabs and lobsters, jellyfish) were excluded.
- Taxa with very small size or cryptic behaviour that makes their identification and abundance assessment less reliable (e.g. amphipods, small-sized gastropods) were excluded.

- Taxa identified with very low taxonomic resolution (e.g. Animalia) were excluded as these were not considered useful for the purpose of the analysis undertaken in this study.
- Taxa recorded in multiple forms in the dataset (e.g. *Spirobranchus* and *Spirobranchus* tubes) were merged because of uncertainty about consistency of recording between observers.
- Sponge taxa were aggregated according to morphology types, where these were known; where not known taxa (generally at family level) were retained. This reduced the number of sponge taxa/forms from 55 to 18 (with six of the latter occurring in less than five samples overall).
- Taxa with very low occurrence in the overall dataset (less than five occurrences of the taxon in the combined Phase 1 and Phase 2 dataset) were identified. This threshold is based on the minimum occurrence considered appropriate for the TITAN analysis (Baker & King 2010; Baker *et al.* 2015a). Where possible, very low occurrences were corrected by merging taxa with taxonomic similarity (e.g. *Salmacina* and *Salmacina dysteri* were merged as *Salmacina*) negating the need to exclude the data.

The method applied when aggregating taxa was as follows:

- Where the groups of taxa to be merged were all recorded based on either count or coverage, the antilog transformation was applied to their numerical (logged) values (where greater than 0) in the samples (i.e. 10x or 2y, using base 10 or 2 for count- or coverage-derived observations, respectively, where x and y are the numerical values for species that were recorded based on count or coverage observations, respectively). The resulting values were summed between the taxa in the group for each sample, and the log transformation was then applied.
- Where the groups of taxa to be merged included a mix of record types (taxa recorded from count and coverage observations, across different surveys), the above criterion could not be applied due to the different log bases and scale of the anti-logged values. In these instances, the maximum of the numerical (logged) values amongst the taxa within the group was taken as representative for the whole group.

The resulting integrated biological dataset included a total of 258 taxa/forms (Appendix 3: Table 16). This dataset was further processed to create two alternative taxa datasets to be considered for further analysis: conspicuous and aggregated (Appendix 3: Table 17)

2.4.1 Conspicuous taxa

The conspicuous dataset only included taxa and forms (sponges) considered to be observed with higher certainty, and therefore greater confidence, thus giving more emphasis on the reliability of the records. This dataset included sponge morphologies, larger-bodied taxa, and higher-cover taxa, comprising a total of 188 taxa/forms (Appendix 1: Table 13).

2.4.2 Aggregated taxa

The aggregated dataset included all taxa and forms (sponges), with the highest taxonomic resolution being lowered from species to genus to reduce possible noise due to identification variability (e.g. depending on the level of training of the surveyor). Where multiple species belonging to the same genus were present, these were aggregated at genus level (e.g. *Alcyonium digitatum* and *Alcyonium glomeratum* merged as *Alcyonium*). The resulting dataset included a total of 177 taxa/forms (Appendix 1: Table 14).

2.5 Step 5 – Environmental data extraction and harmonisation

2.5.1 Survey data

Environmental variables characterising the habitat and environmental conditions of the sample observations were recorded with the survey data (Step 1; Appendix 2). Substratum composition was used to classify each sample according to its dominant sublittoral rock substratum type (bedrock, boulder, cobble or pebble) and the quantity of sublittoral rock (high, medium or low) using the methodology applied in Phase 1 (Step 2; Strong & Johnson 2023).

2.5.2 Data extracted from environmental spatial layers

Survey sample locations were used to extract additional variables from environmental data layers (including anthropogenic pressure indicators), as in Phase 1. The list of data layers and extracted environmental variables is given in Appendix 2. Most of the data layers and methods for extracting the environmental variables used in Phase 2 corresponded to those used in Phase 1, with a few exceptions described below.

UK SeaMap (2016) was used in Phase 2 in place of the EUSeaMap (2010; from EMODnet seabed habitat portal) used in Phase 1. UKSeaMap (2016) is based on updated data and for many areas provides information at a higher resolution (approximately 100 m) than the EUSeaMap data layer, thus providing more spatially accurate habitat predictions for each sample point. Phase 1 data for the variables extracted from this data layer were also updated. In addition to the categorical habitat variables, as extracted in Phase 1, continuous variables, measuring the kinetic energy at the seabed were also extracted (for both Phase 1 and Phase 2 data).

Updated bathymetric data layers for the UK (DEFRA Astrium bathymetric Data 2016) were used in Phase 2 (Phase 1 used Astrium 2015). This resource includes data layers at variable spatial resolutions (1 and 6 arcseconds) and with variable spatial coverage (lower coverage for the high-resolution layer). A hierarchical approach was adopted to extract bathymetric data for survey sample points (i.e. the use of bathymetry data at higher resolution were prioritised where available, while bathymetry data at lower resolution were only used where this high-resolution data were not available).

The suspension or erosion potential of each grain size category (i.e. the standardised coefficients used for the calculation of the resuspension pressure indicator from abrasion data layers) was derived as an inverse of the Hjulström curve of erosion thresholds (Hjulström 1935). This accounts for the cohesion, and therefore low erosion potential, of very fine sediment and classes the erosion potential for rock as zero (Figure 3). A high-resolution raster layer for suspension potential was then derived using the categorical sediment data from the UKSeaMap (2016).

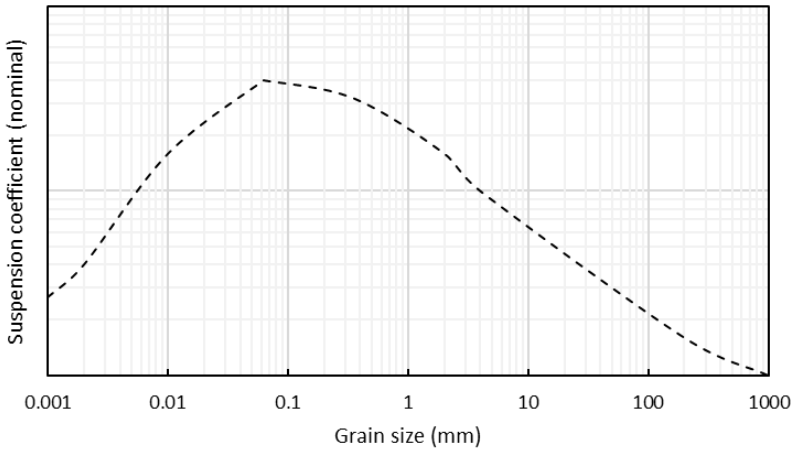

Figure 3. Suspension coefficients based on an inverse of the Hjulström curve of erosion thresholds (Hjulström 1935).

Updated annual pressure data layers characterising surface and subsurface abrasion from fishing activities (Church *et al.* 2016) were provided by JNCC for the years 2009 to 2016. These rasters were resampled to a resolution of 100 m in order to match the high-resolution sediment grid described above. The raster calculator tool was then used to weight the abrasion pressure raster for each year (2009 to 2016) by the resuspension potential raster, and to obtain the proxy indicator for anthropogenic resuspension due to surface abrasion (SA0 and SA.1 for the given survey years or the years before, respectively) and subsurface abrasion (SBA0 and SBA.1 for the given survey years or the years before, respectively), as done in Phase 1. The resulting proxy indicator ranged in the studied dataset between 0 and 7.3 for SA0 and SA.1, and between 0 and 1 for SBA0 and SBA.1. These rasters were further processed using the Focal Statistics tool to recalculate the value of each raster cell as an average of the surrounding radii (500 m). This gave consideration to the substratum and abrasion pressure of the surrounding area rather than the survey site location.

The abrasion from fishing pressure layers used were calculated from Vessel Monitoring System (VMS) data (Church *et al.* 2016), which account for the intensity of fishing activities (combines different gears). VMS data layers (by gear) were also obtained from the JNCC to allow exploration and potential creation of an additional pressure indicator. The physical abrasion from accidental contact of fishing gear, such as potting fleets, was considered a pressure of particular relevance for rocky habitats. While abrasion pressure layers do not include potting amongst the fishing activities (Church *et al.* 2016), VMS data layers included data for pots. However, the available VMS data layers only included the cumulative values across the period 2009 to 2015, therefore preventing any realistic association with the SACFOR survey data that were collected in different years. In addition, on a preliminary exploration of the potting VMS data layer, a very small spatial overlap was observed between areas of potting pressure and the survey sites in the studied datasets (this occurred for only 26% of the survey sites, cumulatively for Phase 1 and 2 sites). A decision was thus made not to pursue the development of a second pressure indicator any further within this phase of the contract.

Eighteen of the sample sites in the Phase 2 dataset fell outside the area covered by some of the environmental data layers, and therefore environmental variables could not be obtained for these sample locations (e.g. backscatter, POC). This prevented their inclusion in further data exploration, and they were therefore excluded from the combined dataset (Phase 1 and 2 combined), reducing its size to 6,867 samples.

2.6 Step 6 - Environmental gradient analysis and stratification

The collinearity between the environmental variables (continuous and ranked variables, including the pressure indicators) was explored by means of Spearman's rank correlation. Collinear variables with correlation coefficient less than -0.3 or greater than 0.3 were excluded from further analysis. Variance Inflation Factors (VIF) for the variables included in the final selection were checked, to ensure that multiple collinearity was low (VIF less than 3; Zuur *et al.* 2010).

The importance of the selected environmental gradients (including the pressure indicator) in the combined dataset were investigated by means of Principal Components Analysis (PCA). Where skewness in the data distribution and the influence of outliers needed to be reduced, the environmental data were transformed by natural logarithm or square root (where environmental data (x) included zero values, the transformations were applied to x+1; the natural base was used for log-transformations). Data were also normalised before undertaking PCA in order to control for different measurement units and distribution ranges (Clarke & Warwick 2001). Categorical variables (e.g. habitat type, rock type) were visualised in PCA plots using point symbology to allow identification of additional environmental differentiations in the dataset.

Conceptual Ecological Models (CEMs) for sublittoral rock habitats, as published in Alexander *et al.* (2015), were examined to identify a possible alternative stratification method to that used in Phase 1 (Strong & Johnson 2023). In particular, the model for temporarily or permanently attached active filter feeders (sub model 2; Figure 4) was considered as the most representative of the rock habitats included in this analysis. However, due to the qualitative nature of the CEM, these models were not deemed suitable for the purpose of extracting quantitative thresholds needed for the data stratification. Nevertheless, the model verified that the environmental variables considered (Section 3.2) in the present study accounted for the most important environmental drivers of biological communities in the rock habitats.

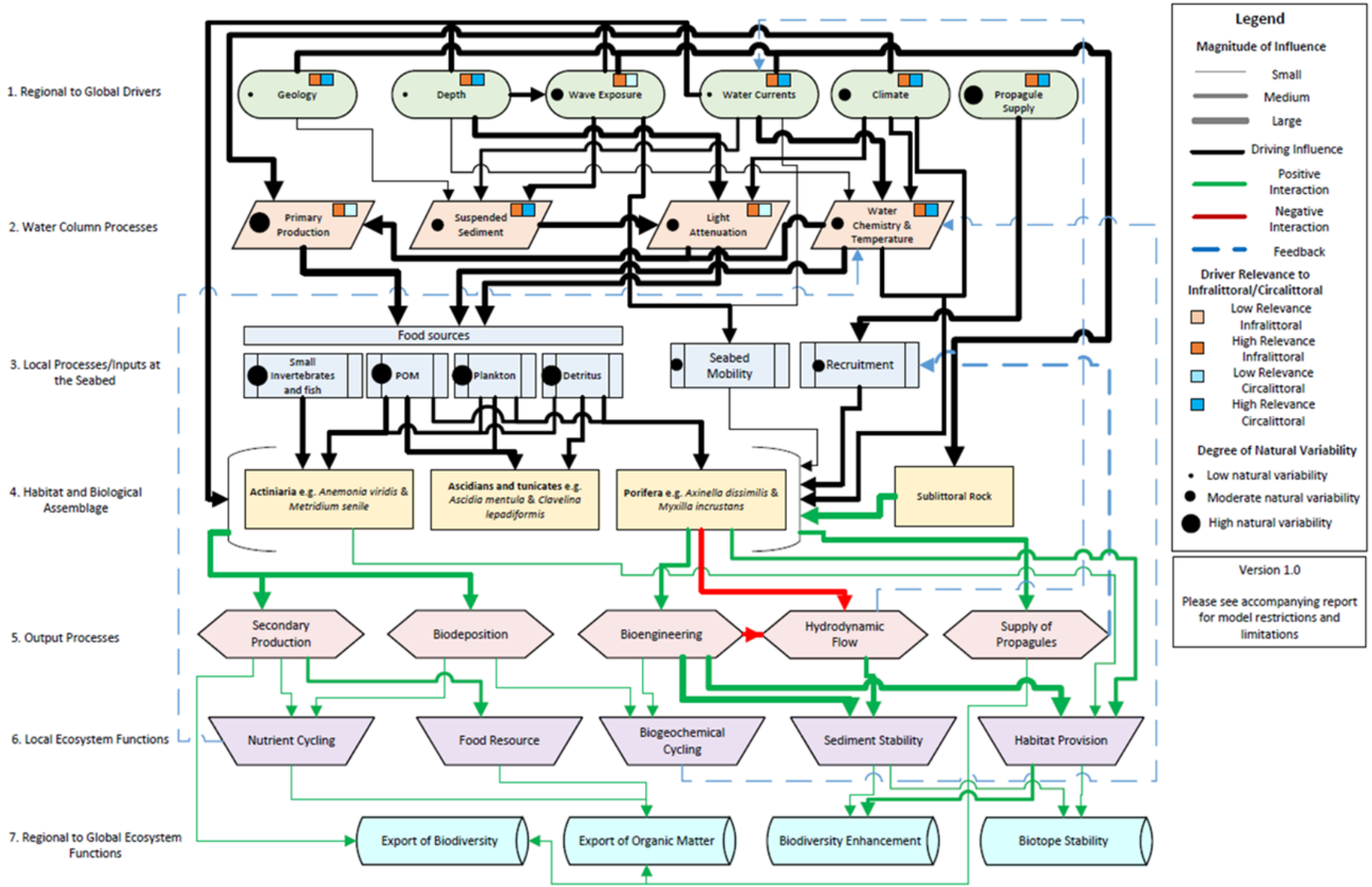

Figure 4. Conceptual Ecological Model for temporarily or permanently attached active filter feeders on sublittoral rock (sub model 2 from Alexander *et al.* 2015).

The stratification approach used in this analysis was developed based on objective differentiations in the data in order to reduce possible subjectivity in the strata determination. Differentiations were initially identified using PCA, with the environmental variables responsible for the main separations within the survey data used to stratify in a sequential manner. Three different criteria were combined to accept a given stratification:

1. The number of samples included in the resulting strata was used to assess whether the stratification led to an excessive reduction in the dataset size after stratification.
2. The gradient of the proxy indicator for anthropogenic resuspension (from now on referred to as pressure indicator) was assessed to ensure a sufficient gradient was maintained within the strata. An excessive reduction of the gradient is expected to reduce the power of the final analysis and therefore the validity of its results.
3. The biological sample data (community composition) was used to validate the stratification. These data were compared between the resulting strata to confirm that the environmental differentiation corresponded to a differentiation in the structure of biological communities. A non-parametric analysis of similarities (ANOSIM, 999 permutations) was applied to the biological data matrix after calculation of Bray-Curtis Similarity. This test was applied separately for the two datasets analysed (Conspicuous taxa and Aggregated taxa) with the resulting R statistics used as a criterion for validation. R ranges between 0 and 1, with 0 indicating a complete overlap in the community composition between the groups, and 1 indicating a complete separation. Very low R values (e.g. less than 0.1) were considered indicative of no substantial differentiation in the community composition of the environmental stratification applied, and therefore that level of stratification was rejected. R values were also used to choose between alternative stratifications when there was not a clear dominant environmental gradient.

2.7 Step 7 – Rare species removal (within strata)

The biological datasets within each of the strata identified in Step 6, for the two datasets (conspicuous and aggregated taxa), were further explored and taxa with less than five occurrences in the stratum dataset were identified and excluded from analysis. The choice of this threshold was again driven by the minimum occurrence considered appropriate for the TITAN analysis (Baker & King 2010; Baker *et al*. 2015a). This differs from the Phase 1 approach which removed taxa with less than 2% commonality across the dataset (i.e. represented by 137 or fewer observations across the Phase 1 dataset which consisted of 6,852 observations).

TITAN has been designed to deal explicitly with biological survey data that are commonly characterised by sparse matrices (i.e. absences occurring in nearly any sampling unit, leading to many zeros in the dataset) and noisy data (with high levels of variability) (Baker & King 2013). Taxa occurring with low frequency in the analysed dataset are more likely to show weak and/or inconsistent changes along the studied environmental gradient. As species are analysed separately in TITAN before combining their response at community level, these taxa can be filtered out of the analysis *a posteriori*, if needed. Therefore, no further exclusion of taxa on account of their low frequency of occurrence was undertaken.

2.8 Step 8 – Threshold Indicator Taxa ANalysis (TITAN)

The TITAN was applied to the selected stratified datasets (Conspicuous and Aggregated taxa) using the TITAN2 package in R (Baker *et al*. 2015b), as in Phase 1. All data within each stratum were included in the analysis in order to represent the full pressure gradient within a stratum, including baseline conditions (i.e. data with a pressure indicator value of zero).

Similarly, as with Phase 1, indicator taxa were selected as those 'filtered' taxa that met purity and reliability criteria (i.e. showing consistent change (in direction and magnitude) in over 95% of the cases during bootstrap resampling). The response of taxa not meeting the purity and reliability criteria was considered uncertain, and therefore these taxa were not considered as suitable indicators of change along the studied gradient.

In Phase 1, the 'indicator quality' score ('IndVal') was used. In addition, taxa with IndVal values in the top ten were considered as indicators in combination with the 'filtered' taxa outputs (Strong & Johnson 2023). However, this additional criterion very rarely resulted in additional taxa being included in the indicator list (i.e. almost all the taxa selected according to the 'indicator quality' criterion had already been selected as 'filtered' taxa based on purity and reliability criteria). For those few additional taxa selected based on the 'indicator quality' criterion, they often showed a comparatively small magnitude of change and/or a marked inconsistency in their response along the pressure gradient. For example, *Alcyonium digitatum* in the bedrock subset identified in Phase 1, had an IndVal value of only 1.24% (denoting a small magnitude of change) and showed a consistent positive change along the gradient only in 51% of the cases during bootstrap resampling. Due to the uncertainty introduced by the inclusion of these taxa in the analysis, the use of the 'indicator quality' criterion was therefore abandoned in Phase 2.

Community change points ('cp') identify the points along the pressure gradient where the highest synchronisation between taxa showing either a negative (z-) or positive change (z+) occurs. These were used as reference points for the calculation of benchmarks and for validation purposes, similarly to Phase 1. TITAN calculates community change points by considering the whole set of taxa in the community (sumz-.cp and sumz+.cp) or by only including the 'filtered' taxa (fsumz-.cp and fsumz+.cp). The latter change points were used as reference in this study, to avoid the influence of taxa that are non-reliable and non-pure (i.e. taxa showing inconsistencies in the direction and magnitude of the response on bootstrap resampling).

2.9 Step 9 – Benchmark abundance

Benchmark abundance values were calculated following the method described in Phase 1. For each selected indicator taxon, benchmark abundance values (below and above the taxon change point) were obtained as the mean of the abundance index (logged values as in the input datasets) between the samples in the resulting dataset partitions (i.e. below and above the observed cp), using the change point relevant to the specific taxon (i.e. fsumz-.cp for taxa showing a negative change along the gradient and fsumz+.cp for taxa showing a positive change).

2.10 Step 10 – Validation

The benchmark validation allows assessment of the degree of accuracy of the established benchmarks for the selected indicator taxa can provide in predicting whether an observation is from above or below the relevant change points. The accuracy score takes into account the predictive ability of each indicator taxon and combines this taxon-specific results into an average (as percentage accuracy) across all the indicator taxa selected as indicators for a given stratified dataset.

The validation of the obtained benchmarks was undertaken following the approach used in Phase 1 by estimating their accuracy in classifying a community as below or above change point based on the selected indicator taxa through random sub-sampling of the dataset partitions. Due to limitations in the size of the partitions in the stratified datasets analysed in Phase 2, randomised subsets of data were selected to include 25% of the dataset available

above and below the community change points. The variability in the number of samples thus considered for the validation is shown in the results.

3 Results

3.1 Data integration

The biological datasets obtained from the data preparation (Steps 1 to 5) and used as input data for the stratification analysis were:

- Conspicuous taxa dataset ('consp'), including 188 taxa/forms and 6,852 samples; and
- Aggregated taxa dataset ('aggrt'), including 177 taxa/forms and 6,852 samples.

The two datasets shared the same set of samples, including 6,837 samples from Phase 1 and 15 samples from Phase 2. A preliminary exploration of the environmental characteristics of the sample survey sites included in these datasets showed the existence of a notable differentiation of habitats represented by samples from Phase 1 and Phase 2, reflecting the different nature of the surveys. Diving surveys (Phase 2) are normally undertaken in shallower areas and closer to the coastline compared to video surveys (Phase 1). This was reflected in the habitat distribution of the data, with 46% of the new sample records for Phase 2 collected in the infralittoral zone (the remaining being circalittoral), whereas data used in Phase 1 only included circalittoral or deeper habitats. Further environmental variability was explored in detail through gradient analysis (Section 3.2).

The taxa included in the two datasets (Appendix 1: Table 13 and Table 14) was the result of a series of harmonisations and exclusions described in Steps 4 and 7 (see also Appendix 3 for details). There was a substantial overlap between the resulting taxa lists in the two datasets, with 89% of the taxa/forms occurring in both datasets. The lower number of taxa in the 'aggrt' dataset was generally due to taxa occurring as different species in 'consp' which were merged according to genus in 'aggrt'.

3.2 Environmental gradients and collinearity

The correlation analysis highlighted multicollinearity between the environmental variables (including pressure indicators; Table 6). As a result, collinear variables were excluded (Table 7), and the following variables were retained for further analysis:

- Lat (latitude)
- Depth
- Slope
- Curr (current speed)
- Backs (backscatter, as a proxy for turbidity)
- POC
- Kwav (kinetic energy due to waves)
- RockQnum (ranked value for the high/moderate/low quantity of rock)
- EnerC (ranked value for the high/moderate/low energy due to currents and waves)
- SA0 (indicator of sediment resuspension pressure).

Table 6. Absolute Spearman's rank correlation coefficients between the environmental variables (also including pressure indicators) for the studied integrated dataset. Correlation coefficients between -0.3 and 0.3 are not shown. See Appendix 4 for variables abbreviations.

	Lat	Long	Dist	Depth	Slope	STemp	Curr	Mix	Backs	POC	KCurr	Kwav	SA0	SA.1	SBA0	SBA.1	RockQnum	BiozC	EnerC
Lat	1	-	-	-	-	-	0.41	-	-	-	-	-	-	-	-	-	-	0.43	-
Long	-	1	-	-	-	-	0.54	-	0.45	-	0.40	-	-	-	-	-	-	-	0.39
Dist	-	-	1	0.54	-	-	-	0.83	-	-	-	-	-	-	-	-	-	-	-
Depth	-	-	0.54	1	-	-	-	0.77	-	-	-	-	0.39	0.35	0.38	0.36	-	0.48	-
Slope	-	-	-	-	1	-	0.40	-	-	-	-	-	-	-	-	-	-	0.32	-
STemp	-	-	-	-	-	1	-	-	0.77	0.52	0.77	-	-	-	-	-	-	-	-
Curr	0.41	0.54	-	-	0.40	-	1	-	-	-	-	-	-	-	-	-	-	0.45	-
Mix	-	-	0.83	0.77	-	-	-	1	-	-	-	-	-	-	-	-	-	0.48	-
Backs	-	0.45	-	-	-	0.7709	-	-	1	0.47	0.69	-	-	-	-	-	-	-	-
POC	-	-	-	-	-	0.5157	-	-	0.47	1	0.39	-	-	-	0.31	-	-	-	-
KCurr	-	0.40	-	-	-	0.7721	-	-	0.69	0.39	1	-	-	-	-	-	-	-	0.60
Kwav	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
SA0	-	-	-	0.39	-	-	-	-	-	-	-	-	1	0.86	0.97	0.87	-	-	-
SA.1	-	-	-	0.35	-	-	-	-	-	-	-	-	0.86	1	0.85	0.96	-	-	-
SBA0	-	-	-	0.38	-	-	-	-	-	0.31	-	-	0.97	0.85	1	0.90	-	-	-
SBA.1	-	-	-	0.36	-	-	-	-	-	-	-	-	0.87	0.96	0.90	1	-	-	-
RockQnum	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
BiozC	0.43	-	-	0.48	0.32	-	0.45	0.48	-	-	-	-	-	-	-	-	-	1	-
EnerC	-	0.39	-	-	-	-	-	-	-	-	0.60	-	-	-	-	-	-	-	1

Table 7. Variables excluded from further analysis due to multi-collinearity (correlation was considered as high when absolute value of Spearman's rank correlation greater than0.8, moderate when between 0.5 and 0.8, and lower when between 0.3 and 0.5).

Variables removed	Reason for exclusion
SA.1	High positive correlation with SA0 (+ SA.1 has missing values for survey data from 2009)
SBA.1	High positive correlation with SBA0 (+ SBA.1 has missing values for survey data from 2009)
SBA0	High positive correlation with SA0 (SA0 is also less correlated with other environmental variables)
Mix	High positive correlation with Dist, moderate positive correlation with Depth, and lower positive correlation with BiozC (depth ranks)
Kcurr	Moderate positive correlation with STemp, EnerC, Backs, and lower positive correlation with Long and POC
STemp	Moderate positive correlation with Kcurr, Backs and POC
Long	Moderate positive correlation with Curr, and lower positive correlation with Backs, Kcurr and EnerC
Dist	High positive correlation with Mix, moderate positive correlation with Depth
BiozC	Lower correlation with Mix, Depth, Curr, Lat and Slope

A preliminary data exploration undertaken on these variables highlighted that Lat had a bimodal distribution in the studied dataset, due to the data being distributed in North (50 to 52° N) and South areas (58 to 62° N). Therefore, this variable was transformed into a categorical one (N & S) and included as such in the analysis. Although less evident than for Lat, there was also a general separation of Backs data into two groups, with values less than 0.005 shown by approximately two thirds of the data, and values greater than 0.008 in the remaining data. The variable was kept as continuous variable in the analysis (after log transformation), but the data were also categorised as low and high turbidity to ease the interpretation of the two groups. Depth, Slope, Curr and SA0 were log-transformed before the analysis, whereas a square-root transformation was applied to POC.

A PCA was applied to identify the main environmental gradients in the studied dataset. The gradual increase in the cumulative variation explained by each axis of the analysis (Figure 5) suggested that there was not a predominant gradient, but rather all environmental variables contributed to the variability in the dataset. Nevertheless, a clear separation of the sample data was observed according to latitude (N/S areas), depth (as also shown by shallow and deep biozones), energy and turbidity levels, whereas the separation between rock types and quantity was less evident in the main dataset (Figure 6). The pressure gradient (SA0 vector in the PCA plot) was generally perpendicular to the direction of these separations which suggested a low correlation between SA0 values and the separating factors, although the pressure gradient range is likely to vary between the different groups of data (as suggested by the different spread of the data in the direction of the SA0 vector; Figure 6).

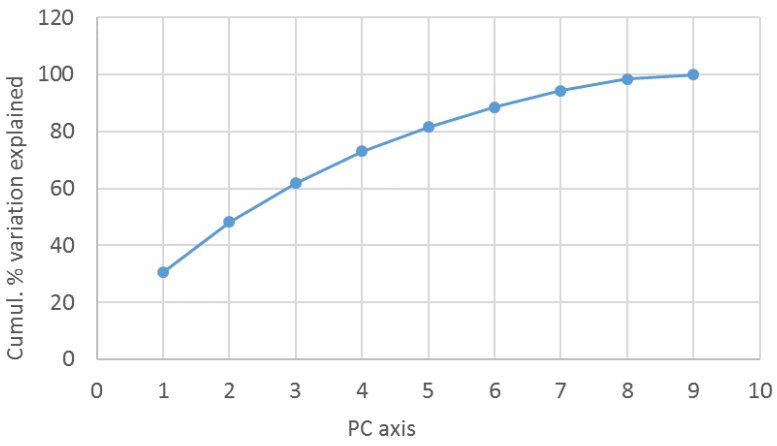

Figure 5. Cumulative percentage variation in the data explained by the PC axes in the PCA undertaken on the overall dataset (6,852 samples).

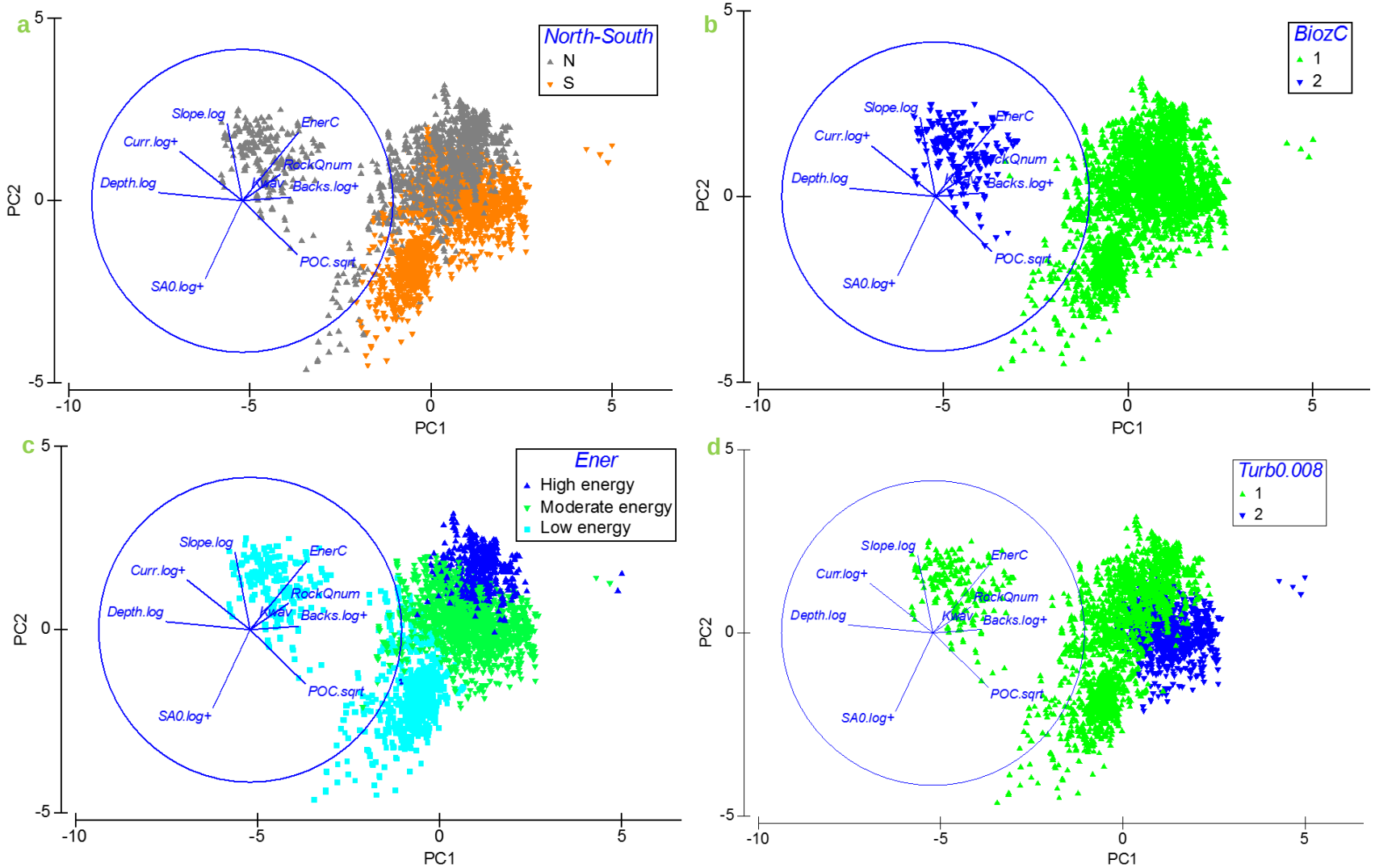

Figure 6. PCA plots with sample data categorised by: a) latitude (N, S); b) Biozone (1 = shallow (infralittoral to deep circalittoral habitats), 2 = deep (bathyal habitats)); c) Energy (low, moderate, high); and d) Turbidity (1 = low, 2 = high). Additional categorisation is shown overleaf.

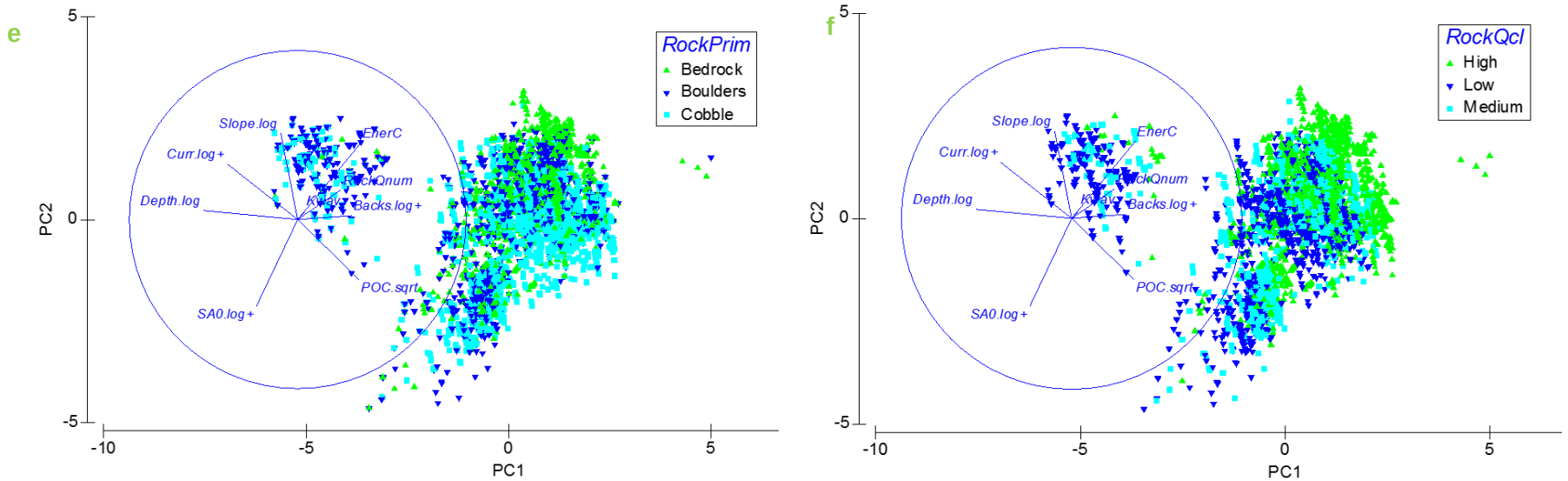

Figure 6. Continued. PCA plots with sample data categorised by: e) primary type of rock substratum (bedrock, boulders, cobble): and f) quantity of rock substratum (low, medium, high).

3.3 Dataset stratification

The separations between the data, according to the environmental factors identified in the PCA, were used in combination with the correspondent differentiation of the biological communities (as assessed by ANOSIM analysis) to inform the data stratification (Appendix 4).

First, the data were stratified according to latitude (North and South areas), also in consideration of possible community differentiation between biogeographic areas, as confirmed by the ANOSIM test (Appendix 4; Table 18).

Within the North sample group (Figure 6a), data were clearly differentiated between shallow and deeper areas (Figure 6b), a stratification that was supported by the analysis of the biological communities (Appendix 4: Table 18). Additional stratifications of the northern shallow sub-group (Figure 6a) were explored (energy and rock type, Figure 6c and 6e respectively) with energy levels corresponding to a stronger separation between biological communities (i.e. higher R value; Appendix 4: Table 18). It was noted that this shallow sub-group only included low turbidity samples (Figure 6d). Based on the characteristics of the pressure gradient range, the three energy subsets were initially considered sufficiently representative of the original pressure gradient (Appendix 4: Table 18). However, further exploration of the data distribution along the pressure gradient within the three subsets highlighted that the samples in the high energy subset were highly skewed towards zero pressure (86% of the data; Figure 10). This, combined with the reduction in pressure gradient, led to the exclusion of this high energy stratum from further analysis. No further stratification was applied to the shallow sub-group to avoid excessive reduction of the dataset size and of the pressure range represented within each resulting stratum. For the deep sub-group, the pressure gradient represented in this dataset was substantially reduced (to 15% of the original gradient), and it was not considered representative enough of the overall gradient for this stratum to be further analysed (Appendix 4: Table 18).

The South sample group (Figure 6a) was only composed of shallow samples (Figure 6b), and a reduced pressure gradient (46% of the original one) was represented in the data from this area. Other stratifications of this group were explored (energy, turbidity, rock type; Figure 6c, 6d and 6e respectively). Stratification between rock types was selected for its strong separation between biological communities, while also maintaining balanced dataset sizes and pressure gradients sufficiently representative of the biogeographic area (Appendix 4: Table 18). Of the stratifications explored for the southern bedrock sub-group (energy and turbidity, Figure 6c and d respectively), turbidity demonstrated the strongest separation between biological communities (Appendix 4: Table 18). However, the southern bedrock high turbidity subset (Figure 6d) only included three samples and therefore it was not considered further in the analysis. For the low turbidity subset (Figure 6d), a clear environmental differentiation between energy levels was observed, but this was not supported by a change in biological communities, and therefore this further stratification of the southern, low turbidity, bedrock habitat was initially rejected. However, due to timing limitations in the computation of the TITAN analysis (possibly due to the big size of the datasets for this stratum, including more than 2,000 samples), a choice was made to apply this further stratification based on energy. This had the effect of excessively reducing the dataset size for the high energy subset (including only one sample) and the pressure gradient represented in the moderate energy subset (to 11% of the original gradient), and therefore the southern bedrock low energy stratum was only considered for further analysis. For the southern boulders sub-group stratifications of energy and turbidity (Figure 6c and 6d) were explored and the former was selected due to a correspondent stronger differentiation in biological communities (Appendix 4: Table 18). However, the data subsets for moderate and high energy showed an excessive reduction in dataset size (one sample only within the southern boulder high energy subgroup) or pressure gradient range (9% of the original one

at moderate energy), and therefore the southern boulder low energy stratum was only considered for further analysis. This stratum was characterised by samples with low turbidity. The southern cobble sub-group was also further stratified according to energy, as this was supported by a stronger change in biological communities compared to a turbidity stratification (Appendix 4: Table 18). Due to the excessive reduction of the pressure gradient range in the moderate energy subset (11% of the original gradient), the low energy subset was only considered for further analysis (no high energy samples were present in the southern cobble sub-group). All samples within this low energy stratum were also characterised by low turbidity.

The resulting strata considered for the analysis are summarised in Table 8. The stratification led to a substantial homogenisation of the environmental variability along the pressure gradient within each stratum (Appendix 4: Figure 12 to Figure 16), thus likely reducing the effect of this natural variability in the final results. None of the selected strata included samples from the Phase 2 dataset, as these were obtained from areas of moderate energy (in the South) and high energy (in the North and South) that were not analysed here (Appendix 4: Table 18).

Table 8. Final stratification applied to the datasets before the TITAN analysis. 'Number of taxa' symbols refer to conspicuous dataset (*); and aggregated dataset (†).

Stratum	Selected characteristics	Additional characteristics	Number of Taxa	Number of Samples	Representation of SA0 gradient
N1	North, Shallow (deep circalittoral), Low energy	Low turbidity; variable rock type	48*, 47†	183	Good (0–7.3, 100% gradient)
N2	North, Shallow (shallow-deep circalittoral), Moderate energy	Low turbidity; variable rock type	87*, 84†	673	Reduced (0–2.5, 34% gradient)
S1a	South, Bedrock, Low turbidity, Low energy	Shallow (deep circalittoral)	63*, 62†	767	Reduced (0–1.7, 23% gradient)
S2	South, Boulders, Low energy	Shallow (deep circalittoral); low turbidity	49*, 50†	407	Reduced (0–3.4, 46% gradient, but full gradient in South data)
S3	South, Cobble, Low energy	Shallow (deep circalittoral); low turbidity	61*, 62†	596	Reduced (0–2.3, 32% gradient)

3.4 Threshold Indicator Taxa Analysis (TITAN)

The TITAN was undertaken on a total of 10 datasets, consisting of the 'consp' (conspicuous) and aggrt' (aggregated) datasets, each subdivided into the five environmental strata N1, N2, S1a, S2 and S3 (Table 8).

For each dataset community change points were identified along the pressure indicator gradient (SA0), with values for groups of taxa showing a negative change (decrease) along the gradient and the group showing a positive change (increase) identified (Table 9). Negatively responding taxa tend to show a change at lower levels along the pressure

indicator gradient compared to positively responding taxa, as also observed for the analysis undertaken in Phase 1.

The 90% percentile interval, as generated by 500 bootstrap resampling, provides information on the uncertainty around the observed change points. This interval, and therefore the uncertainty, is generally smaller for the community change points associated with negatively responding taxa compared with change points for taxa responding positively (Table 9 and Figure 7). This denotes a higher synchronisation between negatively responding taxa of where a change in the taxon-specific frequency and abundance occurs along the gradient, and therefore the community change point can be considered representative of the taxon-specific changes with a high degree of certainty. In turn, a higher uncertainty is associated with the community change point for taxa showing an increase along the studied gradient, due to the wider variation of taxon specific positive change points (Appendix 6).

Table 9. Community change points identified along the pressure gradient (SA0) within the datasets analysed with TITAN, as resulting from the cumulative responses of indicator ('filtered') taxa (i.e. meeting the reliability and purity criteria) showing a negative response and those showing a positive response. For each change point, the table also shows the 90% percentile interval resulting from 500 bootstrap resampling, and the number of taxa contributing to defining that community change point. The mean and range of variability of the SA0 pressure gradient within each dataset are also given for reference. Note 'consp' and 'aggrt' refer to conspicuous data set and aggregated dataset.

Stratum	Taxa	Variable	Negative response	Positive response
N1	consp	observed change point	0.07	0.41
		90% percentile interval	0.06–0.27	0.19–1.93
		number of indicator taxa	18	2
		SA0 pressure	range 0.004–7.27 (mean = 1.66)	
	aggrt	observed change point	0.07	0.41
		90% percentile interval	0.06–0.19	0.19–1.93
		number of indicator taxa	18	2
		SA0 pressure	range 0.004–7.27 (mean = 1.66)	
N2	consp	observed change point	0.01	0.12
		90% percentile interval	0–0.01	0.12–1.19
		number of indicator taxa	15	23
		SA0 pressure	range 0–2.48 (mean = 0.19)	
	aggrt	observed change point	0.01	0.12
		90% percentile interval	0.01–0.01	0.12–1.36
		number of indicator taxa	15	21
		SA0 pressure	range 0–2.48 (mean = 0.19)	
S1a	consp	observed change point	0.32	0.32
		90% percentile interval	0.22–0.36	0.32–0.95
		number of indicator taxa	14	13
		SA0 pressure	range 0–1.67 (mean = 0.21)	
	aggrt	observed change point	0.32	0.32
		90% percentile interval	0.29–0.36	0.32–0.95

Stratum	Taxa	Variable	Negative response	Positive response
		number of indicator taxa	14	12
		SA0 pressure	range 0–1.67 (mean = 0.21)	
S2	consp	observed change point	0.45	no indicator taxa
		90% percentile interval	0.38–0.47	-
		number of indicator taxa	9	0
		SA0 pressure	range 0–3.38 (mean = 0.7)	
	aggrt	observed change point	0.38	1.06
		90% percentile interval	0.22–0.7	1.02–1.26
		number of indicator taxa	8	1
		SA0 pressure	range 0–3.38 (mean = 0.7)	
S3	consp	observed change point	0.1	0.51
		90% percentile interval	0.05–0.24	0.49–1.62
		number of indicator taxa	9	4
		SA0 pressure	range 0–2.32 (mean = 0.63)	
	aggrt	observed change point	0.09	1.59
		90% percentile interval	0.05–0.44	0.49–1.62
		number of indicator taxa	10	5
		SA0 pressure	range 0–2.32 (mean = 0.63)	

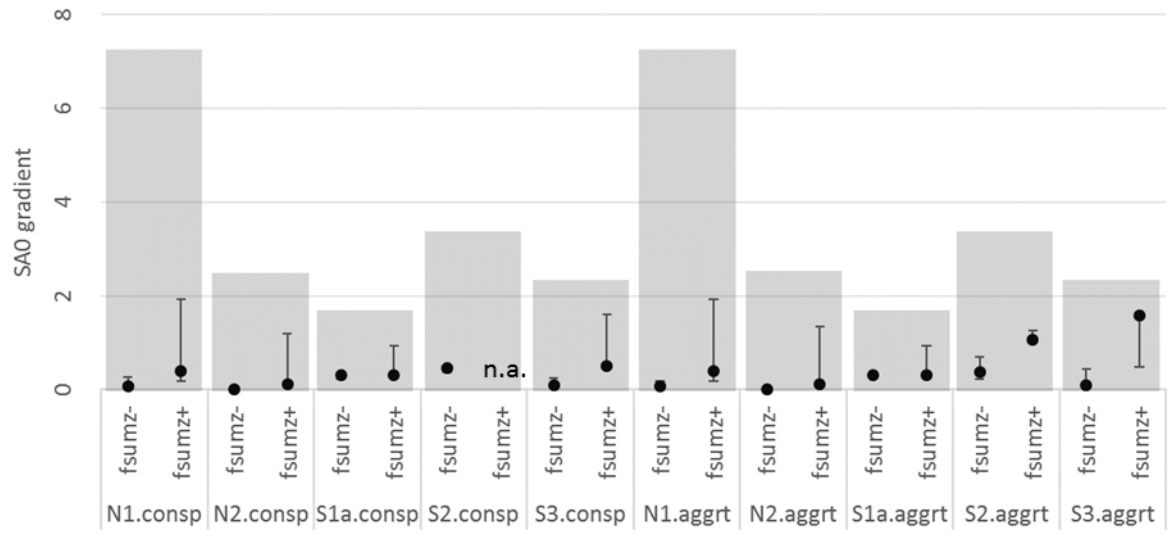

Figure 7. Community change points identified within datasets analysed along the pressure gradient (SA0) analysed with TITAN, resulting from the cumulative responses of indicator ('filtered') taxa. The observed change point for indicator taxa (circle) and the associated 90% percentile interval resulting from 500 bootstrap resampling (5% to 95% percentile whiskers) are shown for taxa responding negatively (fsumz-) and positively (fsumz+) along the SA0 pressure gradient. Shaded areas show the pressure gradient range represented in each dataset analysed. No indicator taxa responding positively to the gradient were identified for the dataset 'S2.consp' (n.a.).

The number of indicator taxa (i.e. meeting the purity and reliability criteria) selected for each stratified dataset are also provided in Table 9. Negatively responding indicator taxa were identified for all of the datasets, whereas none of the positively responding taxa in the dataset 'S2.consp' met the purity and reliability criteria and therefore could not be selected as indicator taxa. Full results for taxon-specific responses (also including non 'filtered' taxa) are available in Appendix 6.

A general agreement in the indicator taxa identified between the 'consp' and 'aggrt' datasets for each stratum was observed, likely due to the high similarity between the two datasets (Table 10). Some taxa frequently selected as indicators consistently showed a negative (e.g. Sertulariidae, Ophiuroidea, Brachiopoda, *Swiftia pallida*) or a positive response (e.g. Actiniaria, Encrusting sponges, *Munida*, Paguroidea) across most strata. Other taxa showed a mixed response, depending on the stratum of occurrence (e.g. *Porania pulvillus* (negative response in N1 and S1a, positive in N2), Hydrozoa (negative response in S1a and S2, positive in N2), *Parazoanthus* (negative response in N1 and S2, positive in N2)). A notable differentiation between the direction of responses for the same taxa was identified between the two strata in the North area (N1 and N2), which primarily differed in their level of energy from currents and tides (higher in N2). Numerous other taxa were only selected as indicators within one or two strata, most commonly within N2 and S1a strata.

Table 10. Summary of the direction of response of the indicator taxa (i.e. meeting purity and reliability criteria) within each stratum and dataset analysed: 'consp' – conspicuous taxa list, 'aggrt' – aggregated taxa list; N – negative response; P – positive response (where the cell is empty, the taxon was not selected as an indicator in the specific dataset). The taxa are ordered by decreasing frequency of being selected as candidate indicator across the datasets. Note some taxa are not represented in both 'consp' and 'aggrt' datasets, differences represented as N/A.

Stratum	**N1**	**N2**	**S1a**	**S2**	**S3**
Area	North	North	South	South	South
Biozone	Shallow	Shallow	Shallow	Shallow	Shallow
Energy	Low	Moderate	Low	Low	Low
Turbidity	Low	Low	Low	Low	Low
Rock type	Variable	Variable	Bedrock	Boulders	Cobble

Stratum	**N1**		**N2**		**S1a**		**S2**		**S3**		
Taxa	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**Freq**
Sertulariidae	N	N			N	N	N	N	N	N	8
Brachiopoda					N	N	N	N	N	N	6
Hydrozoa			P	P	N	N	N	N			6
Ophiocomina nigra			N	N	P	P			N	N	6
Ophiothrix fragilis	N	N			P	P			N	N	6
Ophiuroidea	N	N	N	N	N	N					6
Palmiskenea skenei	N	N					N	N	P	P	6
Porania pulvillus	N	N	P	P	N	N					6
Swiftia pallida					N	N	N	N	N	N	6
Caryophyllia				N	N	N			P	P	5
Parazoanthus	N	N	P	P			N				5
Porella				P	N	N			N	N	5
Actiniaria			P	P					P	P	4

Stratum	N1		N2		S1a		S2		S3		
Taxa	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**Freq**
Balanoidea	N	N	P	P							4
Bryozoa			P	P	N	N					4
Encrusting (Porifera)	P	P	P	P							4
Flustra foliacea	N	N	N	N							4
Hexacorallia	N	N	P	P							4
Hymedesmiidae	N	N	P	P							4
Massive (Porifera)							N	N	N	N	4
Munida			P	P					P	P	4
Paguroidea			P	P	P	P					4
Reteporella	N	N	P	P							4
Scleractinia	N	N	P	P							4
Serpulidae	N	N	P	P							4
Ophiura albida	N	N/A	P	N/A	P	N/A					3
Parasmittina	N	N	N								3
Porifera			P		P	P					3
Sabellida					P	P		P			3
Actiniidae			N	N							2
Alcyonidium					N	N					2
Arborescent (Porifera)	P	P									2
Ascidiacea					N	N					2
Ascidiidae			N	N							2
Asterias rubens	N	N									2
Buccinidae									N	N	2
Calliostoma					N	N					2
Caryophyliidae	N	N									2
Celleporidae			N	N							2
Corallinaceae			N	N							2
Corynactis					P	P					2
Crossaster papposus			N	N							2
Ebalia			P	P							2
Edwardsiidae							N	N			2
Flabellate (Porifera)			P	P							2
Flustrina			N	N							2
Galatheoidea			P	P							2
Globular (Porifera)									N	N	2
Holothuroidea							N	N			2
Lanice conchilega	N	N									2
Mesacmaea mitchellii					P	P					2
Nemertesia			P	P							2

Stratum	N1		N2		S1a		S2		S3		
Taxa	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**consp**	**aggrt**	**Freq**
Ophiactidae					P	P					2
Ophiura		N		P							2
Pagurus			N	N							2
Papillate (Porifera)					P	P					2
Pectinidae					P	P					2
Repent (Porifera)					N	N					2
Rhodophyta			N	N							2
Smittinoidea			N	N							2
Spirobranchus						P				P	2
Styelidae					P	P					2
Terebellida			P	P							2
Trochidae					N	N					2
Tubular (Porifera)			N	N							2
Alcyonium digitatum			N	N/A							1
Nudibranchia									N/A	N	1
Parazoanthus anguicomus			P								1
Porella compressa			P	N/A							1
Spirobranchus triqueter					P	N/A					1

3.5 Indicator taxa benchmark abundance

The benchmark abundance index was calculated for each indicator taxon within each stratified dataset (Appendix 7; Taxa abbreviations provided in Appendix 5).

3.6 Validation

The highest accuracy levels were observed for the stratum S1a, whereas the lowest accuracy was for N1 (Table 11). This result was influenced by dataset size with larger datasets showing higher accuracy. The dataset size affected the number of samples within each partition below and above the observed change point and limited the number of randomised samples that could be resampled for validation purposes. These validation results should therefore be taken with caution, due to the randomised datasets used for the validation not being independent from the data used to generate the benchmark values.

Table 11. Classification accuracy for the suite of indicator taxa/forms for each stratified dataset analysed. The mean accuracy and standard deviation (SD) were calculated on randomly selected subsets including 25% of the data (n shows the resulting number of samples included in the subset partitions for negative/positive indicator taxa).

Stratum	Accuracy	Consp. dataset		Aggrt. dataset	
		below cp	above cp	below cp	above cp
N1	mean	79%	89%	82%	94%
	SD	10%	6%	8%	4%
	n	4/21	42/25	4/21	42/25
N2	mean	92%	86%	91%	86%
	SD	4%	6%	4%	8%
	n	75/110	94/59	78/110	90/59
S1a	mean	94%	89%	95%	90%
	SD	5%	5%	3%	5%
	n	155/155	37/37	155/152	37/40
S2	mean	79%	90%	80%	81%
	SD	10%	10%	10%	7%
	n	18/-	87/-	8/85	94/17
S3	mean	85%	98%	85%	90%
	SD	8%	3%	8%	7%
	n	4/53	146/96	4/144	146/5

4 Discussion

4.1 Comparison with Phase 1

As with Phase 1, many limitations were encountered during this phase regarding data quality and availability, representation of the environmental and pressure variability, and uncertainty and confidence issues (discussed further below). Despite these limitations, indicator taxa were identified for rock communities in given environmental conditions (as defined by the stratification). The validation of the indicator taxa demonstrated generally high levels of confidence, as attested by the measured accuracy being greater than 80% in most cases (often greater than or equal to 90%). A detailed comparison between these results and the results obtained from Phase 1 is prevented due to the differences in datasets with different environmental characteristics defining the strata and methodological modifications applied to the analysis. However, in general terms, the predictive accuracy of the method has substantially improved in the present study compared to Phase 1 (Figure 8).

4.1.1 Impact of Dataset Size and Stratification

In Phase 1 the size of the analysed dataset (number of samples) was suggested as a key factor influencing the number of indicator taxa that are identified by the analysis and the accuracy of the method (Strong & Johnson 2023). This led to the inclusion of additional survey data in the initial data processing undertaken in Phase 2, with the aim of increasing the sample size. However, this had only a negligible effect on the overall dataset size suitable for analysis (with the new samples only accounting for 0.2% of the total dataset), and the new data did not meet the criteria for the final strata selected for analysis. In addition, the different stratification used in the present study led to datasets of generally smaller size than those analysed in Phase 1. Despite this, and despite the more restrictive criteria used in the present study for the selection of indicator taxa (based only on purity and reliability), a general improvement in the predictive accuracy and in the number of selected indicator taxa was obtained in Phase 2 (Figure 8b, Figure 9). This demonstrated that other components of the methodological approach, most likely the data stratification and the choice of indicator taxa, were more critical in affecting the final results than mere dataset size.

This does not mean that, within a given approach, the analysis may not benefit from an increase in dataset size for a given stratum. When considering solely the results obtained in Phase 2, a positive effect of the dataset size on the accuracy of the method is apparent (Figure 8a). This is valid in particular for the accuracy in predicting observations from below the community change point, which increased from approximately 80% at a dataset size less than 500 samples (strata N1 and S2) to 95% at a dataset size greater than 700 samples (stratum S1a). In turn, the accuracy in predicting observations above the community change point seems to remain good (around 90%) independent from dataset size (Figure 8).

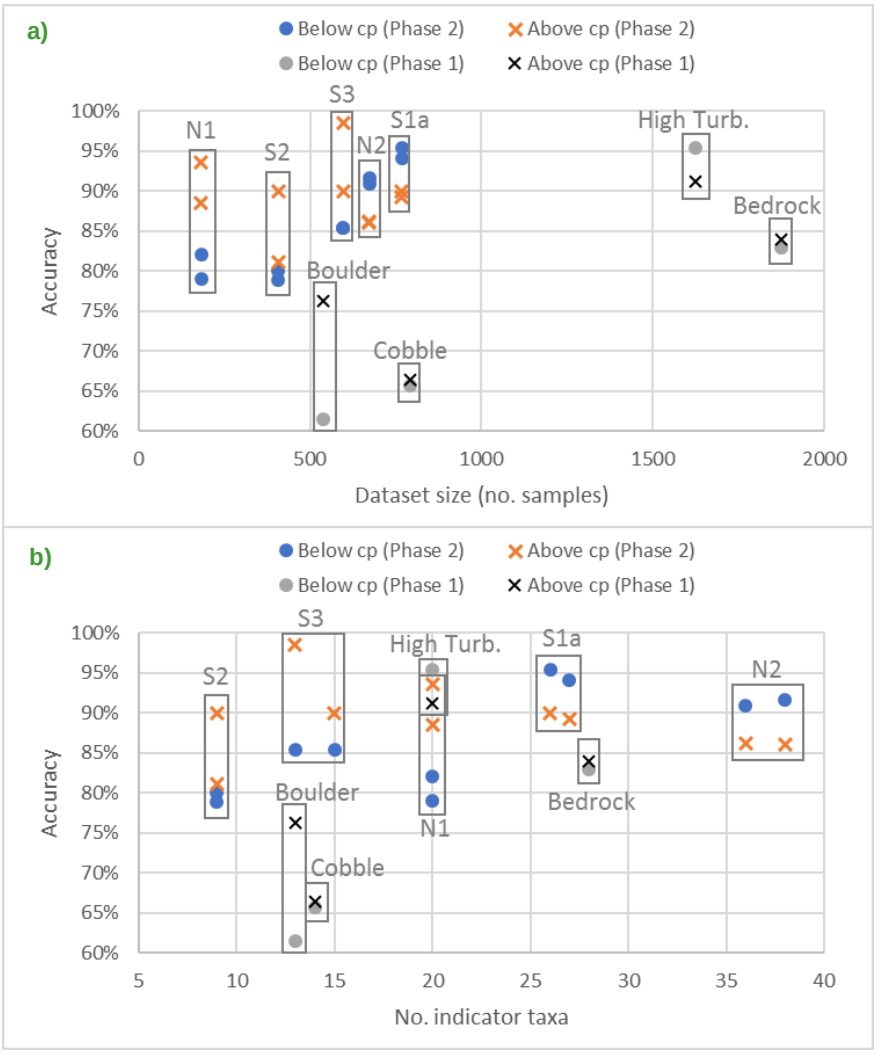

Figure 8. Predictive accuracy of the selected suite of indicator taxa for above and below the community change point (cp) in Phase 2 (including results for both 'consp' [conspicuous taxa list] and 'aggrt' [aggregated taxa list] datasets) and Phase 1 (as assessed using 400 random observations) in relation with: a) the size of the analysed dataset (number of samples); and b) the number of indicator taxa selected in the analysis. Boxes and labels indicate the different stratified datasets as analysed in Phases 1 and 2.

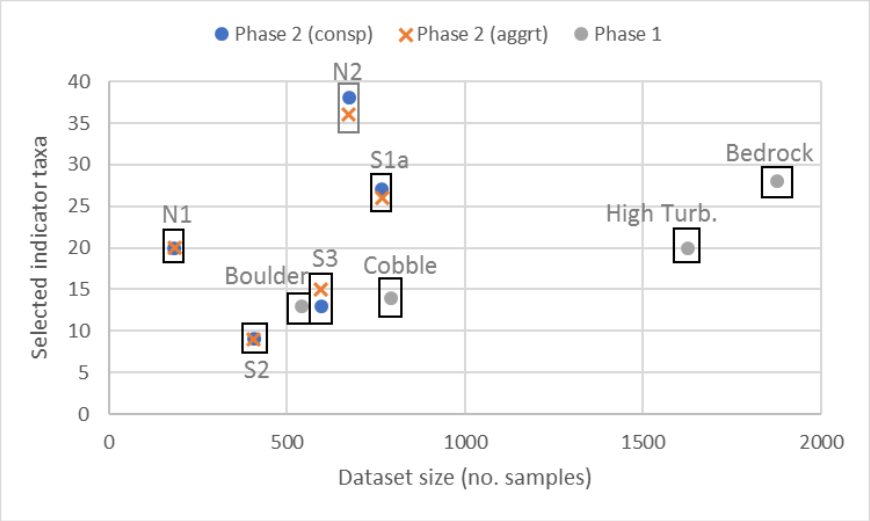

Figure 9. Relationship between number of indicator taxa selected in Phase 1 and Phase 2 (for the different stratified datasets analysed) and the size of the analysed datasets (number of samples). Boxes and labels indicate the different stratified datasets as analysed in Phases 1 and 2.

In Phase 2, the stratified datasets with the highest sample size identified more indicators than the smaller datasets (e.g. strata N2 and S1a compared to N1, S2, and S3; Figure 9). This is an expected effect, as a larger number of observations are more likely to capture a higher number of taxa overall (following the relationship expressed by the species accumulation curve; Ugland *et al.* 2003). As a result, a higher number of taxa are more likely to show consistent changes along the studied gradient and therefore be selected as indicators by the analysis. Although this might be true for the N2 dataset (87 and 84 taxa/forms), the N1 dataset identified more indicators than the S2 and S3 datasets despite having the lowest number of samples and taxa/forms. The high number of indicators in the N1 dataset might be a result of it having the full gradient of pressure present (SA0 0 to 7.3), all other datasets having a SA0 pressure gradient of 0 to 3.4 or less.

Additional benefits of increasing the number of samples within the stratified datasets also relate to the ability of undertaking a formal validation of the recommended indicator taxa. The validation undertaken in Phase 1 and 2 and the resulting accuracy estimates are likely to be positively biased due to the randomised datasets selected for the validation not being independent from the data used to generate the results. Starting with a larger dataset representing a stratum would allow for splitting it into a calibration (generally 75% of the data) and a validation (25%) dataset. This would enable the former to be used for the analysis (and consequently the identification of change points, indicator taxa and associated benchmarks), and the latter for the validation, without compromising the results due to limitations in the dataset size.

The data stratification carried out prior to the application of the TITAN has been identified as a pivotal element of the method. The choices made on data stratification impact the size of the datasets (strata) that will be analysed using TITAN, the representativeness of the pressure gradient within each stratum, and the residual environmental variability that can influence our ability to observe biological responses (e.g. by masking or interacting with the pressure). In Phase 1, the stratification prioritised larger dataset size and having a pressure representative across the gradient however, it could not account for important sources of variability in the biological data. For, example the effects of the geographical location of samples, likely reflecting biogeographic distribution of taxa in different regions (Figure 1) was not accounted for in the stratification, despite latitude and longitude always ranking amongst the top three explanatory variables of biological community variability in the RDA analyses (Strong & Johnson 2023). Consequently, environmental variability was still predominant

even within the selected stratified datasets (as confirmed by RDA results for sub-divided datasets) compared to the pressure gradient that always ranked lower in the list of explanatory variables.

RDA was not used in the present study due to the analysis (and associated F-test) assumptions not being met by the type of data, and an alternative stratification approach, PCA, was used. PCA proved to be more effective in reducing the residual natural variability within the selected strata compared to RDA, while also taking into account the effect of this variability on the biological communities (as assessed using ANOSIM). This improved homogenisation of the environmental conditions within each stratified dataset likely contributed to clearer and stronger responses of the indicator taxa to the pressure indicator gradient alone. This was suggested by the IndVal scores which indicates the magnitude of change in the taxon frequency and abundance between the two partitions of the gradient, below and above the observed change point. Higher IndVal scores were associated with several taxa in Phase 2 compared to the same taxa in Phase 1 (e.g. negatively responding Ophiuroidea in Phase 2 showed IndVal values mostly greater than or equal to 5%, compared to values mostly less than 20% in Phase 1 results). This likely resulted in the higher predictive accuracy of the tool in Phase 2, despite the smaller dataset sizes and reduced gradient range compared to strata in Phase 1. Notably, some of the strata obtained in Phase 2 had an excessive reduction in dataset size and/or pressure gradient range and therefore they were not analysed (e.g. high-energy shallow habitats or deeper habitats in the North, high and moderate energy shallow habitats in the South, high turbidity, or deep habitats). An increase in the survey data available for these conditions, while representing as wide a gradient of pressure as possible, would be beneficial, enabling the analysis of these additional strata and thereby obtain a suite of indicator taxa for these habitats.

4.1.2 Indicator Taxa

The choice of indicator taxa may also be one of the critical elements that affected the improvement of the method performance (as measured by predictive accuracy) in Phase 2 compared to Phase 1. A more restrictive approach for indicator taxa selection was used in Phase 2 which was based solely on the purity and reliability criteria from TITAN. In comparison, Phase 1 also used purity and reliability criteria, but also identified additional taxa (albeit these were only a few) according to top values of an ‘indicator quality’ metric (Strong & Johnson 2023). This led to the inclusion of taxa with more uncertain response to the pressure gradient (i.e. less pure and reliable) and likely contributed to the lower accuracy of the resulting indicators in Phase 1.

Despite the changes in methodology, there were similarities in the indicator taxa selected in Phase 1 and Phase 2, and their responses to the pressure indicator gradient (a proxy for sediment resuspension). For example, Ophiuroidea, as a class, consistently showed a negative response to the pressure gradient, where selected as an indicator taxon, hence being identified as sensitive to the sediment resuspension pressure. However, at species level there was variability in the response, with *Ophiocomina nigra*, *Ophiura albida* and *Ophiothrix fragilis* showing both negative and positive responses to the pressure gradient. Both *O. nigra* and *O. fragilis* inhabit areas of hard substrata and *O. fragilis* is known to be moderately sensitive to smothering (Jackson 2008) however, the sensitivity of this species to increased turbidity and abrasion is low. Given the low resolution of the pressure data and that the measure of pressure is not direct (i.e. a proxy has been used), it is not clear what *O. fragilis* is responding to. Like many species of brittlestars, *O. albida* inhabits muddy substrata (Wilson 1999) and is therefore unlikely to exhibit sensitivity to increased turbidity or sedimentation, unless excessive. Whilst this species showed negative and positive responses to the pressure gradient, the frequency of positive responses was higher. Given the mixed response of the individual species and the variability in their habitat requirements, records of ‘Ophiuroidea’ (i.e. at class level) are too broad for consideration as an indicator

taxon. Other indicator taxa showing a mixed response included *Caryophyllia*, *Palmiskenea skenei, Parazoanthus, Porania pulvillus, Reteporella,* Serpulidae, Hymedesmiidae, Hexacorallia, Hydrozoa and Bryozoa. It is likely that the variable response reflects the variability in the tolerance and habitat requirements of the individual species within these higher-level classifications.

Regarding the indicator taxa recorded to the level of species, the response of *Swiftia pallida* to the pressure gradient was consistently negative across the greatest number of data subsets, although the frequency of observations was low. This species is known to be moderately intolerant of sediment deposition/smothering and abrasion but is not thought to be sensitive to increased turbidity (Wilson 2007). Of the remaining species which only showed a negative response, many are classed as having low or no sensitivity to smothering/sediment deposition, abrasion or increased turbidity (MarESA sensitivity assessment; Tyler-Walters *et al.* 2018). These include *Alcyonium digitatum, Asterias rubens, Flustra foliacea* and *Lanice conchilega*. Current understanding of the biology of the majority of the species highlighted as potential indicator species is poor and their sensitivity to anthropogenic pressures is generally not known.

While massive and tubular sponges showed negative responses, encrusting sponges showed positive responses, suggesting a wider tolerance, confirming the results of Phase 1. Bell (2002) and Pineda *et al.* (2016) found massive, encrusting and cup (broadly comparable to tubular in the classification used in this study; Figure 2) sponge morphologies were the most sensitive to sediment deposition. While this is contrary to some results of the present study (where only repent, massive, globular and tubular species showed negative responses), the low resolution and indirect measurement of the pressure may have influenced this result. Additionally, Pineda *et al.* (2017) demonstrated low sensitivity to sediment deposition in a variety of sponge species.

Some species were shown to display a positive response to pressure. This included *Spirobranchus triqueter* which has been classed as having moderate sensitivity to sediment deposition, but low sensitivity to abrasion and increased turbidity (Riley & Ballerstedt 2005). In this study, in addition to this species demonstrating a positive response to the pressure gradient, so did the genus *Spirobranchus* which was listed as a separate indicator taxon. The validity of *S. triqueter* as an indicator is questionable as, depending on recorder experience or image quality, *S. triqueter* could be misidentified within *Spirobranchus* or Serpulidae categories (which displayed a mixed response).

4.1.3 Community Change Points

Similar to Phase 1, the results of Phase 2 showed that community responses were triggered at low levels of the measured pressure indicator, particularly when considering negatively responding taxa. However, the distribution of sample data along the gradient was uneven in the investigated dataset, with most of the data at lower levels of the pressure gradient. While TITAN is considered to be quite robust to skewed samples (i.e. non-uniform distribution along the gradient (Baker & King 2015)), the higher frequency of available sample data towards the lower end of the pressure gradient might have influenced the identification of change points in that area of the gradient

Contrary to Phase 1, data with zero pressure were included in the analysis in Phase 2 in order to account for reference conditions that are presumed to occur where there is no pressure. This, and the different scale of the pressure indicator measured in Phase 2 compared to Phase 1 prevent specific comparisons of the change point values between the two phases. For negatively responding taxa, community change points were generally identified with good certainty in Phase 2, as attested by the small 90% percentile intervals associated with these change points. These negative change points were the lowest in

Northern areas (N1 and N2, characterised by a mix of rocky substrata on shallow, low turbidity conditions, with low to moderate energy), and in the southern cobble habitats (S3, characterised by shallow, low turbidity and low energy). Bedrock and boulder habitats in these same conditions (S1a and S2) had a negative community change point at a slightly higher level of pressure. Positively responding taxa tended to show changes at higher points along the pressure gradient compared to negatively responding taxa. These were also generally associated with a higher uncertainty (wider 90% percentile intervals) due to a lower synchronisation in the response of different taxa belonging to this group. Taxa responding positively to a pressure gradient are likely to be tolerant to the pressure (sediment resuspension in this case), and their increase along the gradient may be influenced by factors other than the pressure itself. For example, the loss of sensitive taxa that are competitors for the same resources or predators. The positive responses are therefore likely to be taxon specific, and a synchronous tolerant community response may not be expected (Baker & King 2010).

4.2 Sources of uncertainty

TITAN is quite robust against data variability and sparseness, having been specifically designed for the analysis of biological survey data that commonly have these characteristics (Baker & King 2013). However, the validity of the results obtained through this analysis is highly dependent on the validity of the data used as input. A desirable feature of the indicator method developed in this project is its flexibility in accommodating data from different sources (i.e. collected with different methods/standards), as attempted by including Seasearch survey data in Phase 2. This is also particularly relevant when considering that different surveys may target different habitats (e.g. Seasearch surveys mostly in the infralittoral zone, video surveys mostly in circalittoral habitats, but also covering deeper areas) thus allowing a better representation of the wider variability of environmental, and likely, pressure conditions. Comprehensive sample metadata is key when preparing data for analysis. This would ensure a better assessment of the full gradients existing on rock habitats and therefore a more robust stratification of the overall data for the analysis (discussed in Section 5 Recommendations).

Despite the additional Phase 2 (Seasearch) data not being included in the TITAN analysis (filtered out during the stratification process), their exploration and integration in the initial dataset highlighted several sources of uncertainties associated with the input data that may influence the validity of the results obtained with TITAN. These sources of uncertainty are summarised below.

4.2.1 Minimum survey data requirements for use in the analysis

Surveys of rock habitats normally collect species occurrence and abundance data in a semi-quantitative manner, using the SACFOR scale. The TITAN analysis requires numerical data, and therefore a conversion from SACFOR classes into numerical values indicating abundance was developed in Phase 1 and used in this study. The methodology developed for SACFOR conversion into numerical values required:

- The SACFOR classification of each taxon in a sample.
- The type of observation the SACFOR classification was based on (count or coverage).
- The size class of individuals (for count-derived data), or the growth form category (for coverage-derived data).

To allow the use of survey data that do not meet these minimum requirements for the SACFOR conversion (e.g. Seasearch survey data in Phase 2 BIO dataset), a method was proposed in this phase of the project to derive the information from existing datasets (e.g. Phase 1 BIO dataset). Through matching taxa (or proxy taxa) in data where the minimum

requirements were missing (i.e. Phase 2 BIO) with data where the minimum requirements were recorded (i.e. Phase 1 BIO), it was possible to extrapolate the missing information to enable the SACFOR conversion. However, this procedure involved making several assumptions that could introduce uncertainty in the data.

When there was not an exact match in the taxonomic identities recorded in Seasearch surveys with those recorded in the Phase 1 dataset a proxy-taxa was used, introducing some uncertainty. This occurred in 71% of the taxa recorded in Phase 2 dataset (233 out of 328 taxa), including 19 sponge, 6 anthozoan and 208 other taxa. In most of these cases the correspondence between taxa was approximate (i.e. similar taxa were identified in the two datasets but with different taxonomic detail). For example, the missing information for the arborescent sponges *Axinella damicornis* and *Axinella dissimilis* present in the Phase 2 dataset was extracted from the genus *Axinella* which was the closest match available in the Phase 1 dataset. Where a match between the taxa in the two datasets could not be established even at higher taxonomic levels, the type of record, size and/or form were allocated based on expert judgement on the generic characteristics of the species. Instances of this include the lobster *Homarus gammarus*, the horseshoe worm *Phoronis hippocrepia* and a few brown seaweed species, which were only present in the Phase 2 dataset which included taxa from shallower and more inshore habitats than present in Phase 1.

Uncertainty could also be introduced with the assumption that the determination of the dominant type of record for each taxon (count or coverage, size class and/or growth form) was the same among datasets and phases. The uncertainty here is derived from the fact that the possible variability between datasets (e.g. due to different habitats or environmental conditions covered by different surveys) is not considered with this assumption. Potentially the greatest uncertainty was associated with taxa that were recorded in different ways (count and coverage) or with different sizes or growth forms in different sample observations within a dataset.

Uncertainty can also be introduced through the need to match size classes which were defined differently between the MNCR and Seasearch SACFOR scales (Table 4 and 5). In particular, species or individuals (e.g. life stages) of small-medium size (3 cm to 5 cm), assigned to the class 3 cm to 15 cm in the MNCR SACFOR scale were allocated to size class greater than 5 cm in the Seasearch SACFOR scale, thus introducing an error in the transformation.

A degree of uncertainty can be introduced when allocating sponge morphologies solely based on the taxonomic identification. Sponge morphologies are dynamic, and a single taxon may exist in different forms depending on adaptations to variable environmental conditions (e.g. depth, currents, exposure; Bell & Barnes 2000); *Amphilectus fucorum* was classified in the dataset as encrusting, but it can also exist as cushions, or massive, lobose or branched structures. This uncertainty is further compounded by the matching of taxa between Phase 2 and Phase 1, which was also used to allocate morphological types to sponge taxa that were recorded in Phase 2 dataset. This process relied heavily on expert judgement rather than on direct survey observation, as the majority of sponge records in the Phase 2 dataset (32 out of 35 taxa) had no information on morphological type (written or photographic record). However, as the Phase 2 data was deemed unsuitable for testing with the TITAN method, this will have had no impact to the determination of indicator taxa.

4.2.2 Type, quality and accuracy of survey and derived data

Additional sources of uncertainty were identified regarding variability in the standards for data collection, data quality and characteristics.

4.2.2.1. Data collection and recording policies

Data obtained from different sources are often associated with different methods of collection and standards, as observed for Seasearch diving surveys compared to the video surveys used in Phase 1. In some cases (as in the Seasearch surveys), although survey guidance and training are given, survey design can vary depending on the habitat or site surveyed, introducing variation in terms of survey area, effort, and techniques used (e.g. transect survey, point observations, scale of the area assessed at a specific site). As a result, there may be a high variability (the degree of which is unknown) in the survey effort (e.g. area explored by the surveyor and to which a sample record refers to), compared with data obtained from the examination of video stills. This may highly influence the number of taxa recorded in a sample observation, thus leading to variability in the data that are not directly related with environmental or pressure conditions, but rather with the effect of data collection methods.

Similarly, surveys of different nature (diving versus video) may have different taxonomic resolution of the records, depending on the survey methods and on the training of the person collecting the data (directly during the diving survey or from the analysis of video stills). The variables provided with the survey data include a judgment on data quality, and these need to be taken into account, particularly if lower quality data are included in the analysis as this may influence the confidence in the final results (depending on the incidence of the lower quality data in the final analysed dataset).

Other variables (e.g. underwater visibility) may also contribute to assessing the confidence of the data. Combining this information from different types of surveys may be difficult as 'data quality' may have different meaning (e.g. image quality for video surveys, surveyor's level of training in Seasearch diving surveys), and 'underwater visibility' is only recorded for Seasearch survey data.

The classification of sponge morphologies used in this study included 10 morphotypes, following the classification in Berman *et al.* (2013; after Bell *et al.* 2006). However, other morphological classifications exist (e.g. Boury-Esnault & Rützler 1997), with over 30 morphotypes), and raw survey records of sponge morphologies (where available from Seasearch data and for most sponge records in Phase 1 data) made use of a mix of morphotypes from these classifications that needed to be standardised to the Berman's (2013) classification on data preparation. The allocation of morphotypes *a posteriori*, based on sometimes insufficient or unclear descriptions, is likely to be less accurate than direct observations using the same agreed classification.

4.2.2.2. Pressure data

A proxy for anthropogenic sediment resuspension was used as an indicator of indirect pressure in this study, as in Phase 1. The derivation of alternative/additional pressure indicators (e.g. associated with abrasion from potting activities) was not possible due to limitations in the temporal resolution and spatial coverage of the available data layers. Therefore, the pressure indicator was derived from maps of abrasion that originated from fishing activity records (VMS data) aggregated by year and to raster grids at a resolution of 0.05 decimal degrees (i.e. 3 km to 5 km grid at the latitudes of this study; Church *et al*. 2016). The abrasion maps were therefore available at a coarser spatial and temporal resolution than the scale of the survey sample data. As such, the resulting pressure indicator can only be considered as an approximation of the actual pressure to which the habitat at the surveyed sites were subjected. The degree of approximation, and therefore associated uncertainty, depends on the actual spatial and temporal distribution of the VMS data (within the grid cell and within a given year) in relation to the location and timing of the surveys. In fact, the distance (in space and time) of the survey sites from where and when the fishing

activities actually took place may determine whether the derived abrasion pressure and associated sediment resuspension are relevant or not to a specific survey observation. It should also be considered that predominant currents in the area may affect the direction and distance of transport of suspended sediments.

4.2.2.3. Habitat data

For consistency with the method used in Phase 1, EUNIS habitat and sediment type identification for the survey sample points was based on the predicted habitat according to seabed maps (using the updated UK Seamap 2016 in Phase 2) rather than being based on the EUNIS habitat classification recorded in the survey data. It is acknowledged that predicted habitat is likely to be a less accurate assessment than the habitat effectively observed in the sample site. The integration of map models and results over a coarser spatial scale, compared with the one of survey units (e.g. area covered by the photographic still) was required to combine multiple survey data. These *in situ* variables were not used as determinants of the dataset stratification, and therefore their accuracy did not influence the results of this study. However, this source of uncertainty might be relevant in future calibrations of the method that might benefit from the use of these variables for data stratification.

4.2.3 SACFOR transformation

Key to the TITAN analysis is numerical data that represent the distribution of individual taxa/forms in sample observations collected along the studied gradient. As a result, the recorded SACFOR classes needed to be converted into numerical values. This transformation establishes a direct (unique) correspondence between the allocated SACFOR category and the correspondent count (as density) or coverage (as %) class behind the classification, with the resulting values being rescaled and ranked for comparability by using log transformation (on base 2 or 10 depending on the type of observation). As a result, the final dataset used for the analysis included a mix of values that represent count or coverage classes (for different or the same taxa, depending on how they are recorded in the surveys), and that vary on a similar numerical scale.

Due to the different SACFOR classification applied to taxa of different size or growth form, the transformation applied here effectively maintained the relative (ranked) variation in coverage or count classes between samples (i.e. samples with higher numerical values for a species have higher density and/or coverage of that species compared to other samples), while the relationship between SACFOR classification may be lost (i.e. due to the size/form corrections mentioned above, two records with the same numerical value may represent different SACFOR classes in the original survey records). Therefore, the transformation applied here may alter the relative distribution of taxa along the pressure gradient compared to the distribution of the original SACFOR categories (i.e. two samples that showed a change in SACFOR classification at two different points of the gradient may be represented by the same numerical value after the conversion, and *vice versa*).

Furthermore, the transformation applied implicitly established a correspondence between density and coverage values that is unique (i.e. independent of size and form) and has not been biologically validated. For example, two differently recorded taxa, one based on density 1 to 9 / m^2 and the other based on coverage 20 to 39%, will always have the same numerical value of around 4.9 in the final dataset, even though the effective correspondence between numerical density and spatial coverage may largely vary depending on the size, shape, and form of the studied taxa.

5 Recommendations

Based on the elements discussed above, the following recommendations are given.

5.1 Data requirements, quality standards and survey improvements

It is recommended that a more integrative dataset, covering the wider environmental variability around the UK is analysed to calibrate the final indicator. This would allow to better account for all possible gradients and combinations of environmental conditions (different biogeographic regions, energy levels, habitats, etc.). The data selection should also take into account the coverage of the broader pressure gradient that is assumed as driver of the responses observed for indicator taxa in the analysis. Computational timing restrictions may limit the size of the datasets that can be analysed, so the data pre-selection should be oriented towards the representation of full environmental and pressure variability rather than towards the mere increase in dataset size (this has proved to be of secondary importance compared to the quality and representativity of the data). This will allow the calibration of a methodology (e.g. stratification, indicator taxa selection) which will generate results with wider validity, and therefore an indicator (or a set of indicators, depending on habitat) of wider applicability. Increased dataset size would also allow data to be excluded from initial analysis and used for validation of identified indicators.

The exploration of more detailed spatial layers (e.g. original VMS data rather than abrasion maps averaged over a large grid) should be done to extract more meaningful variables (e.g. distance of the survey site from the nearest trawling line, and time and frequency of trawling at different temporal scales consistent with the survey timing) that can be combined in an indicator of pressure. It is acknowledged that this will be a complex and time-consuming analysis. However, it will provide a simple, direct measure of exposure to fishing-related disturbance that, to some extent, accounts for all pressures associated with fishing.

The use of data from different sources may favour the coverage of wider environmental conditions, and the inclusion of more data from Seasearch surveys will allow the full appreciation of how change in source data (with consequent changes in survey method, confidence etc.) may affect the final results. However, for the integration of data from different sources in the analysis, the standardisation of protocols or records is needed, including standardisation of sponge morphologies. That is, a single sponge classification scheme (chosen by JNCC) should be used by all surveyors and morphologies should be recorded *in situ* or directly from video footage or stills images, and in combination with taxonomic observations (where possible). Many sponges are polymorphic according to environmental conditions (as well as exposure to anthropogenic pressures) making morphological classification simply based on taxonomic data difficult and inaccurate. Without direct, first-hand observation, it is not possible to confidently assess potential morphological variation with pressure.

Similarly, standardised survey protocols should include the collection of the minimum supporting information on type of records (count or coverage), size and growth form that is required for the SACFOR conversion into numerical data. For some surveys, data were entered into Marine Recorder as SACFOR classes, with no information on whether the SACFOR class was allocated based on observation of coverage or count (densities), nor on the size of the organisms counted. Abundances therefore had to be inferred. In order to avoid the introduction of errors and unnecessary variability caused by inference, it is essential that full details of the recording are given, and that raw data are available.

It is also important that measures of abundance are standardised for individual species and that surveyors are informed of this. A major difficulty with the present data set was a number of species recorded as both percent cover and counts.

This study has demonstrated that TITAN can be successfully applied to identify species indicative of responses to anthropogenic pressure. However, the analysis was based on survey data which were not necessarily collected with the aim of establishing a pressure-impact relationship. It would be valuable to re-analyse the raw VMS data and perform the TITAN analysis on a subset, with good corresponding biological and supporting environmental data, representative of a pressure gradient. Alternatively, targeted surveys with simultaneous pressure and biological information could be conducted. This would provide the basis for further validation of the outputs of the TITAN analysis.

5.2 Further improvements in analytical protocol

Further exclusion of taxa identified at higher taxonomic levels (e.g. Ophiuroidea) is suggested as these groups may aggregate taxa with different tolerance/sensitivity to the pressure, different habitat requirements (e.g. hard versus soft substrata), and therefore their response may be biased by the dominant taxa (unknown from the survey data) in the group in a specific area (but these taxa may be different in other areas).

It is recommended that habitat and sediment type identification data for the survey should be based on survey observations rather than on predictive maps (as done in this study, for consistency with Phase 1) to improve accuracy. However, key to this is the standardisation of habitat and sediment type records between different surveys to allow the comparability and integration of the data.

It is recommended that an alternative SACFOR transformation should be trialled and results compared. The validity of using $\log_2$ and $\log_{10}$ transformed data simultaneously, in a single matrix, is questionable. Whilst TITAN (initially) treats taxa individually, the data are still subjected to numerical techniques based on the whole community. Given that the log transformation generates values comparable to those on the SACFOR scale (e.g. 1 to 6), it is unlikely that the outcome would be very different; other analyses would have to be modified in order to account for the categorical nature of the SACFOR scoring system.

A validation of the results should be undertaken by using independent samples (as described in section 4.1 of the discussion) to ensure an unbiased estimation of the accuracy of the indicator. Expanding the dataset as suggested above should be beneficial to this purpose, as dataset size limitations would be reduced, while having a better representation of environmental and pressure variability.

5.3 Gaps

As highlighted in the discussion, some of the steps undertaken within the methodological protocol defined here require making assumptions on the data *a posteriori*, which may introduce uncertainty in the data that are subject to analysis, and therefore likely reduce the confidence in the final outcome. The accuracy estimates derived from the validation of the TITAN analysis, as developed in Phase 1, already provide an assessment of the ability of the selected indicator taxa to predict whether an observation is from above or below the relevant change point along the pressure gradient (Strong & Johnson 2023). However, these estimates only take into account the misclassification error that can be made in using the TITAN results, and therefore it is a confidence assessment on the last step of the analysis only.

It is recommended that a more integrative confidence assessment be undertaken, to also reflect the key uncertainties associated with the data and the other steps of the protocol undertaken during data preparation. A possible approach could be to define and combine different metrics of uncertainty accounting for all the elements of uncertainty associated with the methodological protocol as a whole, including the uncertainty associated with the data quality, the assumptions made on SACFOR data conversion, etc in addition to the predictive accuracy of TITAN results. A similar method has been applied for example in the prediction and mapping of essential fish habitats for the Marine Management Organisation (MMO 2013, 2016), whereby the results of the statistical model validation (also based on misclassification error) were combined with metrics (standardised scores) characterising the confidence in the data used, as input to generate the predictive model, and a resulting integrative measure of confidence was obtained for the final outcome of the methodological protocol that was developed. This approach for the confidence assessment and the resulting confidence estimates (classed as high/medium/low) allowed to qualify the outputs obtained from the analysis (essential fish habitat maps in that project) and were well received by the stakeholders that were consulted during that project (e.g. Cefas, JNCC, Marine Scotland Science, IFCAs, DoENI, AFBI-NI, MMO 2016).

At present, understanding of the relationship between fishing activity and the associated pressures, and the subsequent impacts on rock communities (which are indirectly impacted because trawling on rock is minimal) is lacking in terms of the severity of the impact, the most sensitive species, the spatial scale, and the timescale of the impact.

6 References

Alexander, D., Coates, D.A., Tillin, H. & Tyler-Walters, H. 2015. Conceptual Ecological Modelling of Sublittoral Rock Habitats to Inform Indicator Selection. *JNCC Report No. 560*, *May 2015*. JNCC, Peterborough, ISSN 0963-8091. https://hub.jncc.gov.uk/assets/473b4f8c-b3cb-4224-8e59-c88cf433de6f

Baker, M.E. & King, R.S. 2010. A new method for detecting and interpreting biodiversity and ecological community thresholds. *Methods in Ecology and Evolution,* **1,** 25-37.

Baker, M.E. & King, R.S. 2013. Of TITAN and straw men: an appeal for greater understanding of community data. *Freshwater Science*, **32,** 489-506.

Baker, M.E., King, R.S. & Kahle, D. 2015a. Glades.TITAN – An introduction to Threshold Indicator Taxa Analysis with TITAN2 (v2.1). December, 2015. https://cran.r-project.org/web/packages/TITAN2/vignettes/glades.TITAN.html

Baker, M.E., King, R.S. & Kahle, D. 2015b. TITAN2: Threshold Indicator Taxa Analysis. R package version 2.1. https://CRAN.R-project.org/package=TITAN2

Bell, J.J. 2002. Morphological responses of a cup coral to environmental gradients. *Sarsia: North Atlantic Marine Science*, **87,** 319–330.

Bell, J.J., Burton, M., Bullimore, B., Newman, P. B. & Lock, K. 2006. Morphological monitoring of subtidal sponge assemblages. *Marine Ecology Progress Series,* **311,** 79-91.

Berman, J., Burton, M., Gibbs, R., Lock, K., Newman, P., Jones, J. & Bell, J. 2013. Testing the suitability of a morphological monitoring approach for identifying temporal variability in a temperate sponge assemblage. *Journal for Nature Conservation,* **21,** 173-182.

Boury-Esnault, N. & Rützler, K. 1997. Thesaurus of sponge morphology. *Smithsonian Contributions to Zoology,* **596,** 1-55.

Church, N.J., Carter, A.J., Tobin, D., Edwards, D., Eassom, A., Cameron, A., Johnson, G.E., Robson, L.M. & Webb, K.E. 2016. JNCC Pressure Mapping Methodology. Physical Damage (Reversible Change) – Penetration and/or disturbance of the substrate below the surface of the seabed, including abrasion. *JNCC Report No. 515*. JNCC, Peterborough, ISSN 0963-8091. https://hub.jncc.gov.uk/assets/5874e65d-324b-4f6b-bce2-bfc7aab5ba7f

Clarke, K.R. & Warwick, R.M. 2001. *Change in marine communities: an approach to statistical analysis and interpretation. 2nd Edition*. PRIMER-E: Plymouth.

Jackson, A. 2008. *Ophiothrix fragilis* Common brittlestar. In Tyler-Walters H. and Hiscock K. (eds) Marine Life Information Network: Biology and Sensitivity Key Information Reviews, [Online]. Plymouth: Marine Biological Association of the United Kingdom. Available from: https://www.marlin.ac.uk/species/detail/1198 [Accessed 10-05-2018].

JNCC. 2015. The Marine Habitat Classification for Britain and Ireland Version 15.03 [Online]. JNCC. Available from: https://hub.jncc.gov.uk/assets/0d5cbb79-8098-4bfe-9547-5df3fc65667e [Accessed: 09/02/2018].

Hjulström, F. 1935. The morphological activity of rivers. *Bulletin of the Geological Institution of the University of Upsala.*

MMO. 2013. Spatial models of Essential Fish Habitat (South Coast Inshore and Offshore Marine Plan Areas). A report produced for the Marine Management Organisation by the Institute of Estuarine and Coastal Studies, 73pp. *MMO Project No: 1044*. ISBN: 978-1-909452-21-3. (IECS Authors: Franco A., Thomson S., Bhatia N. and Barnard S.; IECS project code ZBB825; report available at http://webarchive.nationalarchives.gov.uk/20140108121958/http:/www.marinemanagement.org.uk/evidence/1044.htm)

MMO. 2016. Follow on to the Development of Spatial Models of Essential Fish Habitat for the South Inshore and Offshore Marine Plan Areas. A report produced for the Marine Management Organisation by the Institute of Estuarine and Coastal Studies, pp 142. *MMO Project No: 1096.* ISBN: 978-1-909452-40-4 (IECS Authors: Franco A. and Thomson S., IECS project code YBB272; report available at https://www.gov.uk/government/publications/follow-on-to-the-development-of-spatial-models-of-essential-fish-habitat-for-the-south-inshore-and-offshore-marine-plan-areas-mmo1096)

Parry, M.E.V. 2015. Guidance on Assigning Benthic Biotopes using EUNIS or the Marine Habitat Classification of Britain and Ireland. *JNCC Report No. 546.* JNCC, Peterborough, ISSN 0963-8091. https://hub.jncc.gov.uk/assets/f23a26d7-07ad-4291-a42d-b422dad82351

Pineda, M.C., Duckworth, A. & Webster, N. 2016. Appearance matters: sedimentation effects on different sponge morphologies. *Journal of the Marine Biological Association of the United Kingdom*, **96,** 481–492.

Pineda, M.C., Strehlow, B., Sternel, M., Duckworth, A., den Haan, J., Jones, R. & Webster, N.S. 2017. Effects of sediment smothering on the sponge holobiont with implications for dredging management. *Scientific Reports,* **7,** 5156. DOI:10.1038/s41598-017-05243-x

Riley, K. & Ballerstedt, S. 2005. *Spirobranchus triqueter* A tubeworm. In Tyler-Walters H. and Hiscock K. (eds) Marine Life Information Network: Biology and Sensitivity Key Information Reviews, [Online]. Plymouth: Marine Biological Association of the United Kingdom. Available from: https://www.marlin.ac.uk/species/detail/1794 [Accessed 10-05-2018].

Strong J.A. & Johnson M. 2023. The development of an indicator of the condition of sublittoral rock communities: biological correlations with environmental and anthropogenic variables. *JNCC Report No. 727.* JNCC, Peterborough, ISSN 0963-8091. https://hub.jncc.gov.uk/assets/ddfc89a2-6cd8-4683-9c4a-3c6c01c9b06f

Tyler-Walters, H., Tillin, H.M., d'Avack, E.A.S., Perry, F. & Stamp, T. 2018. *Marine Evidence-based Sensitivity Assessment (MarESA) – A Guide. Marine Life Information Network (MarLIN).* Marine Biological Association of the UK, Plymouth, pp. 91. Available from https://www.marlin.ac.uk/publications

Ugland, K.I., Gray, J.S. & Ellingsen, K.E. 2003. The species-accumulation curve and estimation of species richness. *The Journal of Animal Ecology***, 72,** 888-897.

Wilson, E. 1999. *Ophiura albida* Serpent's table brittlestar. In Tyler-Walters H. and Hiscock K. (eds) Marine Life Information Network: Biology and Sensitivity Key Information Reviews, [Online]. Plymouth: Marine Biological Association of the United Kingdom. Available from: https://www.marlin.ac.uk/species/detail/1196 [Accessed 10-05-2018].

Wilson, E. 2007. *Swiftia pallida* Northern sea fan. In Tyler-Walters H. and Hiscock K. (eds) Marine Life Information Network: Biology and Sensitivity Key Information Reviews, [on-line].

Plymouth: Marine Biological Association of the United Kingdom. Available from: https://www.marlin.ac.uk/species/detail/1276 [Accessed 10-05-2018].

Zuur, A.F., Ieno, E.N. & Elphick, C.S. 2010. A protocol for data exploration to avoid common statistical problems. *Methods in Ecology and Evolution,* **1,** 3-14.

Appendices

Appendix 1. Phase 1 and 2 taxa name harmonisation

Table 12. Updates of taxa names and group classification (P, Porifera; A, Anthozoa; O, other) for harmonisation of taxonomic identities in Phase 1 and Phase 2 datasets.

Phase	Old name	Updated name
1	*Adamsia carciniopados*	*Adamsia palliata*
1	*Bowerbankia*	*Amathia*
1	*Brisingella coronata*	*Hymenodiscus coronata*
1	*Calveriosoma fenestratum*	*Araeosoma fenestratum*
1	*Cereus pedunculatus*	Changed from **O** to **A**
1	*Cidaris cidaris*	Changed from **A** to **O**_
1	*Corymorpha*	Changed from **A** to **O**_
1	*Echinus acutus*	*Gracilechinus acutus*
1	*Emarginula rosea*	*Emarginula sicula*
1	Gorgonacea	Alcyonacea
1	*Halcampoides elongatus*	*Halcampoides purpureus*
1	Halcampoididae	Halcampidae
1	Leptothecatae	Leptothecata
1	*Luidia sarsi*	*Luidia sarsii*
1	*Megalomma vesiculosum*	*Acromegalomma vesiculosum*
1 & 2	*Metridium senile*	*Metridium dianthus*
1	Mytiloida	Mytiloidea
1	Neocheilostomatina	Flustrina
1	*Oceanapia robusta*	Changed from **O** to **P**
1	*Ophiura affinis*	*Ophiocten affinis*
1	Osteichthyes	Actinopterygii
1	Pecinidae	Pectinidae
1	*Phakellia*	Labelled as **P**
1	Polyzoniae	Polyzonia
1	*Pomatoceros triqueter*	*Spirobranchus triqueter*
1	*Scleractinia*	Labelled as **A**
2	*Bugula flabellata*	*Bugulina flabellata*
2	*Bugula plumosa*	*Crisularia plumosa*
2	*Bugula turbinata*	*Bugulina turbinata*
2	*Flabellina pedata*	*Edmundsella pedata*
2	*Nassarius reticulatus*	*Tritia reticulata*
2	*Sarcodictyon roseum*	Changed from **O** to **A**

Table 13. List of taxa included in the main dataset for conspicuous taxa, with number of occurrences in the overall dataset (n=188) indicated in brackets.

Porifera		
Encrusting [2693]	Massive [530]	Polymastiidae [27]
Globular [941]	Porifera [489]	Suberitidae [14]
Flabellate [805]	Papillate [266]	Hemiasterellidae [6]
Arborescent [752]	Tubular [264]	
Hymedesmiidae [634]	Repent [121]	

Anthozoans		
Caryophyllia [2828]	*Gersemia rubiformis* [55]	*Stomphia coccinea* [16]
Actiniaria [543]	Zoantharia [55]	*Adamsia* [13]
Alcyonium digitatum [497]	Caryophylliidae [49]	*Sagartia* [13]
Corynactis [430]	Scleractinia [49]	*Parazoanthus* [12]
Sagartiidae [402]	*Madrepora oculata* [44]	*Caryophyllia (Caryophyllia) smithii* [9]
Urticina [399]	*Lophelia pertusa* [41]	*Sagartia elegans* [8]
Swiftia pallida [168]	*Bolocera tuediae* [38]	*Cerianthus lloydii* [6]
Edwardsiidae [87]	*Capnea sanguinea* [33]	Halcampoides [6]
Actiniidae [73]	Cerianthidae [33]	*Alcyonium glomeratum* [5]
Alcyonacea [65]	Halcampidae [32]	*Corynactis viridis* [5]
Mesacmaea mitchellii [65]	Anthozoa [29]	*Metridium dianthus* [5]
Actinostolidae [62]	Hexacorallia [27]	
Parazoanthus anguicomus [57]	Hormathiidae [16]	

Other		
Hydrozoa [4648]	Nemertesia [464]	*Parasmittina* [189]
Serpulidae [3882]	*Echinus esculentus* [428]	Sabellida [185]
Bryozoa [3804]	Tubulariidae [418]	Polyplacophora [175]
Ascidiacea [1368]	*Antedon bifida* [404]	*Palmiskenea skenei* [170]
Porella [1266]	Celleporidae [373]	Crinoidea [166]
Spirobranchus [1262]	*Porania pulvillus* [341]	*Reteporella* [157]
Ophiuroidea [1108]	*Gibbula* [329]	Rhodophyta [154]
Brachiopoda [1078]	Pectinidae [320]	*Stichastrella rosea* [143]
Asteriidae [784]	*Parasmittina trispinosa* [294]	Filifera [129]
Ophiocomina nigra [729]	Trochidae [264]	*Ebalia* [119]
Paguroidea [728]	*Crossaster papposus* [260]	Neogastropoda [110]
Calliostoma [704]	*Securiflustra securifrons* [253]	*Asterias rubens* [108]
Sabellaria spinulosa [700]	*Cidaris cidaris* [247]	Holothuroidea [102]
Alcyonidium [621]	Sertulariidae [245]	*Lytocarpia myriophyllum* [98]

Flustra foliacea [620]	Smittinoidea [243]	*Ophiactis* [79]
Munida [604]	Galatheoidea [242]	*Heliometra glacialis* [73]
Cirripedia [589]	Ophiactidae [233]	Haleciidae [69]
Ophiura [563]	*Henricia* [223]	*Leptasterias muelleri* [67]
Ophiothrix fragilis [536]	*Pentapora fascialis* [221]	*Aglaophenia* [64]
Ophiura albida [521]	Balanoidea [212]	*Cellepora pumicosa* [62]
Corallinaceae [488]	Echinoidea [213]	*Lanice conchilega* [61]

Other	
Majoidea [57]	Tubularia [20]
Amphiura [56]	*Spirobranchus triqueter* [20]
Buccinidae [55]	Valvatida [18]
Terebellida [55]	*Diphasia* [18]
Porella compressa [54]	*Ophiura ophiura* [17]
Diazona violacea [54]	*Gorgonocephalus* [16]
Sabellidae [53]	Bugulidae [15]
Parastichopus tremulus [51]	Crisiidae [15]
Salmacina [51]	*Hippasteria phrygiana* [15]
Chaetopteridae [49]	*Sertularella* [15]
Anomiidae [47]	Tunicata [15]
Pecten maximus [46]	*Ciona intestinalis* [15]
Cyclostomatida [46]	*Marthasterias glacialis* [12]
Pagurus [46]	*Thuiaria thuja* [12]
Corymorpha [46]	Neoloricata [11]
Luidia ciliaris [45]	*Macropodia* [10]
Colus [45]	*Ophiopholis aculeata* [10]
Hyalinoecia [40]	*Luidia* [10]
Crepidula fornicata [39]	Aglaopheniidae [9]
Spirorbis [39]	*Mytilus edulis* [8]
Echinus [38]	*Caberea boryi* [8]
Plumularioidea [38]	*Ditrupa arietina* [8]
Ascidiidae [36]	Clavelinidae [8]
Veneroidea [35]	Flustrina [7]
Bugula [34]	Patellidae [7]
Omalosecosa ramulosa [34]	*Sertularia* [7]
Pentapora foliacea [34]	Styelidae [7]
Inachidae [34]	*Inachus* [6]
Psolus [33]	*Hydrallmania falcata* [6]

Sabella [32]	*Delesseria sanguinea* [6]
Atrina fragilis [31]	*Maja* [5]
Flustridae [31]	*Galathea* [5]
Antedon [31]	*Calliostoma zizyphinum* [5]
Bispira [29]	Anthoathecata [5]
Antedonidae [28]	
Goniasteridae [28]	
Polyzonia [26]	
Cellaria [24]	
Stolonica socialis [24]	
Bivalvia [21]	
Gracilechinus acutus [21]	

Table 14. List of taxa included in the main dataset for aggregated taxa, with number of occurrences in the overall dataset (n=177) indicated in brackets.

Porifera		
Hemiasterellidae [6]	Encrusting [2693]	Repent [121]
Hymedesmiidae [634]	Flabellate [805]	Tubular [264]
Polymastiidae [27]	Globular [941]	Porifera [489]
Suberitidae [14]	Massive [530]	
Arborescent [752]	Papillate [266]	

Anthozoans		
Caryophyllia [2837]	*Mesacmaea mitchellii* [65]	Halcampidae [32]
Actiniaria [543]	Actinostolidae [62]	Anthozoa [29]
Alcyonium [502]	*Gersemia rubiformis* [55]	Hexacorallia [27]
Corynactis [435]	Zoantharia [55]	*Sagartia* [21]
Sagartiidae [402]	Caryophylliidae [49]	Hormathiidae [16]
Urticina [399]	Scleractinia [49]	*Stomphia coccinea* [16]
Swiftia pallida [168]	*Madrepora oculata* [44]	*Adamsia* [13]
Edwardsiidae [87]	*Lophelia pertusa* [41]	*Cerianthus lloydii* [6]
Actiniidae [73]	*Bolocera tuediae* [38]	*Halcampoides* [6]
Parazoanthus [69]	*Capnea sanguinea* [33]	*Metridium dianthus* [5]
Alcyonacea [65]	Cerianthidae [33]	

Other		
Hydrozoa [4648]	*Antedon* [434]	Rhodophyta [154]
Serpulidae [3882]	Tubulariidae [418]	*Stichastrella rosea* [143]
Bryozoa [3804]	Celleporidae [373]	Filifera [129]
Ascidiacea [1368]	*Porania pulvillus* [341]	*Ebalia* [119]
Porella [1312]	*Gibbula* [331]	Nudibranchia [115]
Spirobranchus [1282]	Pectinidae [320]	Neogastropoda [110]
Ophiuroidea [1108]	Trochidae [264]	*Asterias rubens* [108]
Brachiopoda [1078]	*Crossaster papposus* [260]	Holothuroidea [102]
Ophiura [927]	*Pentapora* [255]	*Lytocarpia myriophyllum* [98]
Asteriidae [784]	*Securiflustra securifrons* [253]	*Ophiactis* [79]
Ophiocomina nigra [729]	*Cidaris cidaris* [247]	*Heliometra glacialis* [73]
Paguroidea [728]	Sertulariidae [245]	Haleciidae [69]
Calliostoma [709]	Smittinoidea [243]	*Leptasterias muelleri* [67]
Sabellaria spinulosa [700]	Galatheoidea [242]	*Aglaophenia* [64]

Alcyonidium [624]	Ophiactidae [233]	*Cellepora pumicosa* [62]
Flustra foliacea [620]	*Henricia* [223]	*Lanice conchilega* [61]
Munida [604]	Balanoidea [212]	Majoidea [57]
Cirripedia [589]	Echinoidea [205]	*Amphiura* [56]
Ophiothrix fragilis [536]	Sabellida [185]	*Luidia* [55]
Corallinaceae [488]	Polyplacophora [175]	Buccinidae [55]
Parasmittina [483]	*Palmiskenea skenei* [170]	Terebellida [55]
Echinus [465]	Crinoidea [166]	*Diazona violacea* [54]
Nemertesia [464]	*Reteporella* [157]	Sabellidae [53]

Other	
Parastichopus tremulus [51]	*Marthasterias glacialis* [12]
Salmacina [51]	*Thuiaria thuja* [12]
Chaetopteridae [49]	Neoloricata [11]
Anomiidae [47]	*Macropodia* [10]
Pecten maximus [46]	*Ophiopholis aculeata* [10]
Cyclostomatida [46]	*Janolus cristatus* [10]
Pagurus [46]	Aglaopheniidae [9]
Corymorpha [46]	*Mytilus edulis* [8]
Colus [45]	*Caberea boryi* [8]
Hyalinoecia [40]	*Ditrupa arietina* [8]
Crepidula fornicata [39]	Clavelinidae [8]
Spirorbis [39]	Flustrina [7]
Plumularioidea [38]	Patellidae [7]
Ascidiidae [36]	*Sertularia* [7]
Veneroidea [35]	Styelidae [7]
Bugula [34]	*Inachus* [6]
Omalosecosa ramulosa [34]	*Hydrallmania falcata* [6]
Inachidae [34]	*Delesseria sanguinea* [6]
Psolus [33]	*Maja* [5]
Bispira [32]	*Galathea* [5]
Sabella [32]	Aeolidioidea [5]
Atrina fragilis [31]	Anthoathecata [5]
Flustridae [31]	
Antedonidae [28]	
Goniasteridae [28]	

Flabellina [27]	
Polyzonia [26]	
Cellaria [24]	
Stolonica socialis [24]	
Bivalvia [21]	
Gracilechinus acutus [21]	
Tubularia [20]	
Valvatida [18]	
Diphasia [18]	
Gorgonocephalus [16]	
Bugulidae [15]	
Crisiidae [15]	
Hippasteria phrygiana [15]	
Sertularella [15]	
Tunicata [15]	
Ciona intestinalis [15]	

Appendix 2 – Environmental variables

Table 15. Environmental variables (including pressures) used for the combined Phase 1 and Phase 2 dataset.

Data layer [source]	Environmental variables		Type	Description
	Code name	Full name		
Survey data (as per sample records) [from Marine Recorder, provided by JNCC, Jan 2018]	Lat	Latitude	Continuous	Latitude of observation
	Long	Longitude	Continuous	Longitude of observation
	Bedr Boul Cobb Pebb Grav Sand Mud Shel Maer Biog Artif	Substratum composition	Continuous	Contribution of bedrock, boulder, cobble, pebble, gravel, sand, mud, shell, maerl, biogenic reef and artificial substratum, measured as 0 to 100% coverage in the surveyed area
Derived from local survey data	RockQ	Rock quantity	Categorical / Rank	Classes of sublittoral rock cover: high (3), medium (2), low (1)
	Rock_prim	Rock type	Categorical	Primary rock type: Bedrock, Boulders, Cobble (in the analysed dataset)
UKSeaMap 2016 [JNCC website; accessed Jan 2017].	Substr_pred	Substratum	Categorical	Substratum (modified Folk classes). Composite of high resolution (approx 100 m) broad-scale substratum map and the coarser EUSeaMap 2016 broad-scale substratum map
	Bioz	Biozone	Categorical / Rank	Biozones from observations and models (various classes, ranked as 1 – shallow (infralittoral to circalittoral), and 2 – deep (bathyal)). Composite of high resolution (approx 100 m) broad-scale biozone map and the coarser EUSeaMap 2016 broad-scale biozone map
	Ener	Kinetic energy	Categorical / Rank	Predicted energy zone due to waves and currents: high (3), moderate (2), low (1). Composite of high resolution (approx 100 m) broad-scale energy map and the coarser EUSeaMap 2016 broad-scale energy map
	EUNIS_pred	EUNIS habitat	Categorical	Predicted EUNIS Level 4 habitats. Composite of high resolution (approx 100 m) broad-scale habitat map and the coarser EUSeaMap 2016 broad-scale habitat map

Data layer [source]	Environmental variables		Type	Description
	Code name	Full name		
EMODnet Seabed Habitats broad-scale habitat map (EUSeaMap 2016)	Kcurr	Kinetic energy due to currents	Continuous	Kinetic energy at the seabed due to currents (N/m^2). 90th percentile kinetic energy at the seabed due to currents in the North East Atlantic Sea, Norwegian Shelf, Greater North Sea and Celtic Seas. Created for the EMODnet Seabed Habitats broad-scale habitat map (EUSeaMap 2016). North Sea and Celtic Seas (year 2001): a composite created by ABPmer of NOC POLCOMS CS20 (1.8 km resolution); NOC POLCOMS CS3 (10 km (2007) and NOC POLCOMS North East Atlantic (12.5 km resolution)
	Kwav	Kinetic energy due to waves	Continuous	Kinetic energy at the seabed due to waves (N/m^2). 90th percentile kinetic energy at the seabed due to waves in the North East Atlantic Sea, Greater North Sea and Celtic Seas. This dataset is a raster composite of the outputs of several models, created for display in the EMODnet Seabed Habitats portal. North Sea and Celtic Seas offshore (> 6 km from coast): NOC ProWAM model with a resolution of 12.5 km offshore run for a period of 5 years (2000 to 2005); North Sea and Celtic Seas inshore (< 6 km from coast): DHI MIKE21 Spectral wave model with a resolution of 100 to 300m run for a period of 5 years (2000 to 2005) (12.5 km resolution)
IECS	Dist	Distance to coast	Continuous	Straight-line distance to nearest shoreline (high water polyline) (m)
DEFRA Astrium bathymetric Data 2016 (1 and 6 arcsecond, UK) [provided by JNCC, Jan 2018]	Depth	Depth	Continuous	Depth (m), as inverse of bathymetry
	Slope	Slope	Continuous	Derived from bathymetry (percent rise)

Data layer [source]	Environmental variables		Type	Description
	Code name	Full name		
Atlantic - European North West Shelf - Ocean Physics Analysis and Forecast numerical-model (7 km grid) [CMEMS]	STemp	Sea temperature	Continuous	Annual average temperature at the seabed (kelvin)
Atlantic - European North West Shelf- Ocean Physics Reanalysis (7 km grid) from Met office (1985-2014) [CMEMS]	Curr	Current speed	Continuous	Northing and easting water column (1 to 1,000 m depth) velocity (m/s) converted to a vector and the magnitude used.
EMODnet Seabed Habitats Portal (accessed 2015) - regional data	Mix	Mixing	Continuous	Water column mixing
Ocean Color Web (accessed Jan 2017) - regional data	Backs	Total backscatter at 443 nm	Continuous	Aqua MODIS - whole mission turbidity composite and absorption due to gelbstoff and detrital material at 443 nm (GIOP model at ~ 4 km resolution)
Aqua MODIS (total mission composite) - Ocean Color Web (accessed Jan 2017) - regional data	POC	Particulate Organic Carbon	Continuous	POC in mg m^{-3} (~ 4 km resolution)

Data layer [source]	Environmental variables		Type	Description
	Code name	Full name		
Abrasion spatial layers (annual mean for 2009 - 2016) [provided by JNCC, Feb 2018] UK SeaMap 2016 (for substratum classification - see above)	SA0 SA.1 SBA0 SBA.1	Anthropogenic resuspension due to surface abrasion (SA) and subsurface abrasion (SBA)	Continuous	Resuspension was derived from pressure maps for surface and sub-surface abrasion for each year, combined by the theoretical suspension potential on a normalised scale as derived by substratum type UKSeaMap 2016 and literature values of erosion thresholds (Hjulström, 1935)

Appendix 3. List of taxa excluded from the analysed datasets, including reasons for exclusion.

Table 16. Taxa screened from the initial dataset and reason for exclusion.

Taxon	Reason for exclusion
Abietinaria abietina	Not relevant – pelagic / planktonic
Acanthocardia aculeata	Questionable ID
Acromegalomma vesiculosum	less than 5 occurrences
Actinopterygii	Not relevant – mobile
Aequipecten opercularis	less than 5 occurrences
Ammodytidae	Not relevant – mobile
Anarhichas lupus	Not relevant – mobile
Anomura	less than 5 occurrences
Aphrodita aculeata	less than 5 occurrences
Astropecten irregularis	less than 5 occurrences
Aurelia aurita	Not relevant - pelagic / planktonic
Axinella damicornis	less than 5 occurrences
Axinella dissimilis	less than 5 occurrences
Bathynectes	Not relevant - mobile
Berthella	less than 5 occurrences
Blenniidae	Not relevant - mobile
Bonellia viridis	less than 5 occurrences
Brachyura	Not relevant - mobile
Brisingidae	less than 5 occurrences
Callionymus	Not relevant - mobile
Callionymus lyra	Not relevant - mobile
Cancer pagurus	Not relevant - mobile
Caprella	Not relevant - swimming/inconspicuous
Caprellidae	Not relevant - swimming/inconspicuous
Caprellidira YELLOW	Not relevant - swimming/inconspicuous
Carcinus maenas	less than 5 occurrences
Caridea	Not relevant - swimming
Centrolabrus exoletus	Not relevant - mobile
Chelidonichthys	Not relevant - mobile
Chelidonichthys cuculus	Not relevant - mobile
Chirolophis ascanii	Not relevant - mobile
Chlamys	less than 5 occurrences
Chlorophyta	less than 5 occurrences
Clathrina coriacea	less than 5 occurrences
Cnidaria	Not relevant - pelagic / planktonic
Colossendeis	Not relevant - mobile
Conger conger	Not relevant - mobile
Crangon Crangon	Not relevant - swimming
Crangonidae	Not relevant - swimming
Ctenolabrus rupestris	Not relevant - mobile
Demospongiae	less than 5 occurrences
Desmarestia ligulata	less than 5 occurrences
Dromia personata	less than 5 occurrences
Eledone cirrhosa	Not relevant - mobile
Emarginula sicula	inconspicuous

Taxon	Reason for exclusion
encrusting algae indet.	less than 5 occurrences, too low taxonomic resolution
encrusting algae indet. PINK	Too low taxonomic resolution
Eubranchus farrani	inconspicuous
Eucarida	Not relevant - swimming
Eupolymnia nebulosa	less than 5 occurrences
Filograna implexa	less than 5 occurrences
Fissurellidae	inconspicuous
Gadidae	Not relevant - mobile
Gaidropsarus vulgaris	Not relevant - mobile
Geryonidae	less than 5 occurrences
Gobiidae	Not relevant - mobile
Grantia compressa	less than 5 occurrences
Grantiidae	less than 5 occurrences
Haliclona (Haliclona) oculata	less than 5 occurrences
Haliclona (Haliclona) urceolus	less than 5 occurrences
Haliclona (Rhizoniera) viscosa	less than 5 occurrences
Homarus gammarus	Not relevant - mobile
Hyas araneus	less than 5 occurrences
Hymeniacidon perlevis	less than 5 occurrences
Hymenodiscus coronata	less than 5 occurrences
Jassa falcata	less than 5 occurrences, spurious id
Labridae	Not relevant - mobile
Labrus bergylta	Not relevant - mobile
Labrus mixtus	Not relevant - mobile
Lacuna vincta	inconspicuous
Laminaria hyperborea	Kelp
Lepidorhombus whiffiagonis	Not relevant - mobile
Leptothecata	Not relevant - pelagic / planktonic
Leuconia	less than 5 occurrences
Leucosolenia	less than 5 occurrences
Liocarcinus depurator	Not relevant - mobile
Liparis liparis liparis	Not relevant - mobile
Littorina	inconspicuous
Littorinimorpha	inconspicuous
Lophius piscatorius	Not relevant - mobile
Melanogrammus aeglefinus	Not relevant - mobile
Merlangius merlangus	Not relevant - mobile
Mesogastropoda	inconspicuous
Microcionidae	less than 5 occurrences
Modiolus modiolus	less than 5 occurrences
Molva molva	Not relevant - mobile
Mysida	Not relevant - swimming
Mytiloidea	less than 5 occurrences
Myxilla (Myxilla) incrustans	less than 5 occurrences
Myxillidae	less than 5 occurrences
Necora puber	Not relevant - mobile
Nymphonidae	less than 5 occurrences
Oceanapia robusta	less than 5 occurrences
Ocenebra erinaceus	less than 5 occurrences
Octopodidae	Not relevant - mobile

Taxon	Reason for exclusion
Opisthobranchia	less than 5 occurrences
Pagurus bernhardus	less than 5 occurrences
Palaemon serratus	Not relevant - swimming
Palaemonoidea	Not relevant - swimming
Palinurus elephas	less than 5 occurrences
Pandalidae	Not relevant - swimming
Pandalus montagui	Not relevant - swimming
Parablennius gattorugine	Not relevant - mobile
Parablennius ruber	Not relevant - mobile
Paromola cuvieri	less than 5 occurrences
Patellogastropoda	less than 5 occurrences
Pholis	Not relevant - mobile
Pholis gunnellus	Not relevant - mobile
Phoronis hippocrepia	less than 5 occurrences
Pisidia longicornis	less than 5 occurrences
Pleuronectiformes	Not relevant - mobile
Pollachius pollachius	Not relevant - mobile
Polymastia boletiformis	less than 5 occurrences
Polymastia penicillus	less than 5 occurrences
Polynoidae	less than 5 occurrences
Pomatoschistus minutus	Not relevant - mobile
Porifera boring	less than 5 occurrences
Porifera BRANCHING	less than 5 occurrences
Portunidae	less than 5 occurrences
Prosobranchia	less than 5 occurrences
Pycnogonida	Cryptic, less than 5 occurrences
Raja clavata	Not relevant - mobile
Raspailia (Clathriodendron) hispida	less than 5 occurrences
Raspailia (Raspailia) ramosa	less than 5 occurrences
Rissoidae	less than 5 occurrences
Saccharina latissima	Kelp
Scaphopoda	less than 5 occurrences
Scyliorhinidae	Not relevant - mobile
Scyliorhinus canicula	Not relevant - mobile
Scyliorhinus Eggs	Not relevant - mobile
Solasteridae	less than 5 occurrences
Stelligera rigida	less than 5 occurrences
Suberites carnosus	less than 5 occurrences
Suberites ficus	less than 5 occurrences
Sycon ciliatum	less than 5 occurrences
Symphodus melops	Not relevant - mobile
Taurulus bubalis	Not relevant - mobile
Teleostei	Not relevant - mobile
Thorogobius ephippiatus	Not relevant - mobile
Thymosia guernei	less than 5 occurrences
Triglidae	Not relevant - mobile
Trisopterus	Not relevant - mobile
Trisopterus luscus	Not relevant - mobile
Trisopterus minutus	Not relevant - mobile
Tritia reticulata	less than 5 occurrences

Taxon	Reason for exclusion
Trivia	less than 5 occurrences
Virgularia mirabilis	less than 5 occurrences, sediment species
X_Amphipoda	Not relevant - swimming/inconspicuous
X_AmphipodaTubes	Not relevant - swimming/inconspicuous
X_ANIMALIA	Too low taxonomic resolution
X_Annelid (Tube worm casing)	Too low taxonomic resolution
X_Annelida	Too low taxonomic resolution
X_Crustacea	Too low taxonomic resolution
X_Ctenophora	Not relevant - pelagic / planktonic
X_Decapoda	Too low taxonomic resolution
X_Echinodermata	Too low taxonomic resolution
X_Faunal turf	Too low taxonomic resolution
X_Gastropoda	Too low taxonomic resolution
X_Mollusc	Too low taxonomic resolution
X_Polychaeta tube	Too low taxonomic resolution
Xantho	less than 5 occurrences
Zeugopterus punctatus	Not relevant - mobile

Table 17. Taxa screened from the conspicuous (consp) and aggregated (aggrt) datasets and reasons for exclusion.

Taxon	Excluded from	Reason for exclusion
Actinothoe sphyrodeta	'consp' & 'aggrt' datasets	less than 5 occurrences
Aeolidioidea	'consp' dataset	nudibranch
Aequipecten opercularis	'consp' dataset	less than 5 occurrences
Alcyonidium diaphanum	'consp' dataset	less than 5 occurrences
Anomura	'consp' dataset	less than 5 occurrences
Aplidium	'consp' & 'aggrt' datasets	less than 5 occurrences
Astropecten irregularis	'consp' dataset	less than 5 occurrences
Berthella	'consp' dataset	less than 5 occurrences
Bispira volutacornis	'consp' dataset	less than 5 occurrences
Botryllus schlosseri	'consp' & 'aggrt' datasets	less than 5 occurrences
Brisingidae	'consp' dataset	less than 5 occurrences
Bugulina	'aggrt' dataset	less than 5 occurrences
Bugulina flabellata	consp' dataset	less than 5 occurrences
Bugulina turbinata	consp' dataset	less than 5 occurrences
Calliblepharis ciliata	'consp' & 'aggrt' datasets	less than 5 occurrences
Carcinus maenas	'consp' dataset	less than 5 occurrences
Chlamys	'consp' dataset	less than 5 occurrences
Crisia	'consp' & 'aggrt' datasets	less than 5 occurrences
Crisularia plumosa	'consp' & 'aggrt' datasets	less than 5 occurrences
Dictyopteris polypodioides	'consp' & 'aggrt' datasets	less than 5 occurrences
Dictyota dichotoma	'consp' & 'aggrt' datasets	less than 5 occurrences
Didemnidae	'consp' & 'aggrt' datasets	less than 5 occurrences
Doto	'consp' dataset	nudibranch
Dromia personata	'consp' dataset	less than 5 occurrences
Edmundsella pedata	'consp' dataset	nudibranch
Electra pilosa	'consp' & 'aggrt' datasets	less than 5 occurrences
Epizoanthus	'consp' & 'aggrt' datasets	less than 5 occurrences
Eunicella verrucosa	'consp' & 'aggrt' datasets	less than 5 occurrences
Flabellina	'consp' dataset	nudibranch
Geryonidae	'consp' dataset	less than 5 occurrences
Gibbula cineraria	'consp' dataset	less than 5 occurrences
Heterosiphonia plumosa	'consp' & 'aggrt' datasets	less than 5 occurrences
Hyas araneus	'consp' dataset	less than 5 occurrences
Hymenodiscus coronata	'consp' dataset	less than 5 occurrences
Janolus cristatus	'consp' dataset	nudibranch
Lissoclinum perforatum	'consp' & 'aggrt' datasets	less than 5 occurrences

Taxon	Excluded from	Reason for exclusion
Modiolus modiolus	'consp' dataset	less than 5 occurrences
Morchellium argus	'consp' & 'aggrt' datasets	less than 5 occurrences
Mytiloidea	'consp' dataset	less than 5 occurrences
Nemertea	'consp' dataset	unreliable count
Nudibranchia	'consp' dataset	nudibranch
Ocenebra erinaceus	'consp' dataset	less than 5 occurrences
Pagurus bernhardus	'consp' dataset	less than 5 occurrences
Paromola cuvieri	'consp' dataset	less than 5 occurrences
Patellogastropoda	'consp' dataset	less than 5 occurrences
Pisidia longicornis	'consp' dataset	less than 5 occurrences
Plocamium	'consp' & 'aggrt' datasets	less than 5 occurrences
Polyclinidae	'consp' & 'aggrt' datasets	less than 5 occurrences
Portunidae	'consp' dataset	less than 5 occurrences
Prosobranchia	'consp' dataset	less than 5 occurrences
Prostheceraeus vittatus	'consp' dataset	less than 5 occurrences
Rissoidae	'consp' dataset	less than 5 occurrences
Tritia reticulata	'consp' dataset	less than 5 occurrences
Trivia	'consp' dataset	less than 5 occurrences
Trivia monacha	'consp' dataset	Littorinomorpha v. small, inconspicuous
Xantho	'consp' dataset	less than 5 occurrences

Appendix 4: Data stratification and pressure gradient summary

Table 18. Data stratification of the integrated studied dataset based on predominant environmental gradients observed in the analysis. Dataset size (number of samples) and pressure gradient range maintained within each stratum (as % of the overall gradient ranging 0 to 7.3) are given. ANOSIM results in support of each stratification step are also given as Global R statistics and Pairwise R statistics (where more than two levels were compared), with (1) showing results for the "Conspicuous" dataset, and (2) for the "Aggregated Taxa" dataset.

Stratification level and environmental criterion	Resulting strata			ANOSIM results	Note on community differentiation
1 **Latitude**	**North** dataset size: 1,965 SA0 gradient: 100% (0 - 7.3)	**South** dataset size: 4,887 SA0 gradient: 43% (0 - 3.4) **This stratum has only shallow samples**		Global R: 0.562 (1), 0.430 (2)	Moderate separation between latitude levels. Stratification accepted.
2 **North - Biozone**	**Circalittoral (1)** dataset size: 1394 SA0 gradient: 100% (0 - 7.3) **This stratum has only low turbidity samples**	**Bathyal (2)** dataset size: 571 SA0 gradient: 15% (0 - 1.1) Pressure gradient reduced too much - not analysed		Global R: 0.583 (1), 0.592 (2)	Moderate separation between biozone levels. Stratification accepted.
3 **a. North.Circalittoral - Rock type**	**Bedrock** dataset size: 655 SA0 gradient: 100% (0 - 7.3)	**Boulders** dataset size: 394 SA0 gradient: 100% (0 - 7.3)	**Cobble** dataset size: 345 SA0 gradient: 69% (0 - 5.0)	Global R: 0.174 (1), 0.168 (2) Pairwise R: Bedrock/Boulders: 0.129 (1), 0.128 (2)	Not strong separation between levels overall for both rock types (a) and energy levels (b), but separation is

Stratification level and environmental criterion	Resulting strata			ANOSIM results	Note on community differentiation
	No further stratification - reduces dataset size and/or pressure gradient too much			Bedrock/Cobble: 0.272 (1), 0.265 (2) Boulders/Cobble: 0.077 (1), 0.061 (2)	stronger between energy levels. Stratification by energy level was chosen for the analysis.
3 **b. North.Circalittoral - Energy**	**Low**	**Moderate**	**High**	Global R: 0.188 (1), 0.191 (2) Pairwise R: High/Moderate: 0.138 (1), 0.137 (2) High/Low: 0.557 (1), 0.570 (2) Moderate/Low: 0.053 (1), 0.060 (2)	
	dataset size: 184 SA0 gradient: 100% (0 - 7.3)	dataset size: 674 SA0 gradient: 34% (0 - 2.5)	dataset size: 536 SA0 gradient: 27% (0 - 1.7) *(this stratum includes 5 samples from Phase 2 dataset)*		
	No further stratification - reduces dataset size and/or pressure gradient too much				
2 **a. South - Turbidity**	**Low**	**High**		Global R: 0.129 (1), 0.132 (2)	Not strong separation between levels overall for turbidity (a), energy (b) and rock type (b), but separation is stronger for energy levels and rock type. Stratification by rock type was chosen for the analysis, also considering dataset and pressure gradient size.
	dataset size: 4861 SA0 gradient: 46% (0 - 3.4)	dataset size: 26 SA0 gradient: 4% (0 - 0.3) Dataset size and pressure gradient reduced too much - Not analysed			
2 **b. South - Energy**	**Low**	**Moderate**	**High**		

Stratification level and environmental criterion	Resulting strata			ANOSIM results	Note on community differentiation
	dataset size: 1771	dataset size: 3114	dataset size: 2	Global R: 0.194 (1), 0.193 (2) Pairwise R: High/Moderate: 0.710 (1), 0.670 (2) High/Low: 0.924 (1), 0.924 (2) Moderate/Low: 0.193 (1), 0.192 (2)	
	SA0 gradient: 46% (0 - 3.4) **This stratum has only low turbidity samples**	SA0 gradient: 11% (0 - 0.8) Pressure gradient reduced too much - Not analysed *(this stratum includes 8 samples from Phase 2 dataset)*	SA0 gradient: no gradient Dataset size and pressure gradient reduced too much - Not analysed *(this stratum includes 2 samples from Phase 2 dataset)*		
2 **c. South - Rock type**	**Bedrock**	**Boulders**	**Cobble**	Global R: 0.179 (1), 0.180 (2) Pairwise R: Bedrock/Boulders: 0.159 (1), 0.164 (2) Bedrock/Cobble: 0.237 (1), 0.237 (2) Boulders/Cobble: 0.073 (1), 0.073 (2)	
	dataset size: 2025 SA0 gradient: 23% (0 - 1.7)	dataset size: 918 SA0 gradient: 46% (0 - 3.4)	dataset size: 1944 SA0 gradient: 32% (0 - 2.3) **This stratum has no high energy samples**		
3 **a. South.Bedrock - Turbidity**	**Low**	**High**		Global R: 0.566 (1), 0.572 (2)	Moderate separation between

Stratification level and environmental criterion	Resulting strata			ANOSIM results	Note on community differentiation
	dataset size: 2022 SA0 gradient: 23% (0 - 1.7)	dataset size: 3 SA0 gradient: 3% (0.07 - 0.3)			turbidity levels, weak between energy levels. Stratification by turbidity was chosen for the analysis.
		Dataset size and pressure gradient reduced too much - Not analysed			
3 **b. South.Bedrock - Energy**	**Low**	**Moderate**	**High**	Global R: 0.025 (1), 0.023 (2) Pairwise R: High/Moderate: 0.831 (1), 0.817 (2) High/Low: 0.888 (1), 0.878 (2) Moderate/Low: 0.024 (1), 0.021 (2)	
	dataset size: 768 SA0 gradient: 23% (0 - 1.7)	dataset size: 1256 SA0 gradient: 11% (0 - 0.8) Pressure gradient reduced too much - Not analysed	dataset size: 1 SA0 gradient: no gradient Dataset size and pressure gradient reduced too much - Not analysed		
4 **South.Bedrock.LowTurbidity - Energy**	**Low**	**Moderate**	**High**	Global R: 0.026 (1), 0.023 (2)	Very weak separation between energy levels (R<0.1). Further energy stratification was not applied to bedrock, low turbidity habitat
	dataset size: 768 SA0 gradient: 23% (0 - 1.7)	dataset size: 1253 SA0 gradient: 11% (0 - 0.8) Pressure gradient reduced too much - Not analysed	dataset size: 1 SA0 gradient: no gradient Dataset size and pressure gradient reduced too much - Not analysed		

Stratification level and environmental criterion	Resulting strata			ANOSIM results	Note on community differentiation
3 **a. South.Boulders - Turbidity**	**Low**	**High**		Global R: 0.117 (1), 0.117 (2)	Moderate separation between energy levels, weaker between turbidity levels. Stratification by energy was chosen for the analysis.
	dataset size: 904	dataset size: 14			
	SA0 gradient: 46% (0 - 3.4)	SA0 gradient: 2% (0.02 - 0.1) Pressure gradient reduced too much - Not analysed			
3 **b. South.Boulders - Energy**	**Low**	**Moderate**	**High**	Global R: 0.508 (1), 0.510 (2) Pairwise R: High/Moderate: 0.635 (1), 0.631 (2) High/Low: 0.997 (1), 0.995 (2) Moderate/Low: 0.507 (1), 0.508 (2)	
	dataset size: 407 SA0 gradient: 46% (0 - 3.4) **This stratum has only low turbidity samples**	dataset size: 510 SA0 gradient: 9% (0 - 0.6) Pressure gradient reduced too much - Not analysed	dataset size: 1 SA0 gradient: no gradient Dataset size and pressure gradient reduced too much - Not analysed		
3 **a. South.Cobble - Turbidity**	**Low**	**High**		Global R: 0.119 (1), 0.118 (2)	Moderate separation between energy levels, weaker between turbidity levels. Stratification by
	dataset size: 1935 SA0 gradient: 32% (0 - 2.3)	dataset size: 9 SA0 gradient: 3% (0.1 - 0.3)			

Stratification level and environmental criterion	Resulting strata			ANOSIM results	Note on community differentiation
		Dataset size and pressure gradient reduced too much - Not analysed			energy was chosen for the analysis.
3 **b. South.Cobble - Energy**	**Low**	**Moderate**		Global R: 0.585 (1), 0.586 (2)	
	dataset size: 596 SA0 gradient: 32% (0 - 2.3) **This stratum has only low turbidity samples**	dataset size: 1348 SA0 gradient: 11% (0 - 0.8) Pressure gradient reduced too much - Not analysed			

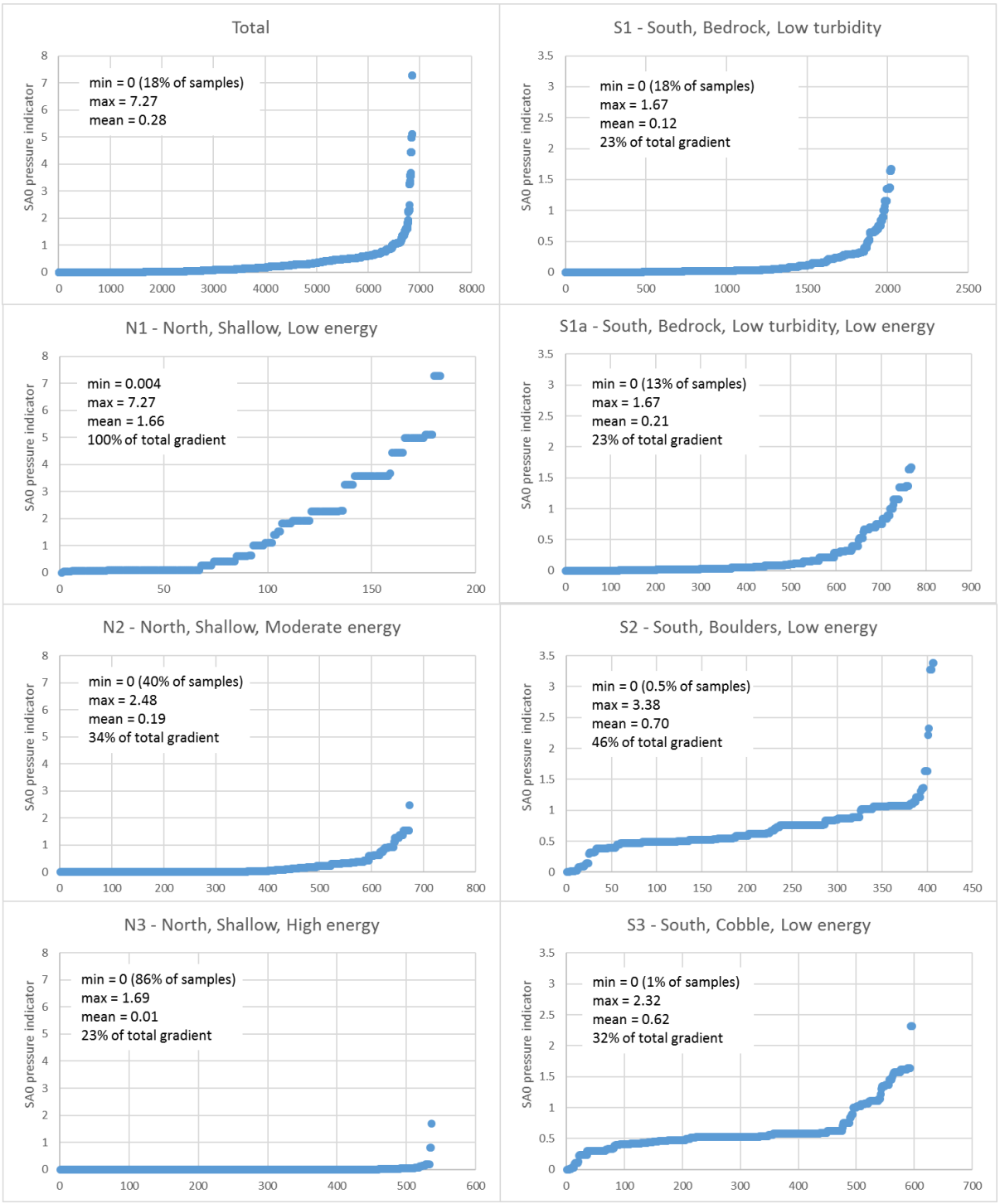

Figure 10. Gradient of the pressure indicator (SA0) in the overall dataset (6,852 samples) and in the strata obtained for the analysis. The pressure gradient was not considered to be sufficiently represented in stratum N3, and therefore this stratum was not considered for the analysis. Due to computational timing limitations in running the TITAN analysis, stratum S1a was used instead of S1.

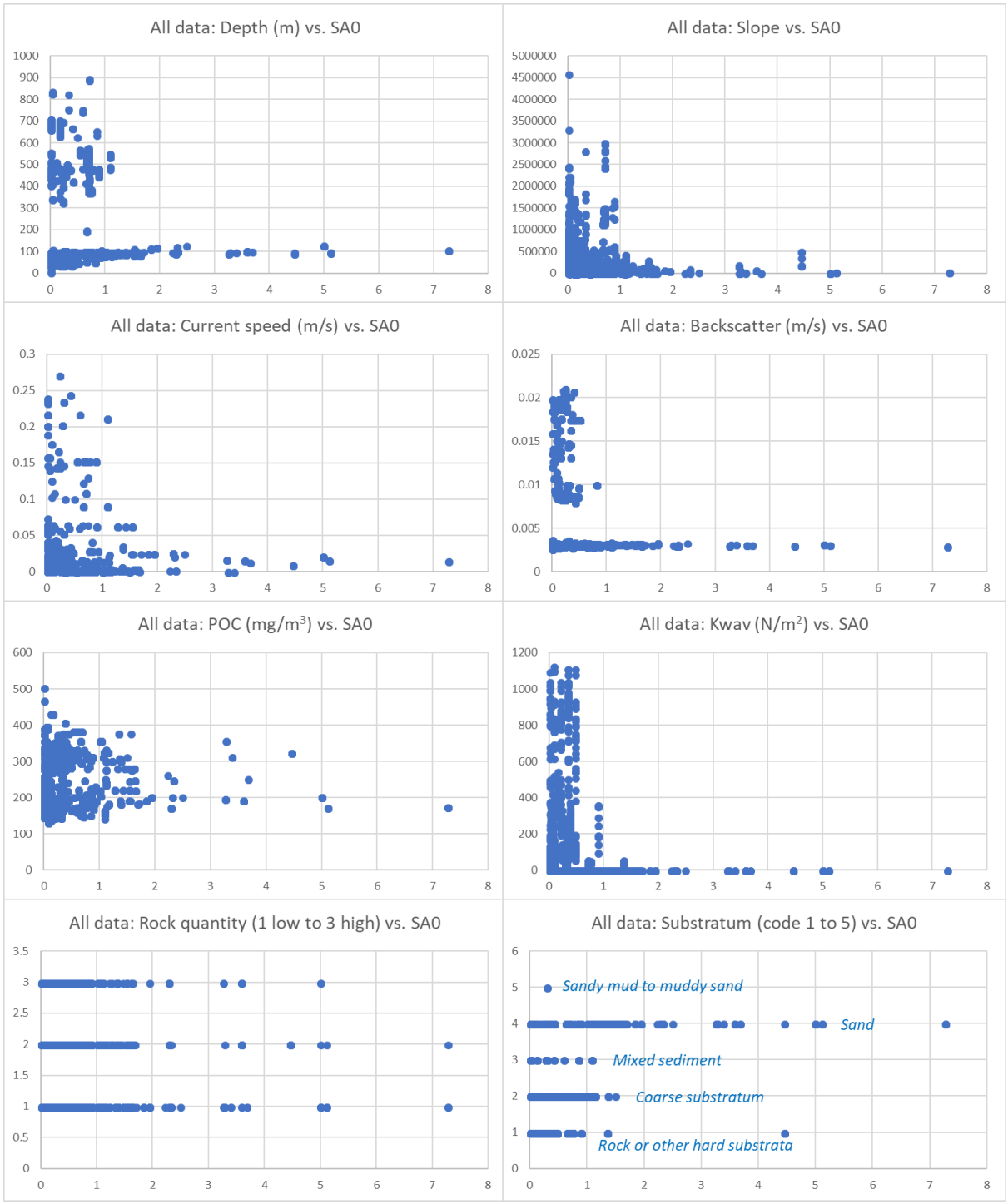

Figure 11. Environmental variability along the pressure indicator (SA0) gradient in the overall dataset (6,852 samples)

Figure 12. Environmental variability along the pressure indicator (SA0) gradient in the N1 dataset (183 samples)

Figure 13. Environmental variability along the pressure indicator (SA0) gradient in the N2 dataset (673 samples).

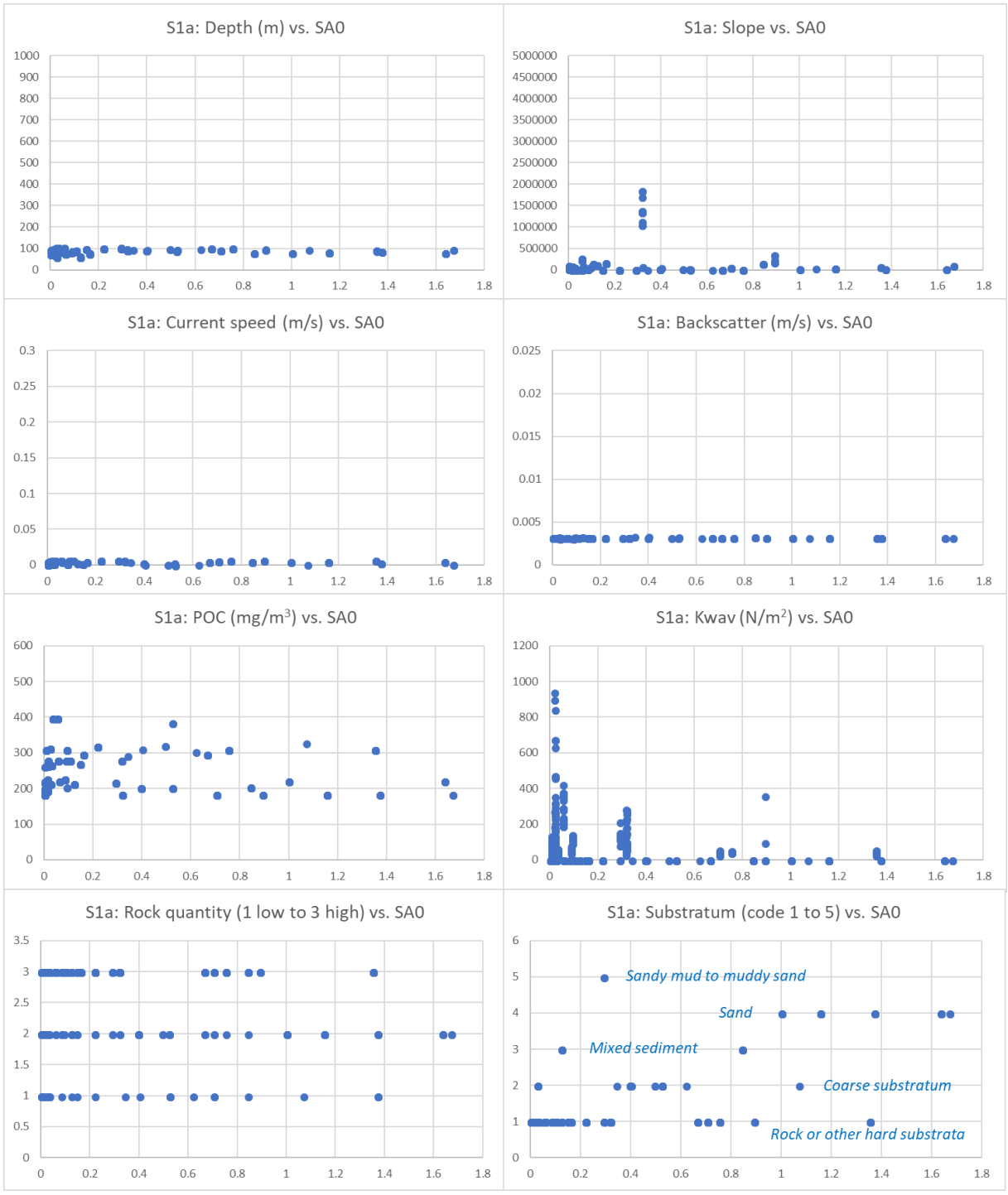

Figure 14. Environmental variability along the pressure indicator (SA0) gradient in the S1a dataset (767 samples).

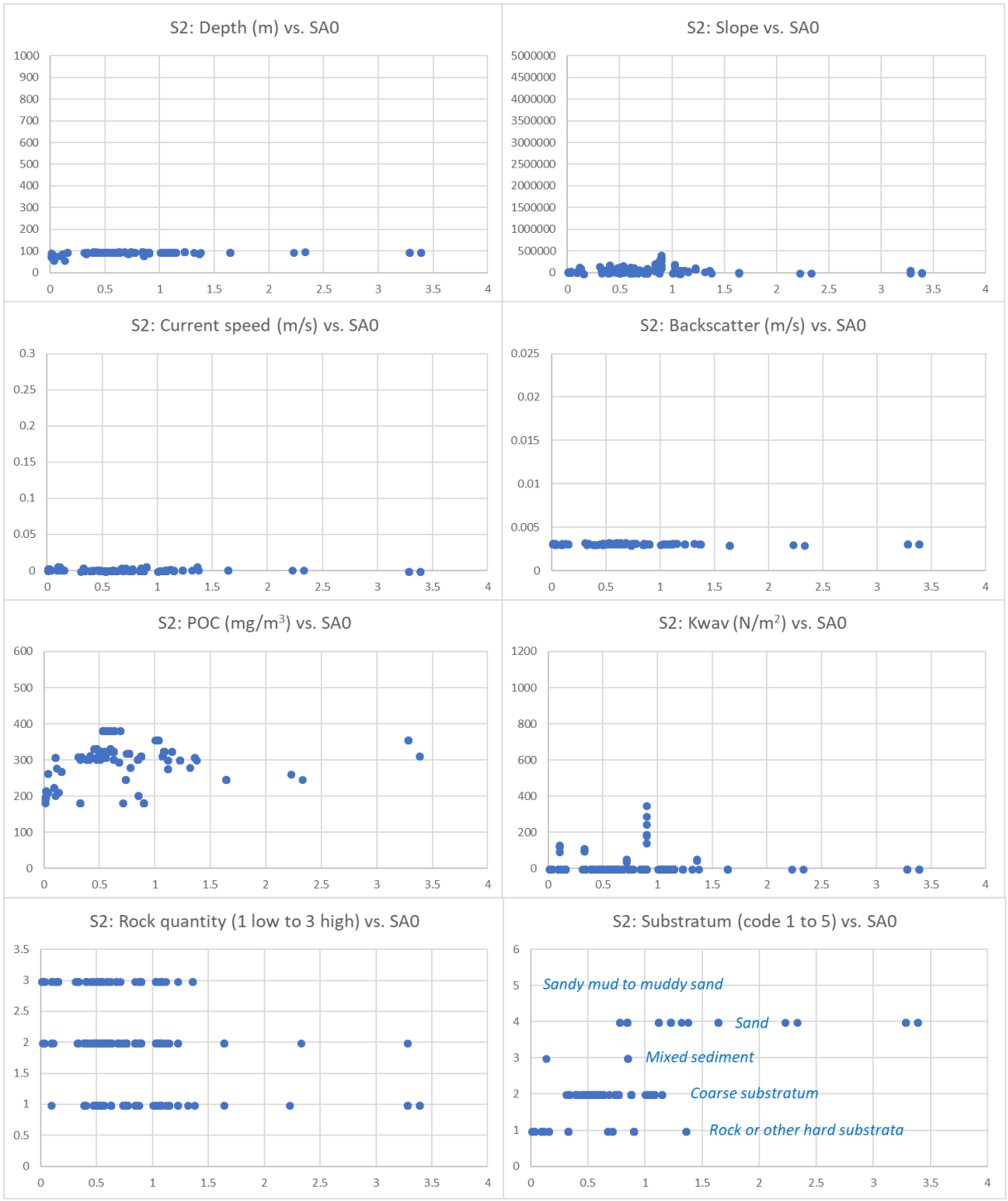

Figure 15. Environmental variability along the pressure indicator (SA0) gradient in the S2 dataset (407 samples).

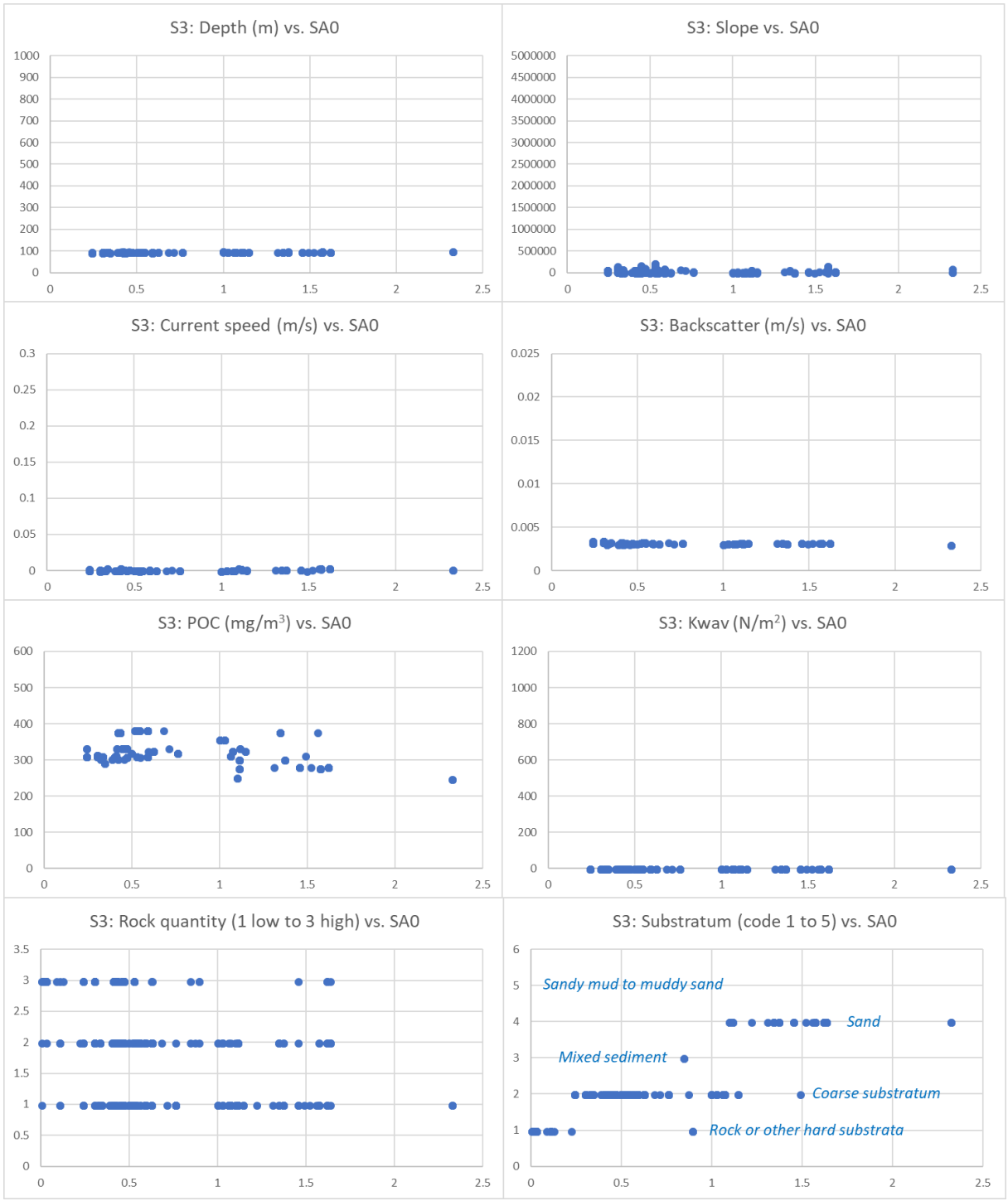

Figure 16. Environmental variability along the pressure indicator (SA0) gradient in the S3 dataset (596 samples).

Appendix 5. Abbreviations and full names of taxa included in the dataset strata analysed.

Table 19. Abbreviations and full names of taxa included in the conspicuous (Consp) dataset analysed. Taxon abbreviations may vary among dataset strata (i.e. an individual taxon may be referred to using a different abbreviation in each of the dataset strata).

Abbreviation	Full name
Actiniar	Actiniaria
Actiniid	Actiniidae
Adamsia	*Adamsia*
Aglaoph1	Aglaopheniidae
Aglaoph2	*Aglaophenia*
Aglaophe	*Aglaophenia*
Alcyodig	*Alcyonium digitatum*
Alcyoglo	*Alcyonium glomeratum*
Alcyonid	*Alcyonidium*
Alcyoniu	*Alcyonium digitatum*
Amphiura	*Amphiura*
Antedon	*Antedon*
Antedonb	*Antedon bifida*
Antedoni	Antedonidae
Anthozoa	Anthozoa
Arboresc	Arborescent
Ascidiac	Ascidiacea
Ascidiid	Ascidiidae
Asterias	*Asterias rubens*
Asteriid	Asteriidae
Atrinafr	*Atrina fragilis*
Balanoid	Balanoidea
Bispira	*Bispira*
Bolocera	*Bolocera tuediae*
Brachiop	Brachiopoda
Bryozoa	Bryozoa
Buccinid	Buccinidae
Bugula	*Bugula*
Bugulida	Bugulidae
Cabereab	*Caberea boryi*
Calliost	*Calliostoma*
Capneasa	*Capnea sanguinea*
Caryoph1	*Caryophyllia*
Caryoph2	Caryophylliidae
Caryophy	*Caryophyllia*
Cellepor	Celleporidae
Ceriallo	*Cerianthus lloydii*
Cerianth	Cerianthidae

Abbreviation	Full name
Chaetopt	Chaetopteridae
Cionaint	*Ciona intestinalis*
Cirriped	Cirripedia
Colus	*Colus*
Corallin	Corallinaceae
Corynact	*Corynactis*
Corynvir	*Corynactis viridis*
Crepidul	*Crepidula fornicata*
Crinoide	Crinoidea
Crossast	*Crossaster papposus*
Diazonav	*Diazona violacea*
Diphasia	*Diphasia*
Ditrupaa	*Ditrupa arietina*
Ebalia	*Ebalia*
Echinoid	Echinoidea
Echinuse	*Echinus esculentus*
Edwardsi	Edwardsiidae
Encrusti	Encrusting
Flabella	Flabellate
Flustraf	*Flustra foliacea*
Flustrid	Flustridae
Flustrin	Flustrina
Galatheo	Galatheoidea
Gibbula	*Gibbula*
Globular	Globular
Gracilec	*Gracilechinus acutus*
Haleciid	Haleciidae
Henricia	*Henricia*
Hexacora	Hexacorallia
Hippaste	*Hippasteria phrygiana*
Holothur	Holothuroidea
Hyalinoe	*Hyalinoecia*
Hydrozoa	Hydrozoa
Hymedesm	Hymedesmiidae
Inachida	Inachidae
Laniceco	*Lanice conchilega*
Leptaste	*Leptasterias muelleri*
Luidiaci	*Luidia ciliaris*

Abbreviation	Full name
Lytocarp	*Lytocarpia myriophyllum*
Majoidea	Majoidea
Marthast	*Marthasterias glacialis*
Massive	Massive
Mesacmae	*Mesacmaea mitchellii*
Munida	*Munida*
Mytiluse	*Mytilus edulis*
Nemertes	*Nemertesia*
Neogastr	Neogastropoda
Neoloric	Neoloricata
Omalosec	*Omalosecosa ramulosa*
Ophiacti	Ophiactidae
Ophiocom	*Ophiocomina nigra*
Ophiopho	*Ophiopholis aculeata*
Ophiothr	*Ophiothrix fragilis*
Ophiualb	*Ophiura albida*
Ophiuoph	*Ophiura ophiura*
Ophiura	*Ophiura*
Ophiuroi	Ophiuroidea
Paguroid	Paguroidea
Pagurus	*Pagurus*
Palmiske	*Palmiskenea skenei*
Papillat	Papillate
Parasmit	*Parasmittina*
Parastri	*Parasmittina trispinosa*
Parazang	*Parazoanthus anguicomus*
Parazoan	*Parazoanthus*
Pectenma	*Pecten maximus*
Pectinid	Pectinidae
Pentafas	*Pentapora fascialis*
Pentafol	*Pentapora foliacea*
Plumular	Plumularioidea
Polyplac	Polyplacophora
Poraniap	*Porania pulvillus*
Porella	*Porella*
Porella_	*Porella*

Abbreviation	Full name
Porellac	*Porella compressa*
Porellaco	*Porella compressa*
Porifera	Porifera
Psolus	*Psolus*
Repent	Repent
Retepore	*Reteporella*
Rhodophy	Rhodophyta
Sabella	*Sabella*
Sabellar	*Sabellaria spinulosa*
Sabelli1	Sabellida
Sabelli2	Sabellidae
Sabellid	Sabellida
Sagartia	*Sagartia elegans*
Sagartii	Sagartiidae
Salmacin	*Salmacina*
Scleract	Scleractinia
Securifl	*Securiflustra securifrons*
Serpulid	Serpulidae
Sertula1	*Sertularella*
Sertula2	*Sertularia*
Sertular	Sertulariidae
Smittino	Smittinoidea
Spirobra	*Spirobranchus*
Spirotri	*Spirobranchus triqueter*
Stichast	*Stichastrella rosea*
Stolonic	*Stolonica socialis*
Stomphia	*Stomphia coccinea*
Styelida	Styelidae
Suberiti	Suberitidae
Swiftiap	*Swiftia pallida*
Terebell	Terebellida
Thuiaria	*Thuiaria thuja*
Trochida	Trochidae
Tubular	Tubular
Tubulari	Tubulariidae
Urticina	*Urticina*

Table 20. Abbreviations and full names of taxa included in the aggregated (Aggrt) dataset analysed. Taxon abbreviations may vary among dataset strata (i.e. an individual taxon may be referred to using a different abbreviation in each of the dataset strata).

Abbreviation	Full name
Actiniar	Actiniaria
Actiniid	Actiniidae
Adamsia	*Adamsia*
Aglaoph1	Aglaopheniidae
Aglaoph2	*Aglaophenia*
Aglaophe	*Aglaophenia*
Alcyonid	*Alcyonidium*
Alcyoniu	*Alcyonium*
Amphiura	*Amphiura*
Antedon	*Antedon*
Antedoni	Antedonidae
Anthozoa	Anthozoa
Arboresc	Arborescent
Ascidiac	Ascidiacea
Ascidiid	Ascidiidae
Asterias	*Asterias rubens*
Asteriid	Asteriidae
Atrinafr	*Atrina fragilis*
Balanoid	Balanoidea
Bispira	*Bispira*
Bolocera	*Bolocera tuediae*
Brachiop	Brachiopoda
Bryozoa	Bryozoa
Buccinid	Buccinidae
Bugula	*Bugula*
Bugulida	Bugulidae
Cabereab	*Caberea boryi*
Calliost	*Calliostoma*
Capneasa	*Capnea sanguinea*
Caryoph1	*Caryophyllia*
Caryoph2	Caryophylliidae
Caryophy	*Caryophyllia*
Cellepor	Celleporidae
Ceriallo	*Cerianthus lloydii*
Cerianth	Cerianthidae
Chaetopt	Chaetopteridae
Cionaint	*Ciona intestinalis*
Cirriped	Cirripedia
Colus	*Colus*
Corallin	Corallinaceae
Corynact	*Corynactis*

Abbreviation	Full name
Crepidul	*Crepidula fornicata*
Crinoide	Crinoidea
Crossast	*Crossaster papposus*
Diazonav	*Diazona violacea*
Diphasia	*Diphasia*
Ditrupaa	*Ditrupa arietina*
Ebalia	*Ebalia*
Echinoid	Echinoidea
Echinus	*Echinus*
Edwardsi	Edwardsiidae
Encrusti	Encrusting
Flabella	Flabellate
Flabelli	*Flabellina*
Flustraf	*Flustra foliacea*
Flustrid	Flustridae
Flustrin	Flustrina
Galatheo	Galatheoidea
Gibbula	*Gibbula*
Globular	Globular
Gracilec	*Gracilechinus acutus*
Haleciid	Haleciidae
Henricia	*Henricia*
Hexacora	Hexacorallia
Hippaste	*Hippasteria phrygiana*
Holothur	Holothuroidea
Hyalinoe	*Hyalinoecia*
Hydrozoa	Hydrozoa
Hymedesm	Hymedesmiidae
Inachida	Inachidae
Janolusc	*Janolus cristatus*
Laniceco	*Lanice conchilega*
Leptaste	*Leptasterias muelleri*
Luidia	*Luidia*
Lytocarp	*Lytocarpia myriophyllum*
Majoidea	Majoidea
Marthast	*Marthasterias glacialis*
Massive	Massive
Mesacmae	*Mesacmaea mitchellii*
Munida	*Munida*
Mytiluse	*Mytilus edulis*

Abbreviation	Full name
Nemertes	*Nemertesia*
Neogastr	Neogastropoda
Neoloric	Neoloricata
Nudibran	Nudibranchia
Omalosec	*Omalosecosa ramulosa*
Ophiacti	Ophiactidae
Ophiocom	*Ophiocomina nigra*
Ophiopho	*Ophiopholis aculeata*
Ophiothr	*Ophiothrix fragilis*
Ophiura	*Ophiura*
Ophiuroi	Ophiuroidea
Paguroid	Paguroidea
Pagurus	*Pagurus*
Palmiske	*Palmiskenea skenei*
Papillat	Papillate
Parasmit	*Parasmittina*
Parazoan	*Parazoanthus*
Pectenma	*Pecten maximus*
Pectinid	Pectinidae
Pentapor	*Pentapora*
Plumular	Plumularioidea
Polyplac	Polyplacophora
Poraniap	*Porania pulvillus*
Porella	*Porella*
Porifera	Porifera
Psolus	*Psolus*
Repent	Repent
Retepore	*Reteporella*
Rhodophy	Rhodophyta
Sabella	*Sabella*
Sabellar	*Sabellaria spinulosa*
Sabelli1	*Sabellida*
Sabelli2	Sabellidae
Sabellid	*Sabellida*
Sagartia	*Sagartia*
Sagartii	Sagartiidae
Salmacin	*Salmacina*
Scleract	Scleractinia
Securifl	*Securiflustra securifrons*
Serpulid	Serpulidae
Sertula1	*Sertularella*
Sertula2	*Sertularia*
Sertular	Sertulariidae

Abbreviation	Full name
Smittino	Smittinoidea
Spirobra	*Spirobranchus*
Stichast	*Stichastrella rosea*
Stolonic	*Stolonica socialis*
Stomphia	*Stomphia coccinea*
Styelida	Styelidae
Suberiti	Suberitidae
Swiftiap	*Swiftia pallida*
Terebell	Terebellida
Thuiaria	*Thuiaria thuja*
Trochida	Trochidae
Tubular	Tubular
Tubulari	Tubulariidae
Urticina	*Urticina*

Appendix 6: TITAN results

TITAN results for “Conspicuous taxa” dataset, stratum N1 - North, shallow (deep circalittoral), low energy habitat (with low turbidity and variable rock type)

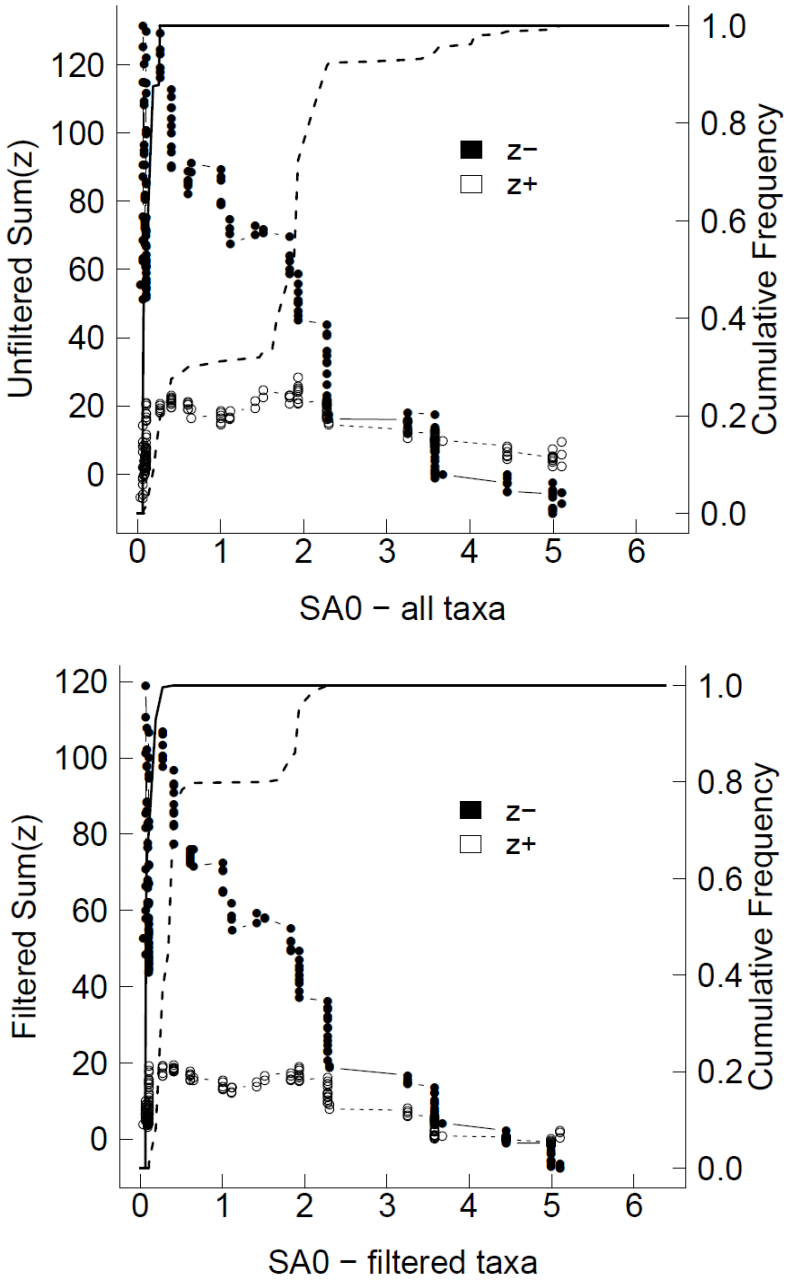

Figure 17. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 – 7.3) within the dataset “N1.conspicuous”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 21. TITAN taxon-specific tabular output for the dataset "N1.conspicuous".Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 19.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Laniceco*	0.05 (0.05 - 0.27)	12	76.01	Yes	1.00	0.98
	Caryoph2*	0.06 (0.06 - 0.08)	10	71.56	Yes	1.00	1.00
	Ophiuroi*	0.07 (0.06 - 0.08)	30	70.85	Yes	1.00	1.00
	Ophiualb*	0.07 (0.06 - 0.27)	19	47.4	Yes	1.00	1.00
	Hexacora*	0.06 (0.06 - 0.09)	6	42.86	Yes	1.00	1.00
	Poraniap*	0.08 (0.05 - 0.19)	33	40.64	Yes	0.97	0.97
	Flustraf*	0.07 (0.05 - 0.27)	11	37.7	Yes	1.00	1.00
	Parazoan*	0.06 (0.06 - 0.27)	9	33.34	Yes	1.00	0.99
	Sertular*	0.08 (0.06 - 0.09)	6	30.03	Yes	1.00	0.97
	Ophiothr*	0.1 (0.09 - 0.11)	30	28.78	Yes	0.97	1.00
	Hymedesm*	0.27 (0.11 - 0.34)	19	24.9	Yes	1.00	1.00
	Serpulid*	0.34 (0.06 - 1.93)	34	24.89	Yes	0.98	1.00
	Parasmit*	0.27 (0.06 - 0.27)	14	19.72	Yes	1.00	1.00
	Scleract*	0.27 (0.11 - 0.34)	11	15.49	Yes	1.00	1.00
	Asterias*	0.09 (0.05 - 1)	8	14.64	Yes	1.00	0.98
	Balanoid*	0.27 (0.04 - 1.67)	13	13.99	Yes	1.00	1.00
	Retepore*	0.11 (0.04 - 0.27)	7	10.94	Yes	1.00	0.97
	Palmiske*	0.27 (0.11 - 0.34)	7	10.29	Yes	1.00	0.98
	Spirobra	5.1 (0.06 - 6.18)	153	67.23	Yes	0.77	0.98
	Bryozoa	5.1 (0.07 - 6.18)	141	66.65	Yes	0.74	0.98
	Caryoph1	0.63 (0.09 - 5.05)	61	30.01	Yes	0.79	1.00
	Globular	0.06 (0.06 - 0.11)	5	21.77	Yes	0.99	0.93
	Securifl	0.08 (0.05 - 2.78)	9	16.07	Yes	0.86	0.83
	Ophiura	0.1 (0.09 - 4.45)	14	15.62	Yes	0.80	0.89
	Ebalia	0.27 (0.11 - 0.41)	14	13.85	Yes	0.94	0.97
	Porifera	0.06 (0.06 - 1)	6	13.43	Yes	0.99	0.83
	Munida	0.41 (0.11 - 3.58)	20	13.41	Yes	0.91	0.90
	Leptaste	1.11 (0.09 - 3.58)	26	12.94	No	0.79	0.72
	Calliost	0.27 (0.1 - 2.34)	18	12.62	Yes	0.90	0.89
	Ditrupaa	0.1 (0.1 - 1.41)	6	10.69	Yes	0.98	0.86
	Massive	0.11 (0.06 - 5.1)	12	8.71	No	0.64	0.77
	Ascidiac	0.1 (0.06 - 4.99)	5	6.04	No	0.76	0.73
	Colus	0.83 (0.11 - 1)	5	5.43	Yes	0.97	0.65

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Urticina	0.11 (0.09 - 2.78)	5	3.63	No	0.77	0.31
Positive	Encrusti*	0.27 (0.07 - 1.93)	121	57.39	Yes	1.00	1.00
	Arboresc*	0.41 (0.27 - 1.93)	75	49.52	Yes	1.00	1.00
	Hydrozoa	1.83 (0.05 - 5.05)	120	44.12	Yes	0.72	0.76
	Flabella	0.1 (0.09 - 3.58)	64	31.99	Yes	0.77	0.94
	Hyalinoe	5.1 (1.06 - 7.27)	5	31.72	Yes	0.99	0.84
	Henricia	4.72 (0.1 - 4.99)	18	21.56	Yes	0.95	0.83
	Echinoid	2.28 (0.1 - 4.45)	29	19.97	Yes	0.94	0.92
	Asteriid	4.45 (0.08 - 4.99)	30	18.99	No	0.70	0.69
	Echinuse	1.83 (0.07 - 4.45)	35	15.09	No	0.61	0.76
	Galatheo	2.28 (0.06 - 5.05)	25	15.02	Yes	0.83	0.83
	Paguroid	0.41 (0.08 - 5.05)	33	14.68	No	0.83	0.66
	Terebell	4.06 (0.09 - 4.45)	14	12.1	No	0.60	0.71
	Thuiaria	1.83 (0.09 - 5.1)	5	4.66	No	0.85	0.63
	Hippaste	0.41 (0.08 - 4.99)	6	3.86	No	0.55	0.44

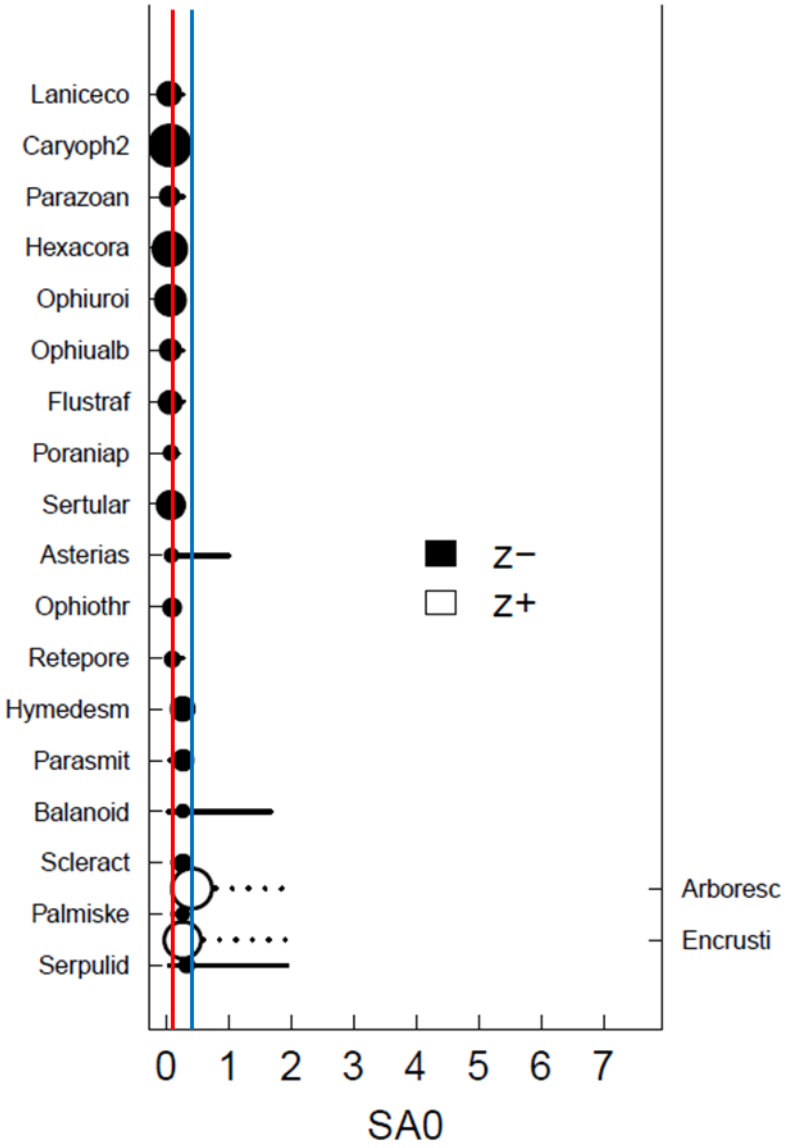

Figure 18. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “N1.conspicuous”. Black symbols correspond to negative (z-) indicator taxa (no positive indicator taxa were found in stratum). Symbols are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa), and horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Vertical lines represent community change point for taxa responding negatively (red) or positively (blue) to the pressure gradient. Taxa name abbreviations are as per Table 19.

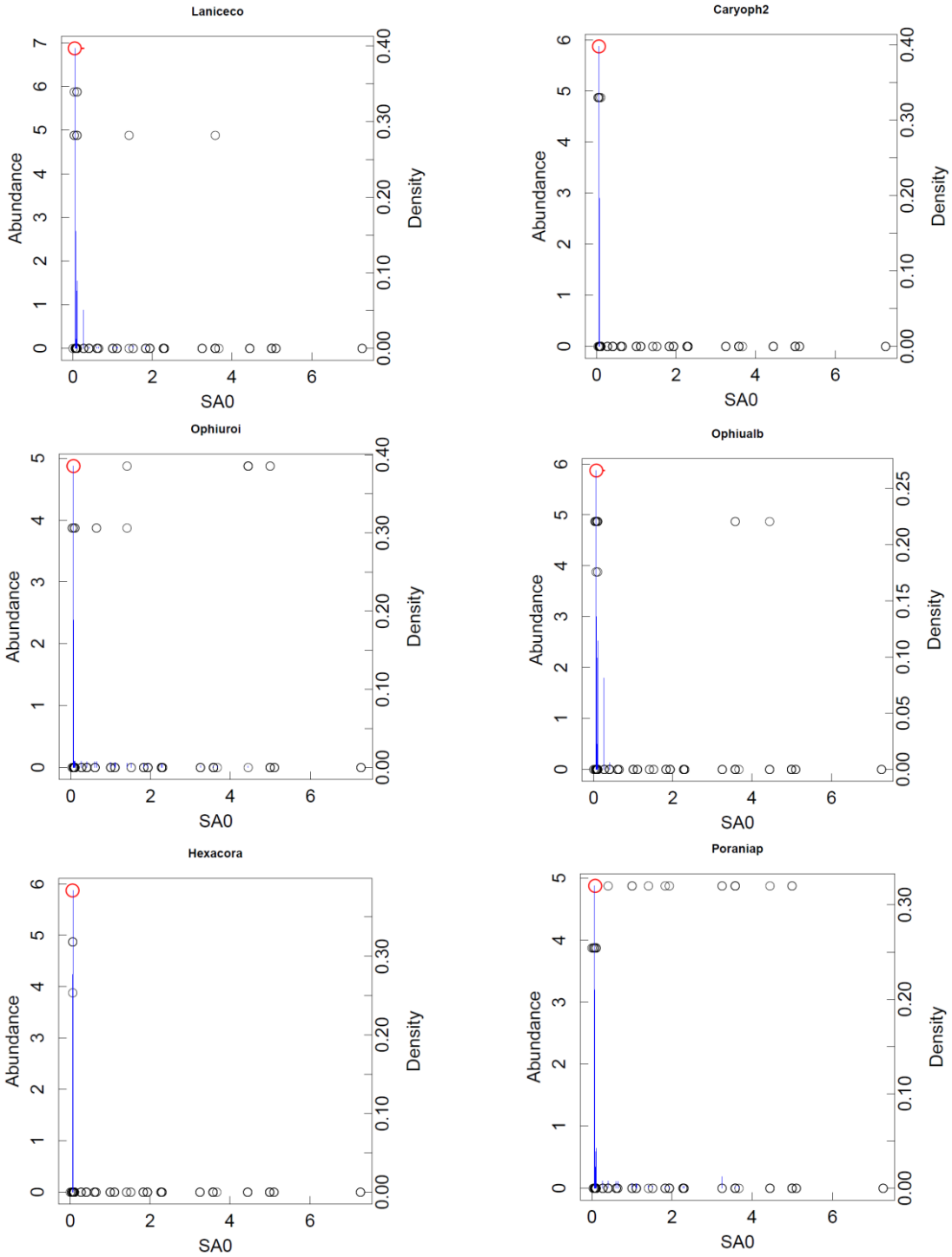

Figure 19. Taxon-specific plots of indicator taxa identified for the dataset “N1.conspicuous”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

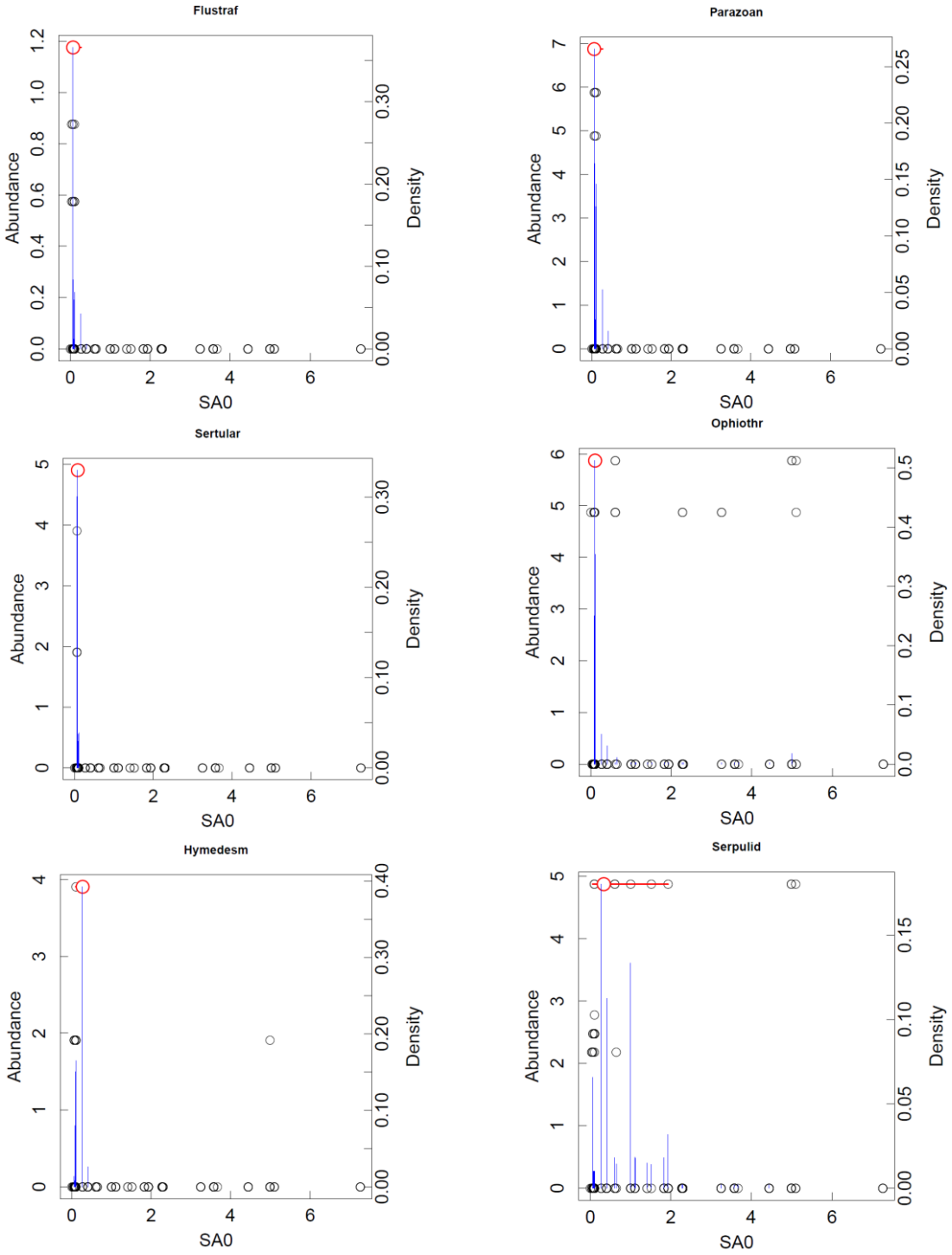

Figure 20. Taxon-specific plots of indicator taxa identified for the dataset “N1.conspicuous”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

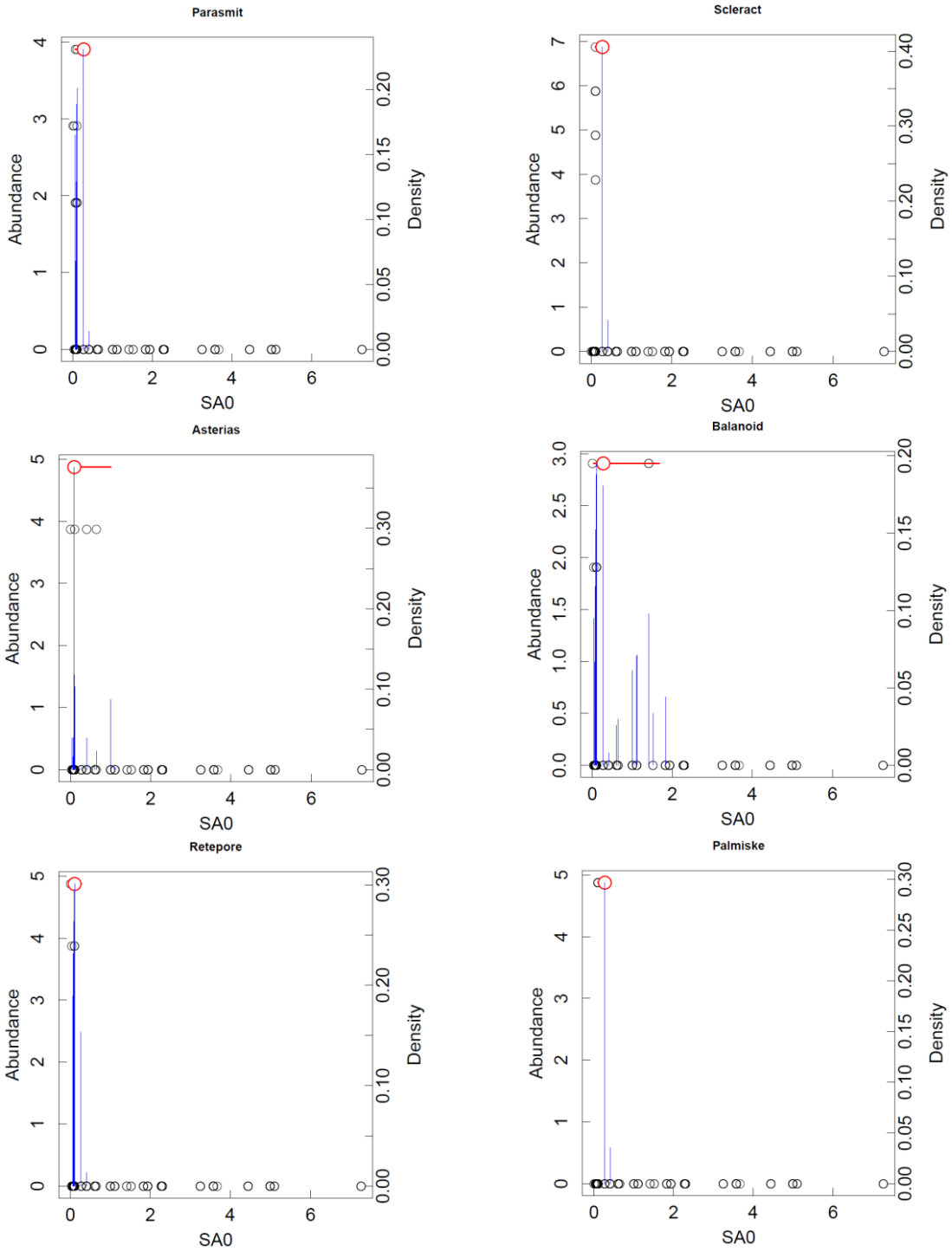

Figure 21. Taxon-specific plots of indicator taxa identified for the dataset “N1.conspicuous”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

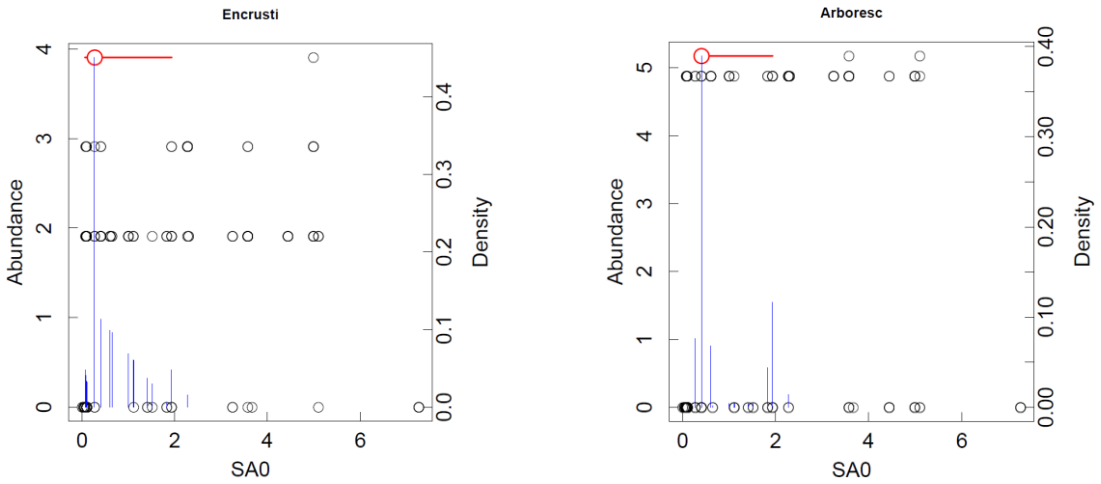

Figure 22. Taxon-specific plots of indicator taxa identified for the dataset “N1.conspicuous”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

TITAN results for “Aggregated taxa” dataset, stratum N2 - North, shallow (deep circalittoral), moderate energy habitat (with low turbidity and variable rock type)

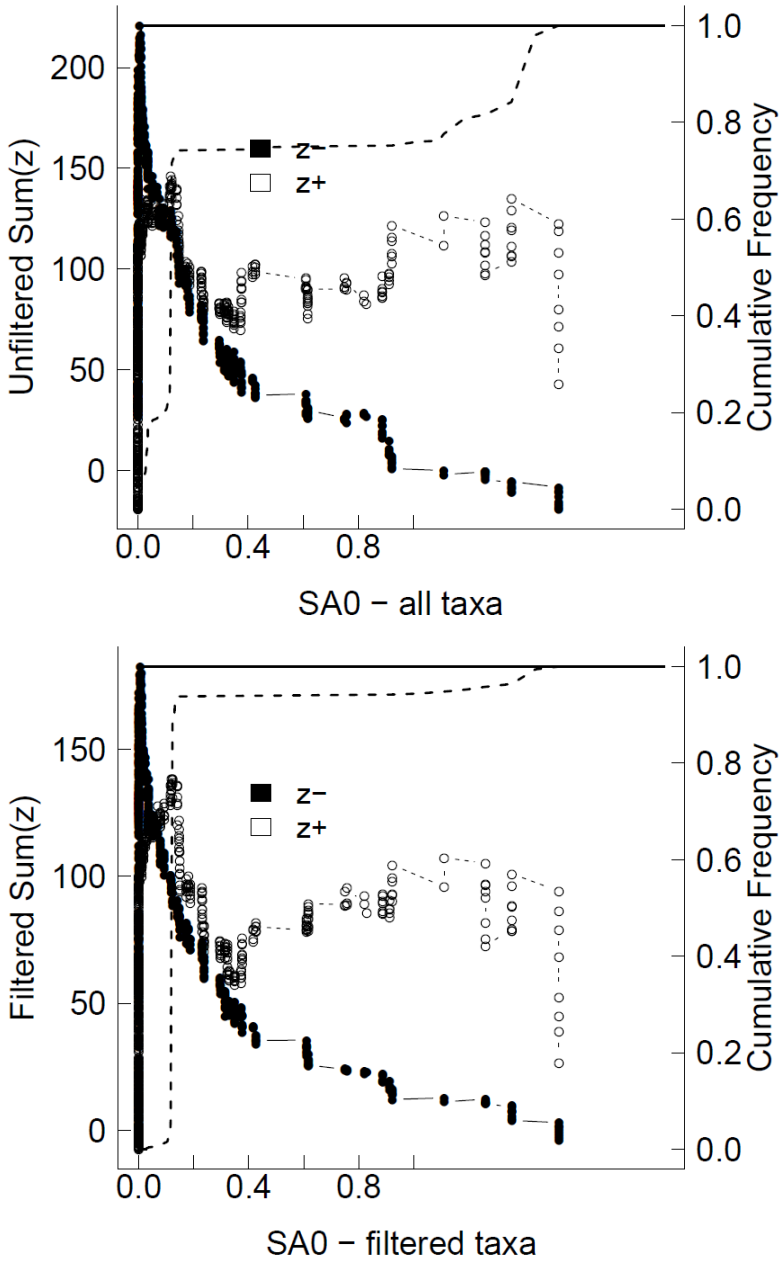

Figure 23. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 2.5) within the dataset “N2.conspicuous taxa”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 22. TITAN taxon-specific tabular output for the dataset "N2.conspicuous taxa". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, (i.e. decreasing or increasing in frequency and abundance with the gradient), respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 19.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Ophiocom*	0.01 (0 - 0.01)	166	48.19	Yes	1.00	1.00
	Corallin*	0.01 (0.01 - 0.01)	155	47	Yes	1.00	1.00
	Cellepor*	0.01 (0 - 0.01)	123	30.36	Yes	1.00	1.00
	Alcyoniu*	0.01 (0 - 0.01)	91	26.18	Yes	1.00	1.00
	Ophiuroi*	0 (0 - 0.01)	143	25.98	Yes	1.00	1.00
	Smittino*	0.36 (0.35 - 0.38)	136	23.9	Yes	1.00	1.00
	Parasmit*	0.35 (0.32 - 0.38)	99	17.46	Yes	1.00	1.00
	Flustraf*	0 (0 - 0.01)	86	16.66	Yes	1.00	1.00
	Actiniid*	0 (0 - 0)	45	16.53	Yes	1.00	1.00
	Crossast*	0 (0 - 0.01)	70	16.51	Yes	1.00	1.00
	Pagurus*	0 (0 - 0)	27	9.67	Yes	1.00	1.00
	Rhodophy*	0.01 (0 - 0.01)	29	6.4	Yes	1.00	0.99
	Ascidiid*	0.01 (0 - 0.04)	15	4	Yes	1.00	1.00
	Tubular*	0 (0 - 0.02)	10	3.74	Yes	1.00	0.99
	Flustrin*	0 (0 - 0)	7	2.63	Yes	1.00	0.98
	Spirobra	1.44 (0 - 1.53)	614	59.9	Yes	0.63	0.99
	Globular	0 (0 - 1.53)	50	54.47	Yes	0.52	0.98
	Laniceco	0 (0 - 1.26)	22	30.92	Yes	0.28	0.84
	Caryoph1	0.12 (0.04 - 0.4)	216	27.95	Yes	0.95	1.00
	Polyplac	0 (0 - 0.24)	16	22.98	Yes	0.47	0.88
	Stomphia	0 (0 - 0.33)	8	18.97	No	0.25	0.65
	Anthozoa	0 (0 - 0.35)	9	18.87	No	0.68	0.61
	Haleciid	0 (0 - 0.33)	13	18.28	No	0.89	0.64
	Calliost	0.01 (0 - 1.44)	100	18.09	Yes	0.94	1.00
	Omalosec	0 (0 - 0.33)	19	16.87	Yes	0.90	0.79
	Antedoni	0 (0 - 0.23)	12	15.34	Yes	0.86	0.72
	Securifl	0.01 (0.01 - 1.53)	96	13.52	Yes	0.91	1.00
	Asteriid	0.12 (0 - 1.36)	113	11.94	Yes	0.65	0.95
	Sertula1	0.32 (0 - 0.34)	34	6.17	Yes	0.85	0.98
	Urticina	0.01 (0 - 0.23)	25	4.69	Yes	0.94	0.92
	Flustrid	0 (0 - 0.19)	20	3.99	Yes	0.98	0.94
	Chaetopt	0 (0 - 0.24)	12	2.42	No	0.56	0.55
	Adamsia	0 (0 - 0.12)	5	2.31	Yes	0.94	0.67

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Caryoph2	0.01 (0 - 0.01)	8	2.22	Yes	0.78	0.92
	Antedon	0.09 (0 - 0.14)	11	1.94	No	0.79	0.64
	Buccinid	0.23 (0 - 0.23)	7	1.38	No	0.58	0.35
	Corynact	0.09 (0 - 0.12)	5	1.16	No	0.80	0.47
Positive	Scleract*	1.36 (1.36 - 1.53)	35	76.07	Yes	1.00	1.00
	Parazang*	1.44 (1.31 - 1.53)	20	67.65	Yes	1.00	1.00
	Hydrozoa*	0.12 (0 - 0.15)	314	51.36	Yes	1.00	1.00
	Paguroid*	1.53 (0.01 - 1.53)	46	49.38	Yes	0.99	0.99
	Hymedesm*	1.19 (0.89 - 1.45)	166	44.81	Yes	0.97	1.00
	Bryozoa*	0.01 (0 - 0.43)	294	43.11	Yes	1.00	1.00
	Munida*	1.53 (0.01 - 1.53)	59	42.77	Yes	0.96	0.98
	Serpulid*	0.12 (0 - 0.32)	319	33.97	Yes	0.98	1.00
	Encrusti*	0.43 (0.01 - 0.43)	153	29.11	Yes	1.00	1.00
	Balanoid*	0.12 (0.12 - 0.89)	118	24.8	Yes	1.00	1.00
	Flabella*	0.43 (0.02 - 1.26)	142	24.09	Yes	0.99	1.00
	Hexacora*	0.92 (0.23 - 1.19)	15	23.34	Yes	1.00	1.00
	Ophiualb*	0.14 (0.04 - 0.15)	112	20.65	Yes	1.00	1.00
	Galatheo*	0.14 (0.04 - 0.23)	106	17.51	Yes	1.00	1.00
	Retepore*	0.12 (0.12 - 1.44)	49	15.96	Yes	1.00	1.00
	Poraniap*	0.14 (0 - 1.53)	96	15.28	Yes	1.00	1.00
	Porifera*	0.79 (0 - 0.82)	34	10.76	Yes	0.96	0.95
	Porellac*	0.12 (0.01 - 0.14)	36	10.7	Yes	1.00	1.00
	Actiniar*	0.15 (0.01 - 0.68)	40	8.8	Yes	1.00	1.00
	Ebalia*	0.12 (0.12 - 1.11)	33	8.41	Yes	1.00	0.99
	Terebell*	0.04 (0.02 - 0.04)	22	5.78	Yes	0.97	0.99
	Nemertes*	0.15 (0.14 - 0.23)	19	5.77	Yes	0.99	0.99
	Parazoan*	0.05 (0.04 - 0.14)	12	3.81	Yes	0.99	0.98
	Parastri	1.44 (0.01 - 1.53)	120	70.27	Yes	0.91	1.00
	Gibbula	1.53 (0 - 1.53)	15	26.58	Yes	0.46	0.99
	Ophiothr	0.42 (0.04 - 0.43)	137	22.87	Yes	0.66	1.00
	Massive	1.26 (0 - 1.26)	62	21.52	Yes	0.90	0.97
	Ophiura	1.53 (0 - 1.53)	10	18.74	No	0.63	0.68
	Arboresc	0.02 (0.01 - 0.43)	86	11.79	Yes	0.91	1.00
	Echinoid	0.42 (0 - 0.61)	59	11.02	Yes	0.80	0.91
	Echinuse	0 (0 - 0.61)	55	7.26	Yes	0.52	0.96
	Inachida	1.44 (0 - 1.53)	7	6.82	No	0.86	0.71
	Leptaste	0.01 (0 - 0.43)	41	6.63	Yes	0.91	0.99
	Suberiti	1.26 (0 - 1.53)	7	6.35	Yes	0.72	0.93
	Trochida	0.43 (0 - 0.62)	19	5.46	Yes	0.95	0.92
	Henricia	0.01 (0 - 0.43)	44	4.95	No	0.59	0.77
	Thuiaria	1.36 (0 - 1.36)	7	4.48	No	0.60	0.48
	Pectenma	0.32 (0 - 1.02)	17	4.31	Yes	0.84	0.88
	Asterias	0.43 (0 - 0.63)	24	3.95	No	0.50	0.72
	Ascidiac	0.31 (0 - 0.92)	23	3.91	No	0.67	0.80

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Hyalinoe	0.01 (0.01 - 1.53)	10	2.87	Yes	0.78	0.95
	Neoloric	0.12 (0 - 0.33)	8	2.32	Yes	0.89	0.83
	Papillat	0.35 (0 - 0.35)	7	2.2	Yes	0.88	0.70
	Ophiopho	0.01 (0.01 - 0.07)	7	2.08	Yes	1.00	0.89
	Sertula2	0.04 (0 - 0.23)	10	1.97	Yes	0.71	0.66
	Luidiaci	0 (0 - 0.32)	12	1.94	No	0.80	0.61
	Stichast	0.12 (0 - 1.36)	11	1.82	No	0.59	0.70
	Alcyonid	0 (0 - 0.32)	9	1.68	No	0.25	0.64
	Hippaste	0.03 (0 - 0.12)	9	1.45	No	0.53	0.58
	Sagartii	0.16 (0 - 0.23)	6	1.09	No	0.55	0.44

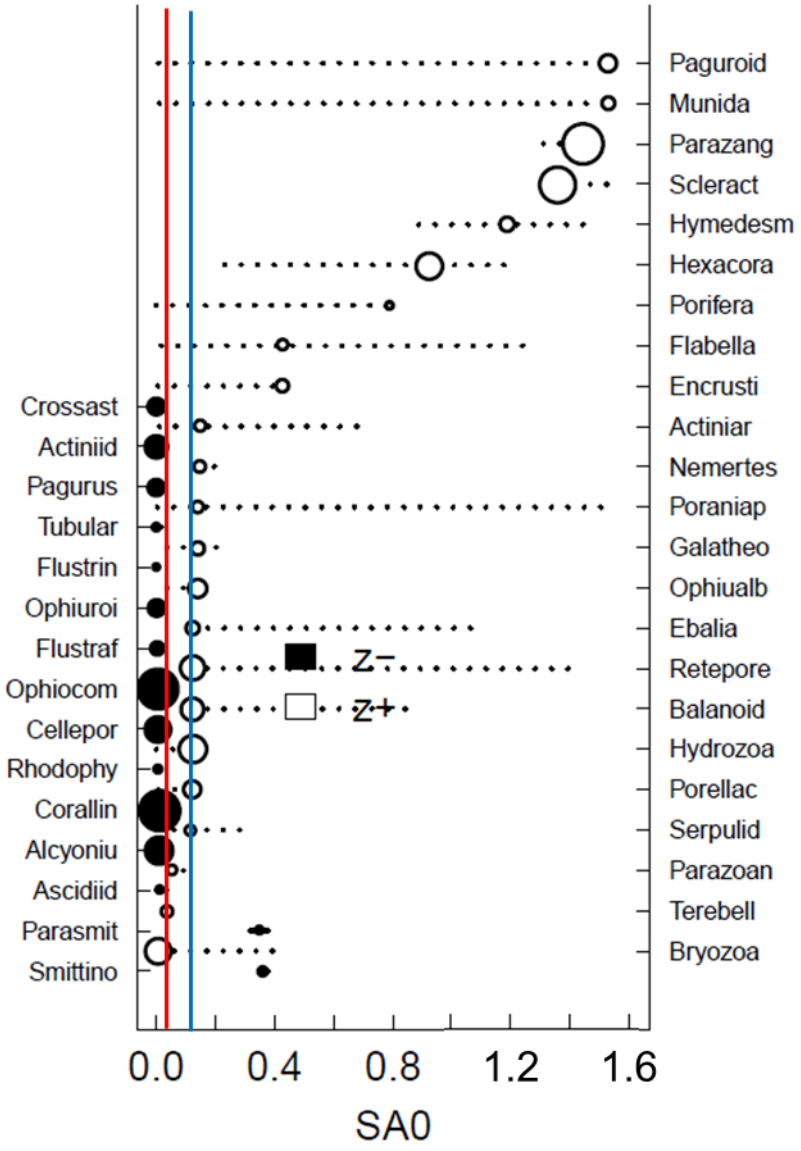

Figure 24. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “N2.conspicuous taxa”. Symbols correspond to negative (z-, full circles) and positive (z-, empty circles) indicator taxa, and are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa). Horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Vertical lines represent community change point for taxa responding negatively (red) or positively (blue) to the pressure gradient. Taxa name abbreviations are as per Table 19.

TITAN results for “Conspicuous taxa” dataset, stratum S1a - South, Low turbidity, Low energy, Bedrock habitat (in deep circalittoral zone)

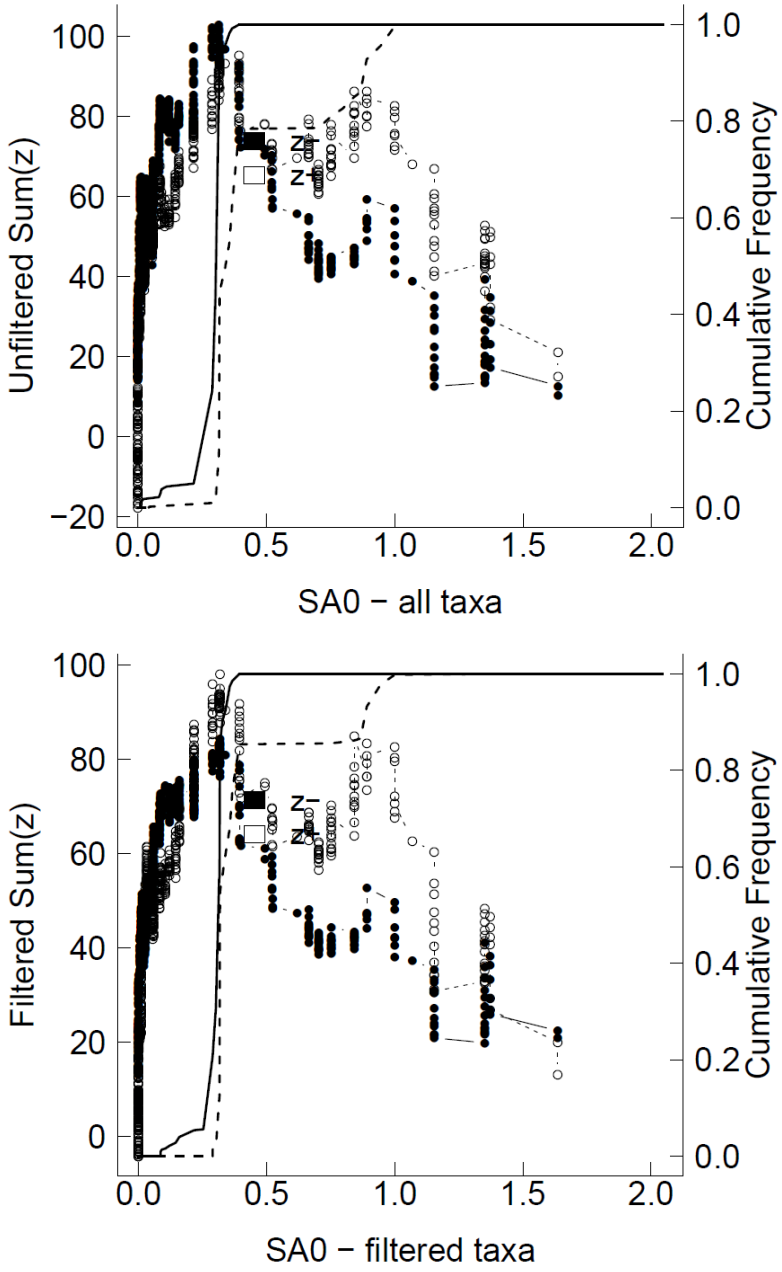

Figure 25. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 1.7) within the dataset “S1a.conspicuous”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 23. TITAN taxon-specific tabular output for the dataset "S1a.conspicuous". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 19.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Hydrozoa*	0.32 (0.29 - 1.37)	698	61.13	Yes	1.00	1.00
	Caryophy*	0.32 (0.02 - 0.39)	607	58.06	Yes	1.00	1.00
	Bryozoa*	0.02 (0.02 - 0.15)	630	54.34	Yes	1.00	1.00
	Porella*	0.95 (0.03 - 1.36)	379	39.89	Yes	1.00	1.00
	Brachiop*	0.29 (0.22 - 0.32)	265	35.85	Yes	1.00	1.00
	Ophiuroi*	0.32 (0.29 - 0.32)	279	35.28	Yes	0.99	1.00
	Ascidiac*	0 (0 - 0.22)	56	23.82	Yes	0.95	0.96
	Alcyonid*	0.02 (0.01 - 0.03)	168	21.15	Yes	1.00	1.00
	Swiftiap*	0 (0 - 0.03)	60	20.08	Yes	1.00	1.00
	Sertular*	0.08 (0.01 - 0.32)	79	10.82	Yes	1.00	1.00
	Repent*	0.04 (0.03 - 0.05)	48	9.26	Yes	1.00	1.00
	Trochida*	0.15 (0 - 0.32)	64	8.8	Yes	0.97	1.00
	Poraniap*	0.03 (0 - 0.32)	59	7.46	Yes	1.00	0.99
	Calliost*	0.06 (0 - 0.32)	49	5.99	Yes	0.99	0.96
	Serpulid	0.22 (0.02 - 0.32)	328	32.07	Yes	0.92	1.00
	Encrusti	0 (0.01 - 1.15)	37	19.24	Yes	0.38	0.98
	Antedonb	0.01 (0.01 - 0.67)	128	16.95	Yes	0.70	1.00
	Flabella	0.02 (0 - 1)	164	14.17	Yes	0.82	0.92
	Globular	0 (0 - 0.84)	9	11.55	Yes	0.67	0.79
	Nemertes	0.08 (0 - 0.36)	111	10.99	Yes	0.90	0.97
	Massive	0 (0 - 1.07)	11	8.67	No	0.24	0.81
	Crinoide	0.05 (0.01 - 0.12)	68	7.69	Yes	0.54	1.00
	Arboresc	0.87 (0 - 0.75)	49	6.87	No	0.45	0.80
	Echinuse	0.32 (0 - 1.35)	55	5.72	No	0.53	0.71
	Echinoid	0.01 (0 - 1.35)	32	5.06	Yes	0.64	0.88
	Bugulida	0 (0 - 0.75)	6	4.04	Yes	0.92	0.94
	Pentafol	0 (0 - 1.35)	9	3.82	Yes	0.74	0.86
	Salmacin	0.01 (0 - 0.15)	18	3.78	Yes	0.98	0.92
	Palmiske	0.32 (0 - 0.32)	19	3.09	Yes	0.72	0.83
	Diazonav	0.01 (0 - 0.06)	7	2.73	Yes	1.00	0.93
	Stichast	0.01 (0 - 0.22)	11	2.52	Yes	0.96	0.78
	Haleciid	0.06 (0 - 0.8)	10	1.82	Yes	0.84	0.75
	Ebalia	0.02 (0 - 0.32)	7	1.69	Yes	0.80	0.75
	Terebell	0.03 (0.01 - 0.12)	10	1.57	No	0.59	0.68

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Cionaint	0.01 (0.01 - 0.84)	6	1.43	No	0.65	0.67
	Asterias	0.09 (0 - 0.09)	5	1.05	No	0.83	0.45
	Gracilec	0.22 (0 - 0.15)	5	0.85	No	0.69	0.39
Positive	Porifera*	0.89 (0.84 - 1)	31	50.42	Yes	1.00	1.00
	Sabelli1*	1.36 (0.09 - 1.37)	12	29.05	Yes	1.00	0.99
	Ophiocom*	0.02 (0.02 - 0.02)	131	19.89	Yes	0.99	1.00
	Paguroid*	0.3 (0.02 - 0.75)	135	18.13	Yes	1.00	1.00
	Corynact*	0.03 (0.03 - 0.04)	64	15.42	Yes	1.00	1.00
	Spirotri*	0.32 (0.32 - 0.9)	20	14.81	Yes	1.00	1.00
	Ophiualb*	0.08 (0.06 - 0.22)	132	14.59	Yes	0.98	1.00
	Ophiacti*	0 (0 - 0.67)	102	13.81	Yes	0.98	1.00
	Ophiothr*	0.02 (0.02 - 0.03)	59	10.16	Yes	0.97	1.00
	Styelida*	0.95 (0.39 - 1.5)	5	8.18	Yes	1.00	0.99
	Mesacmae*	0.32 (0.32 - 1)	9	6.52	Yes	1.00	1.00
	Pectinid*	0.39 (0.12 - 1.15)	7	4.67	Yes	1.00	0.99
	Papillat*	0.05 (0.01 - 1.64)	22	3.75	Yes	0.99	0.99
	Asteriid	1.35 (0 - 1.37)	81	36.57	Yes	0.81	0.99
	Ophiura	0.01 (0.01 - 0.22)	180	16.95	Yes	0.73	0.99
	Lytocarp	1.35 (0 - 1.35)	26	16.06	Yes	0.76	1.00
	Retepore	0.75 (0.01 - 1.15)	43	8.09	Yes	0.77	0.98
	Actiniar	0.08 (0.01 - 0.75)	46	5.64	Yes	0.95	0.91
	Polyplac	0.06 (0 - 0.75)	48	4.65	No	0.47	0.78
	Plumular	0.57 (0.01 - 0.75)	16	4.41	Yes	0.89	0.92
	Munida	0.22 (0 - 1.36)	28	4.38	Yes	0.69	0.93
	Crossast	1.15 (0 - 1.15)	5	2.23	No	0.53	0.69
	Ophiuoph	0.02 (0.02 - 0.75)	9	1.73	Yes	0.76	0.65
	Alcyodig	0.03 (0 - 0.09)	8	1.43	No	0.53	0.64
	Diphasia	0.02 (0.02 - 0.89)	6	1.26	No	0.67	0.57
	Sabella	0.09 (0.03 - 1.35)	5	1.22	No	0.91	0.65

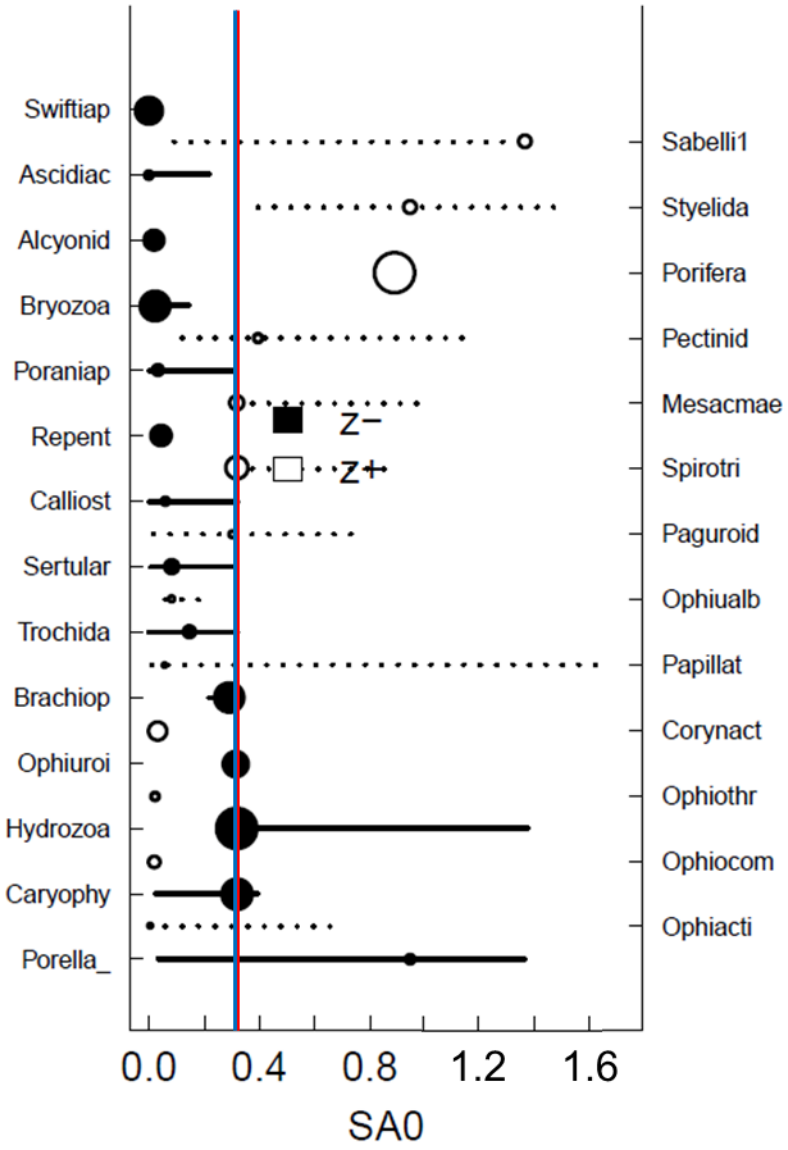

Figure 26. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “S1a.conspicuous”. Black symbols correspond to negative (z-) indicator taxa (no positive indicator taxa were found in stratum). Symbols are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa), and horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. The red vertical line represents community change point for taxa responding negatively to the pressure gradient. Taxa name abbreviations are as per Table 19.

TITAN results for “Conspicuous taxa” dataset, stratum S2 - South, Low energy, Boulders habitat (in deep circalittoral zone and with low turbidity)

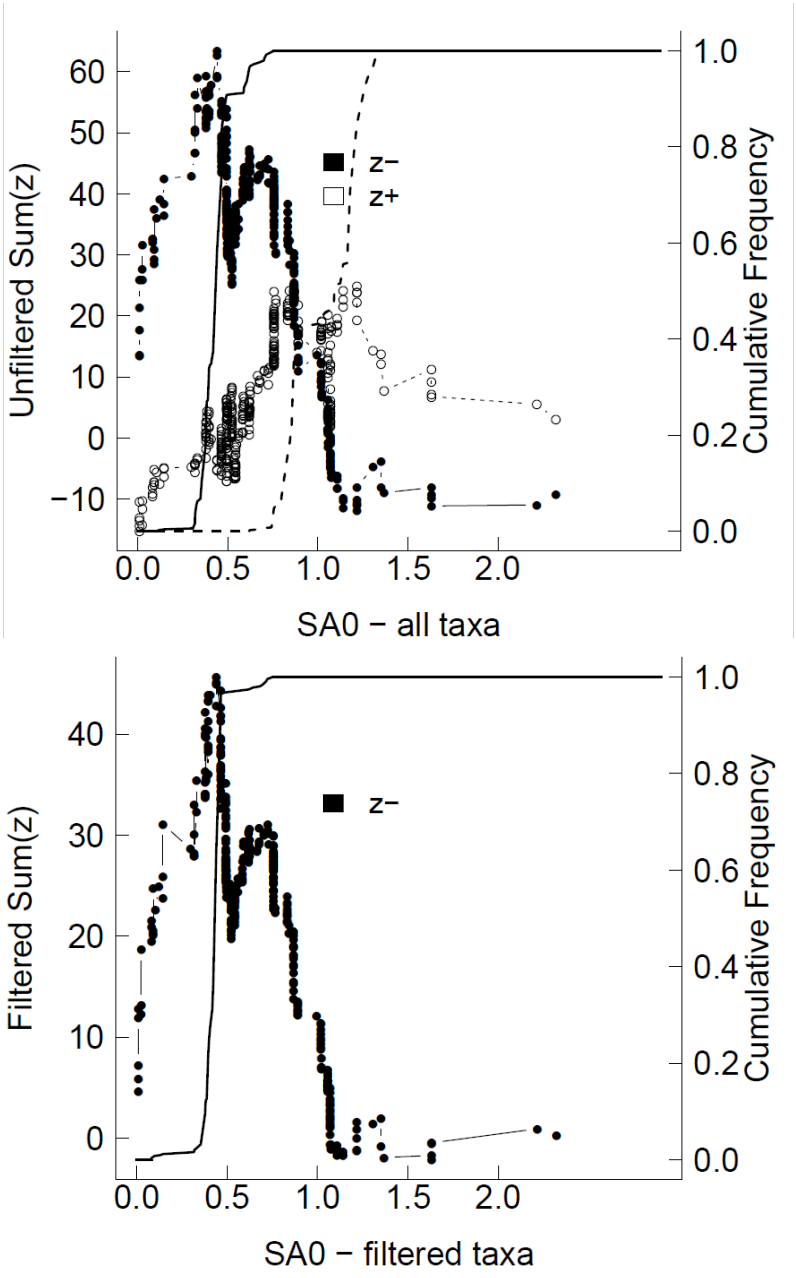

Figure 27. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 3.4) within the dataset “S2.conspicuous”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 24. TITAN taxon-specific tabular output for the dataset "S2.conspicuous".Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 19.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Hydrozoa*	0.62 (0.56 - 1.35)	400	51.42	Yes	0.98	0.99
	Brachiop*	0.62 (0.38 - 0.67)	109	25.78	Yes	1.00	1.00
	Swiftiap*	0.32 (0.01 - 0.32)	5	17.24	Yes	0.99	0.99
	Parazoan*	0.44 (0.4 - 0.47)	9	13.79	Yes	0.96	1.00
	Sertular*	0.38 (0.09 - 0.38)	5	12.82	Yes	1.00	0.99
	Palmiske*	0.76 (0.68 - 0.83)	46	12.71	Yes	0.96	1.00
	Holothur*	0.62 (0.42 - 0.83)	28	9.41	Yes	0.98	0.99
	Edwardsi*	0.76 (0.68 - 0.76)	22	8.24	Yes	1.00	1.00
	Massive*	0.54 (0.38 - 0.76)	14	5.66	Yes	1.00	0.99
	Porella	0.08 (0.05 - 1.63)	232	56.38	Yes	0.89	1.00
	Bryozoa	0.33 (0.32 - 3.27)	358	51.89	Yes	0.78	0.96
	Serpulid	0.49 (0.01 - 1.33)	246	39.88	Yes	0.74	0.98
	Asteriid	0.62 (0.3 - 1.49)	108	19.56	Yes	0.73	0.96
	Antedonb	0.03 (0.01 - 1.06)	27	15.54	Yes	0.68	0.82
	Nemertes	0.7 (0.47 - 1.22)	76	15.43	Yes	0.73	0.99
	Munida	0.76 (0.01 - 0.83)	75	14.93	Yes	0.85	0.86
	Trochida	0.32 (0.09 - 0.63)	12	11.45	Yes	0.95	0.86
	Ophiuroi	0.59 (0.5 - 0.87)	42	11.01	Yes	0.90	0.99
	Aglaophe	0.87 (0.52 - 0.89)	28	9.06	Yes	0.74	1.00
	Stichast	0.48 (0.39 - 1.07)	35	8.5	Yes	0.78	0.76
	Poraniap	0.38 (0.38 - 3.27)	22	8.3	Yes	0.63	0.88
	Papillat	0.73 (0.49 - 1.18)	25	8.16	Yes	0.82	1.00
	Globular	0.59 (0.47 - 1.09)	20	6.73	Yes	0.88	0.95
	Ophiothr	0.38 (0.38 - 0.83)	8	5.99	Yes	0.86	0.70
	Atrinafr	0.38 (0.38 - 1.49)	12	5.31	No	0.45	0.87
	Echinoid	0.38 (0.33 - 1.36)	5	4.85	Yes	0.58	0.72
	Galatheo	0.44 (0.03 - 0.54)	5	4.84	Yes	0.99	0.90
	Ophiocom	0.47 (0.15 - 1.33)	7	4.22	Yes	0.72	0.81
	Encrusti	0.49 (0.47 - 0.62)	8	4.1	Yes	0.96	0.81
	Calliost	0.52 (0.49 - 0.83)	10	4.08	Yes	0.88	0.74
	Bolocera	0.83 (0.49 - 0.87)	11	2.73	No	0.65	0.42
	Pectinid	0.52 (0.09 - 0.76)	5	2.33	Yes	0.95	0.60
Positive	Caryophy	0.76 (0.47 - 1.02)	315	44.98	Yes	0.71	0.99
	Paguroid	1.22 (0.32 - 1.63)	47	25.33	Yes	0.67	0.97

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Echinuse	0.4 (0.36 - 1.5)	76	17.03	Yes	0.81	0.85
	Salmacin	1.35 (0.02 - 1.63)	5	14.71	Yes	0.68	0.90
	Ascidiac	0.87 (0.01 - 1.04)	28	11.65	Yes	0.63	1.00
	Crinoide	1.22 (0.32 - 1.5)	7	11.45	Yes	0.66	0.88
	Sabellid	1.06 (0.4 - 1.26)	9	10.89	Yes	0.93	0.99
	Actiniar	0.76 (0.1 - 1.92)	50	9.32	No	0.69	0.81
	Polyplac	1.18 (0.5 - 1.22)	8	8.66	Yes	0.88	0.73
	Ophiualb	0.83 (0.38 - 1.11)	28	8.63	Yes	0.77	0.93
	Ophiura	0.87 (0.11 - 1.5)	29	8.33	Yes	0.88	0.89
	Ophiacti	0.87 (0.11 - 0.89)	8	4.58	Yes	0.58	0.92
	Alcyoniu	0.76 (0.52 - 1.36)	8	3.87	Yes	0.99	0.88
	Mesacmae	0.52 (0.52 - 0.76)	10	3.82	Yes	0.81	0.84
	Hyalinoe	0.52 (0.52 - 0.76)	7	2.8	Yes	0.88	0.60
	Retepore	0.52 (0.38 - 1.06)	9	2.36	No	0.67	0.49
	Cerianth	0.5 (0.49 - 0.84)	5	1.75	No	0.76	0.35

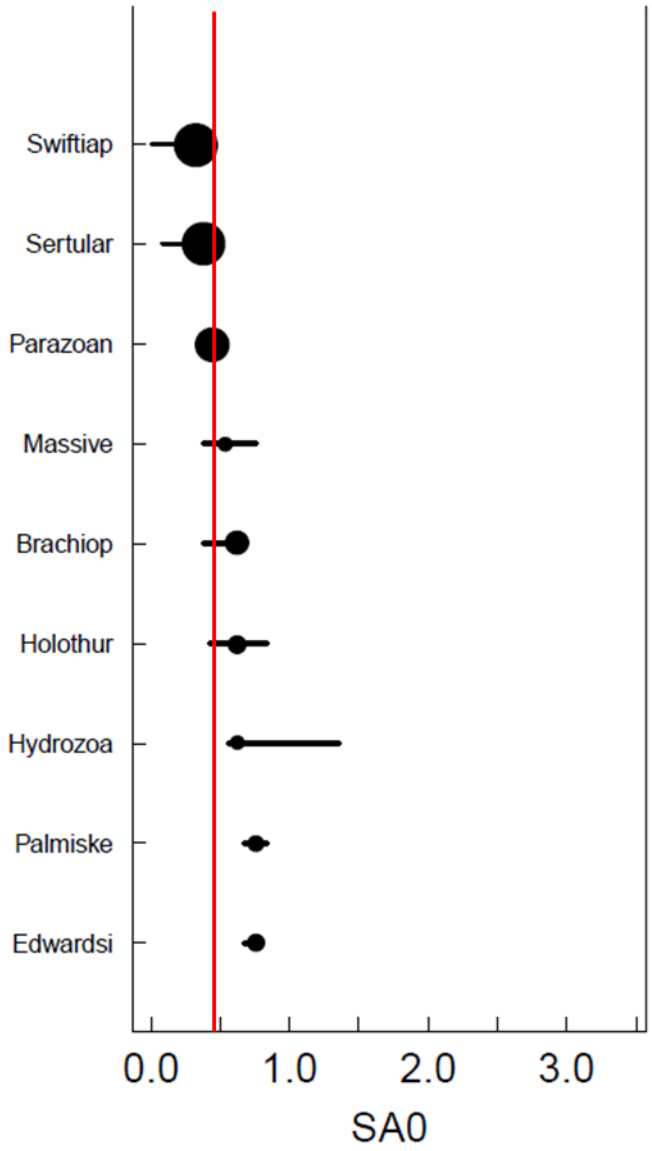

Figure 28. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “S2.conspicuous”. Black symbols correspond to negative (z-) indicator taxa (no positive indicator taxa were found in stratum). Symbols are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa), and horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. The red vertical line represents community change point for taxa responding negatively to the pressure gradient. Taxa name abbreviations are as per Table 19.

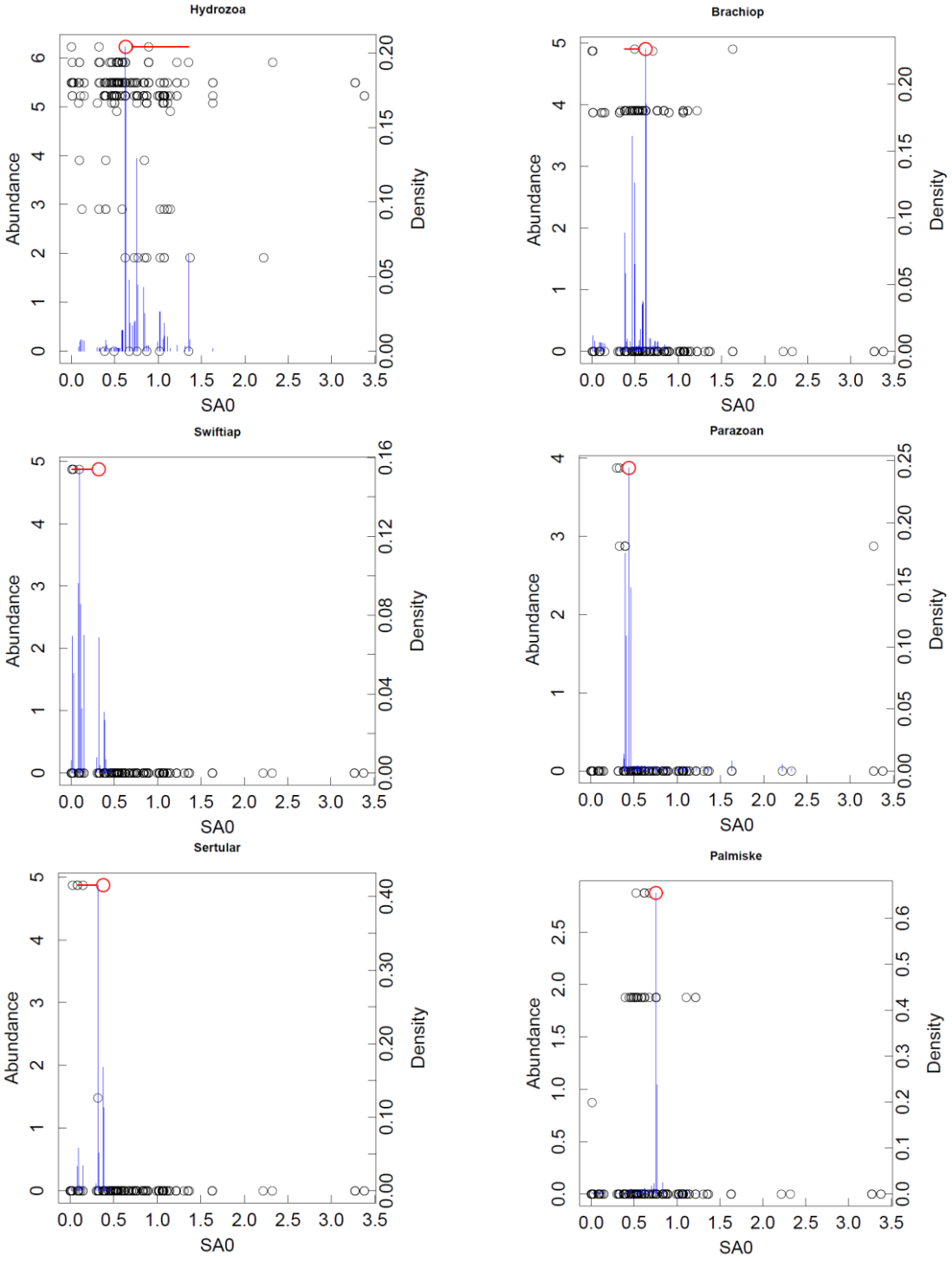

Figure 29. Taxon-specific plots of indicator taxa identified for the dataset “S2.conspicuous”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 3.4). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

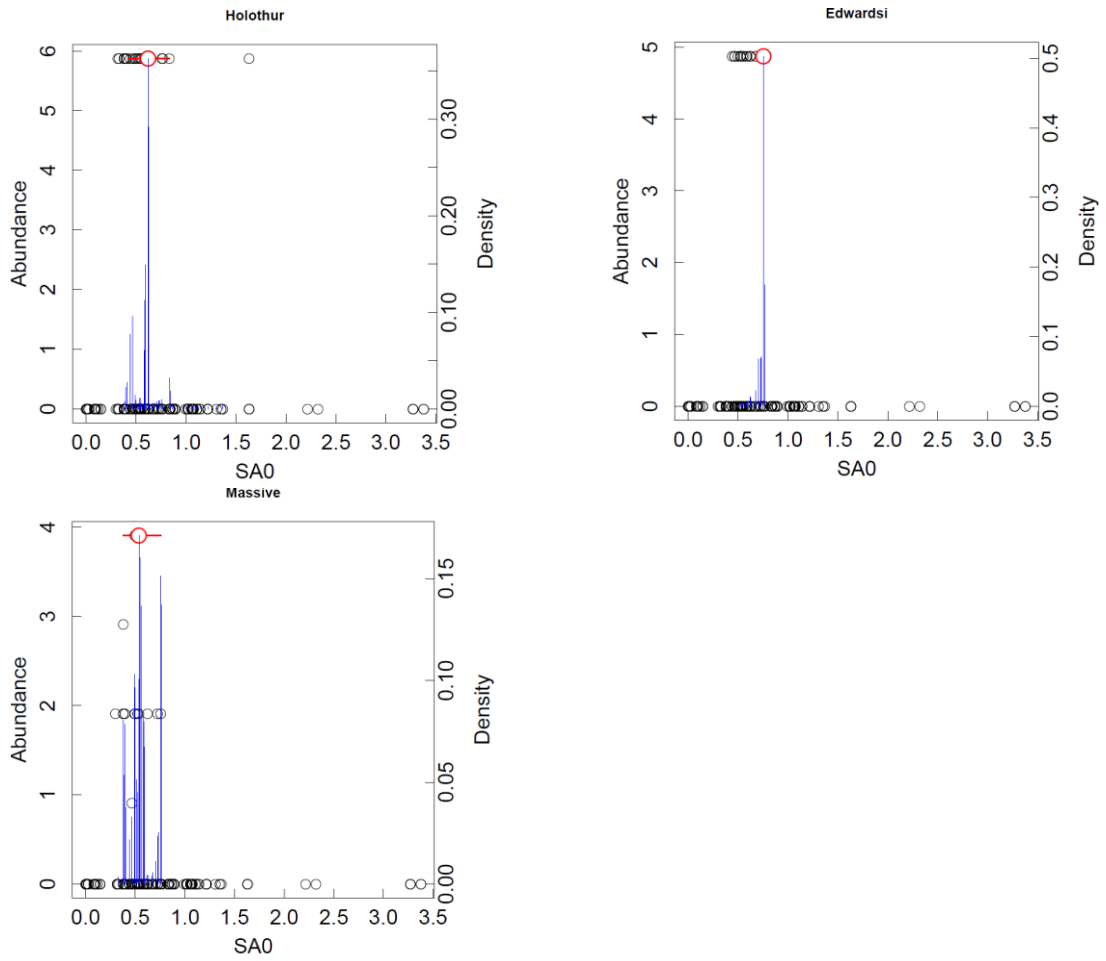

Figure 30. Taxon-specific plots of indicator taxa identified for the dataset “S2.conspicuous”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 3.4). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

TITAN results for “Conspicuous taxa” dataset, stratum S3 - South, Low energy, Cobble habitat (in deep circalittoral zone and with low turbidity)

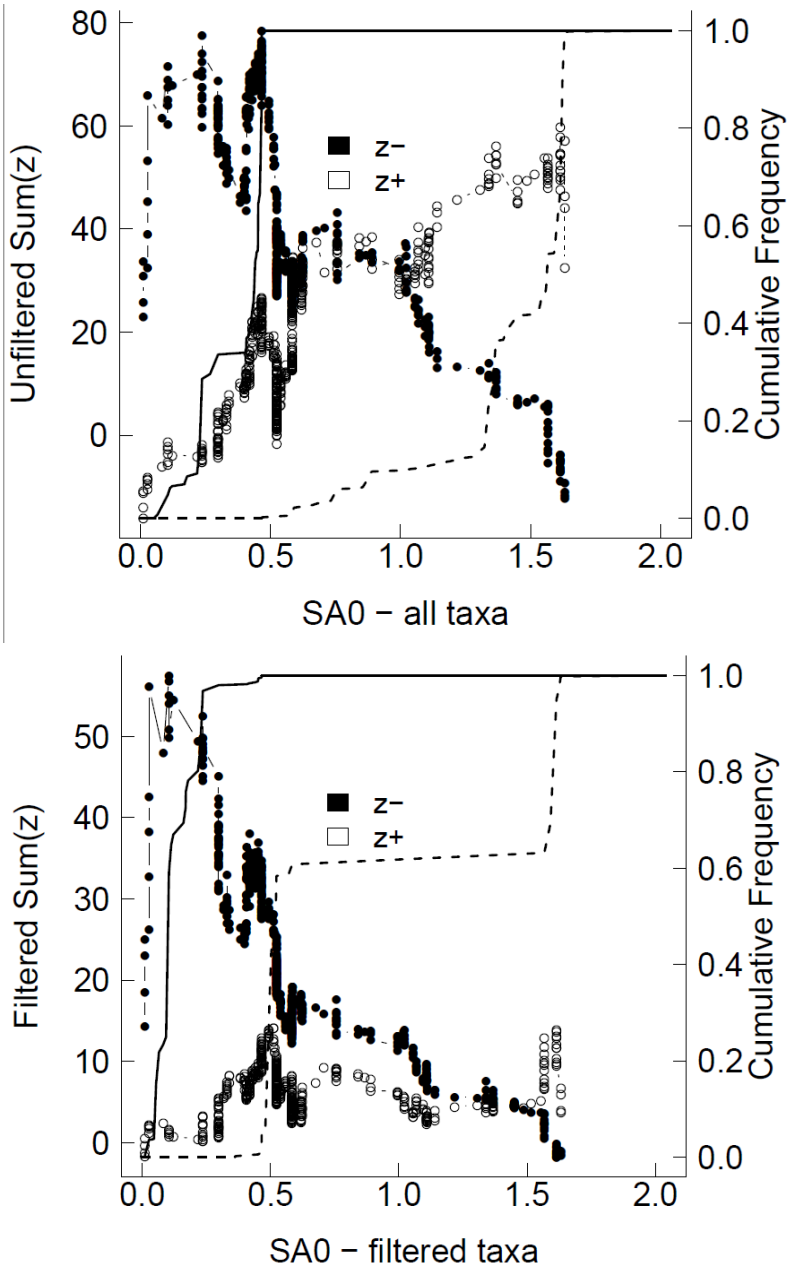

Figure 31. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 2.3) within the dataset “S3.conspicuous”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 25. TITAN taxon-specific tabular output for the dataset "S3.conspicuous". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 19.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Swiftiap*	0.05 (0.05 - 0.24)	8	61.54	Yes	1.00	1.00
	Porella*	0.23 (0.05 - 0.52)	214	54.8	Yes	1.00	1.00
	Brachiop*	0.69 (0.41 - 0.76)	214	30.99	Yes	1.00	1.00
	Sertular*	0.1 (0.01 - 0.24)	5	26.61	Yes	0.99	0.99
	Globular*	0.59 (0.58 - 0.62)	141	26.03	Yes	0.97	1.00
	Ophiothr*	0.45 (0.24 - 0.45)	24	9.95	Yes	0.99	1.00
	Massive*	0.52 (0.34 - 0.99)	27	5.37	Yes	0.98	0.97
	Ophiocom*	0.49 (0.45 - 0.59)	20	4.31	Yes	1.00	0.99
	Buccinid*	0.42 (0.1 - 0.47)	6	4.23	Yes	1.00	0.98
	Hydrozoa	0.89 (0.45 - 1.11)	593	55.51	Yes	0.90	1.00
	Serpulid	0.59 (0.18 - 0.62)	430	45.79	Yes	0.93	1.00
	Ophiuroi	0.01 (0.01 - 0.62)	119	45.19	Yes	0.83	0.86
	Asteriid	0.47 (0.45 - 1.61)	188	26.17	Yes	0.87	1.00
	Paguroid	0.47 (0.42 - 1.63)	124	17.84	Yes	0.34	1.00
	Amphiura	0.43 (0.43 - 1.57)	53	16.01	Yes	0.62	1.00
	Nemertes	0.76 (0.24 - 1.62)	96	13.72	Yes	0.82	0.93
	Ophiura	0.47 (0.4 - 1.63)	63	13.58	Yes	0.62	1.00
	Calliost	0.1 (0.01 - 0.76)	7	12.52	Yes	0.74	0.91
	Diphasia	0.24 (0.1 - 0.59)	6	12	Yes	0.85	0.95
	Poraniap	0.17 (0.03 - 1.11)	31	10.65	Yes	0.89	0.81
	Holothur	0.52 (0.44 - 0.58)	67	10.36	Yes	0.91	0.95
	Papillat	0.3 (0.07 - 1.98)	33	9.61	Yes	0.50	0.99
	Echinuse	0.85 (0.46 - 0.99)	44	8.98	Yes	0.65	1.00
	Echinoid	0.43 (0.31 - 1.61)	30	8.51	Yes	0.68	1.00
	Antedonb	0.23 (0.1 - 1.11)	15	7.34	Yes	0.61	0.84
	Bolocera	0.41 (0.3 - 1.63)	20	6.14	Yes	0.81	0.90
	Ascidiac	0.24 (0.24 - 0.76)	7	5.62	Yes	0.64	0.84
	Polyplac	0.43 (0.01 - 0.65)	24	5.42	Yes	0.95	0.86
	Salmacin	0.1 (0.09 - 1.57)	5	5.04	Yes	0.60	0.79
	Psolus	0.3 (0.24 - 1.57)	7	4.8	Yes	0.76	0.88
	Parazoan	0.41 (0.41 - 0.99)	11	4.53	Yes	0.59	1.00
	Encrusti	0.52 (0 - 0.54)	14	3.83	Yes	0.99	0.94
	Inachida	0.47 (0.24 - 1.61)	7	3.53	Yes	0.80	0.96
	Cerianth	0.3 (0.3 - 0.81)	6	3.09	Yes	0.76	0.51

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Pectenma	0.54 (0.24 - 1.61)	17	2.73	Yes	0.68	0.68
	Trochida	0.47 (0.1 - 0.62)	5	1.8	Yes	0.89	0.72
	Plumular	0.58 (0.33 - 0.58)	5	1.39	Yes	0.68	0.33
Positive	Caryophy*	1.61 (0.58 - 1.61)	371	64.75	Yes	0.99	1.00
	Actiniar*	1.61 (0.43 - 1.63)	78	33.26	Yes	1.00	1.00
	Palmiske*	0.47 (0.44 - 0.52)	85	16.09	Yes	0.99	1.00
	Munida*	0.51 (0.49 - 1.61)	75	11.86	Yes	1.00	1.00
	Bryozoa	1.32 (0.01 - 1.34)	532	50.83	Yes	0.70	0.98
	Sabellid	1.63 (0.3 - 1.63)	9	38.88	Yes	0.90	0.95
	Atrinafr	1.63 (0.52 - 1.98)	18	30.83	Yes	0.96	0.84
	Galatheo	1.61 (0.41 - 1.63)	21	22.26	Yes	0.54	1.00
	Ophiualb	1.34 (0.47 - 1.61)	83	16.01	Yes	0.72	0.95
	Sabella	1.63 (0.4 - 1.63)	7	15.71	Yes	0.74	0.65
	Capneasa	1.63 (0.41 - 1.98)	11	15.13	Yes	0.68	0.59
	Pectinid	1.61 (0.31 - 1.63)	10	13.03	Yes	0.76	0.95
	Edwardsi	0.44 (0.43 - 0.69)	61	12.48	Yes	0.76	1.00
	Mesacmae	1.06 (0.4 - 1.37)	43	10.03	Yes	0.85	0.97
	Retepore	1.53 (0.01 - 1.62)	29	9.06	Yes	0.66	0.89
	Spirobra	1.32 (0.44 - 1.61)	10	8.6	Yes	0.94	0.97
	Ophiacti	0.76 (0.3 - 0.85)	15	6.14	Yes	0.77	0.99
	Stichast	0.58 (0.4 - 0.58)	31	5.21	Yes	0.63	0.92
	Aglaophe	0.52 (0.11 - 0.62)	27	4.77	Yes	0.53	0.98
	Ceriallo	1.07 (0.99 - 1.57)	5	4.75	Yes	0.96	0.94
	Crinoide	1.41 (0.42 - 1.63)	6	4.37	Yes	0.73	0.85
	Alcyoniu	0.52 (0.41 - 1.06)	25	3.42	Yes	0.70	0.64
	Hyalinoe	0.45 (0.41 - 0.76)	18	3.31	Yes	0.94	0.78
	Luidiaci	0.47 (0.47 - 1.57)	6	1.45	Yes	0.82	0.50

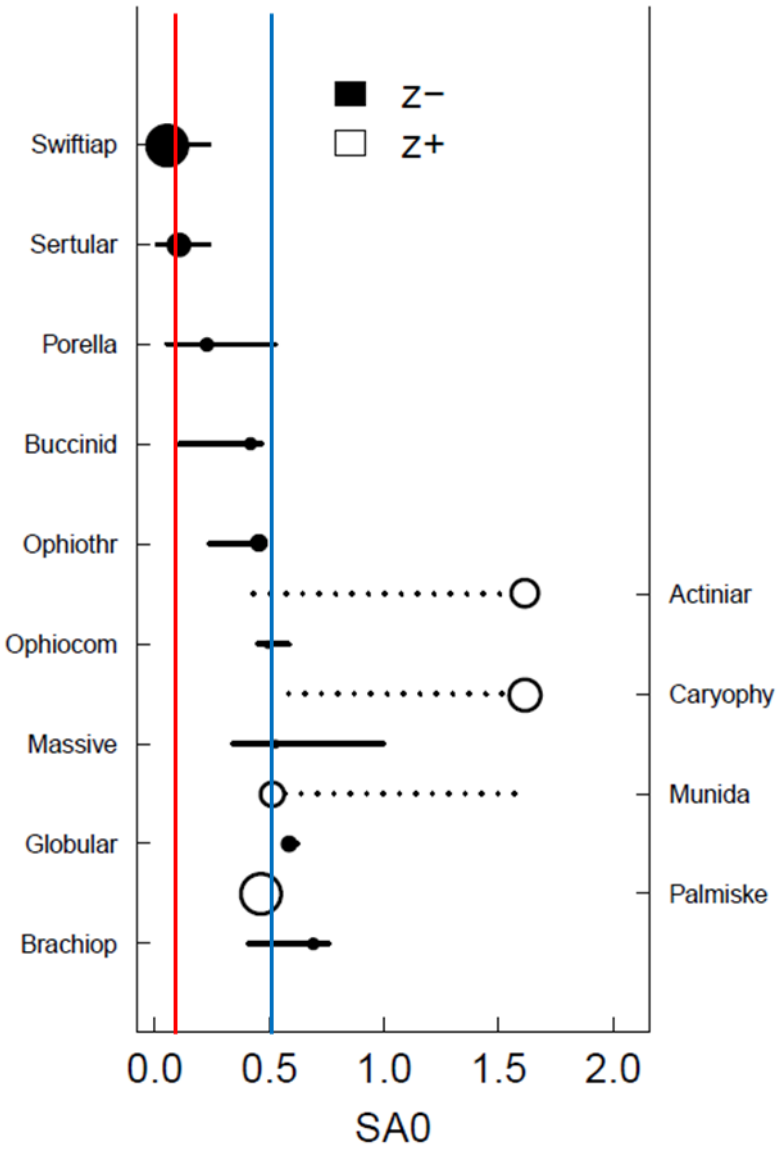

Figure 32 Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset "S3.conspicuous taxa". Symbols correspond to negative (z-, full circles) and positive (z-, empty circles) indicator taxa, and are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa). Horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Vertical lines represent community change point for taxa responding negatively (red) or positively (blue) to the pressure gradient. Taxa name abbreviations are as per Table 19.

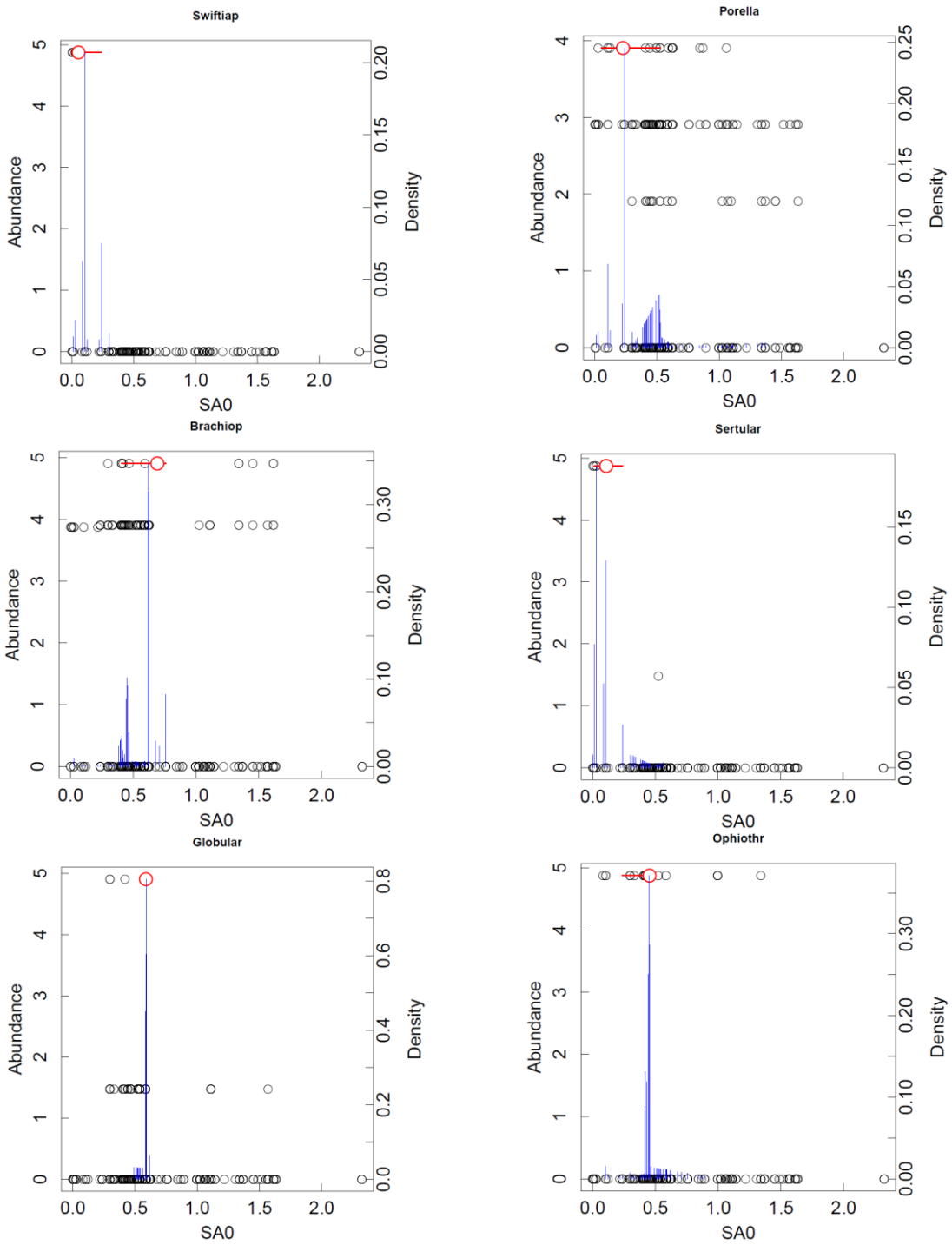

Figure 33. Taxon-specific plots of indicator taxa identified for the dataset “S3.conspicuous taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 2.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

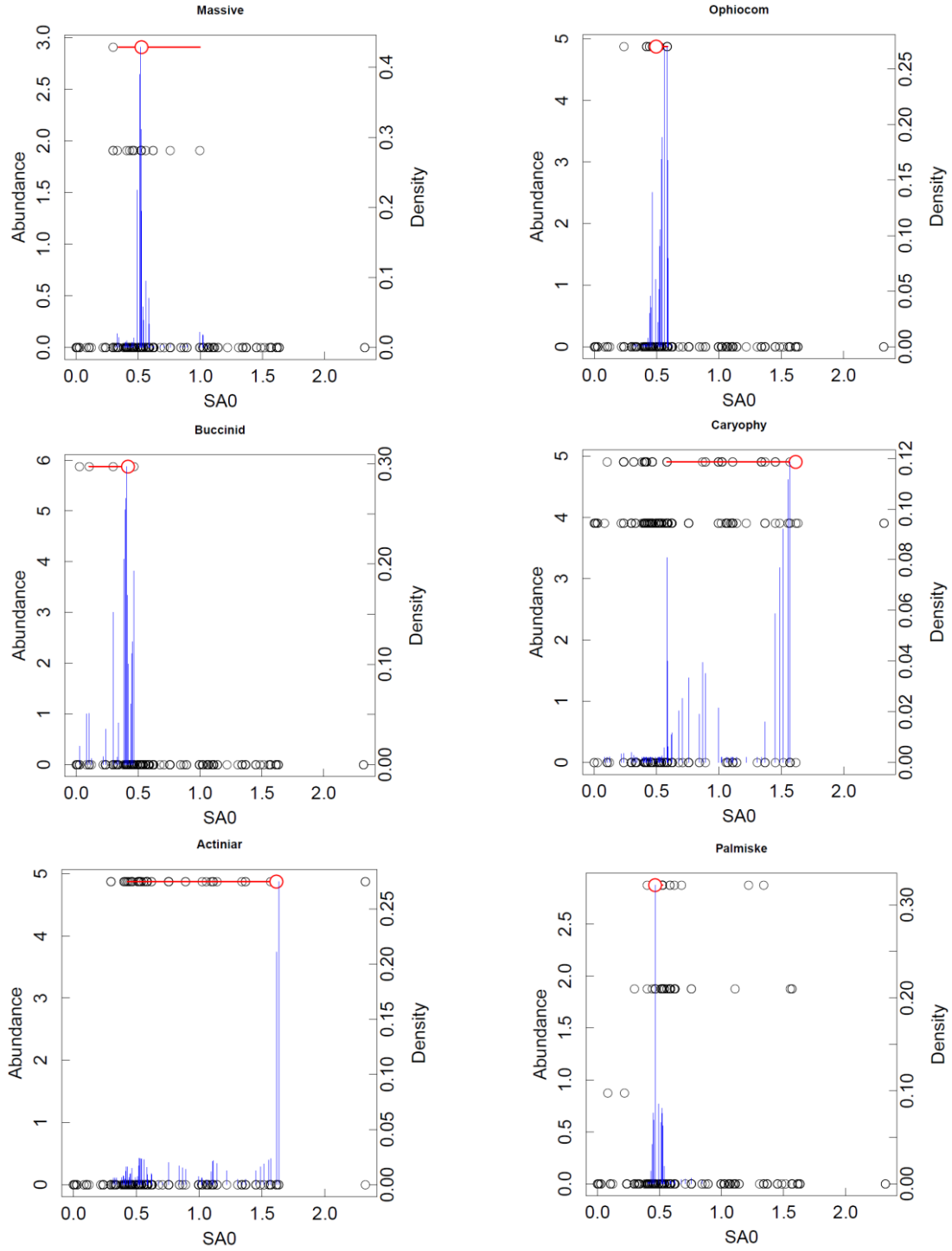

Figure 34. Taxon-specific plots of indicator taxa identified for the dataset “S3.conspicuous taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 2.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

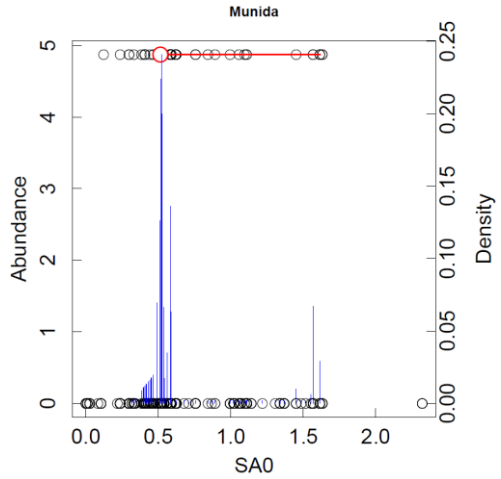

Figure 35. Taxon-specific plots of indicator taxa identified for the dataset “S3.conspicuous taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 2.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

TITAN results for “Aggregated taxa” dataset, stratum N1 - North, shallow (deep circalittoral), low energy habitat (with low turbidity and variable rock type)

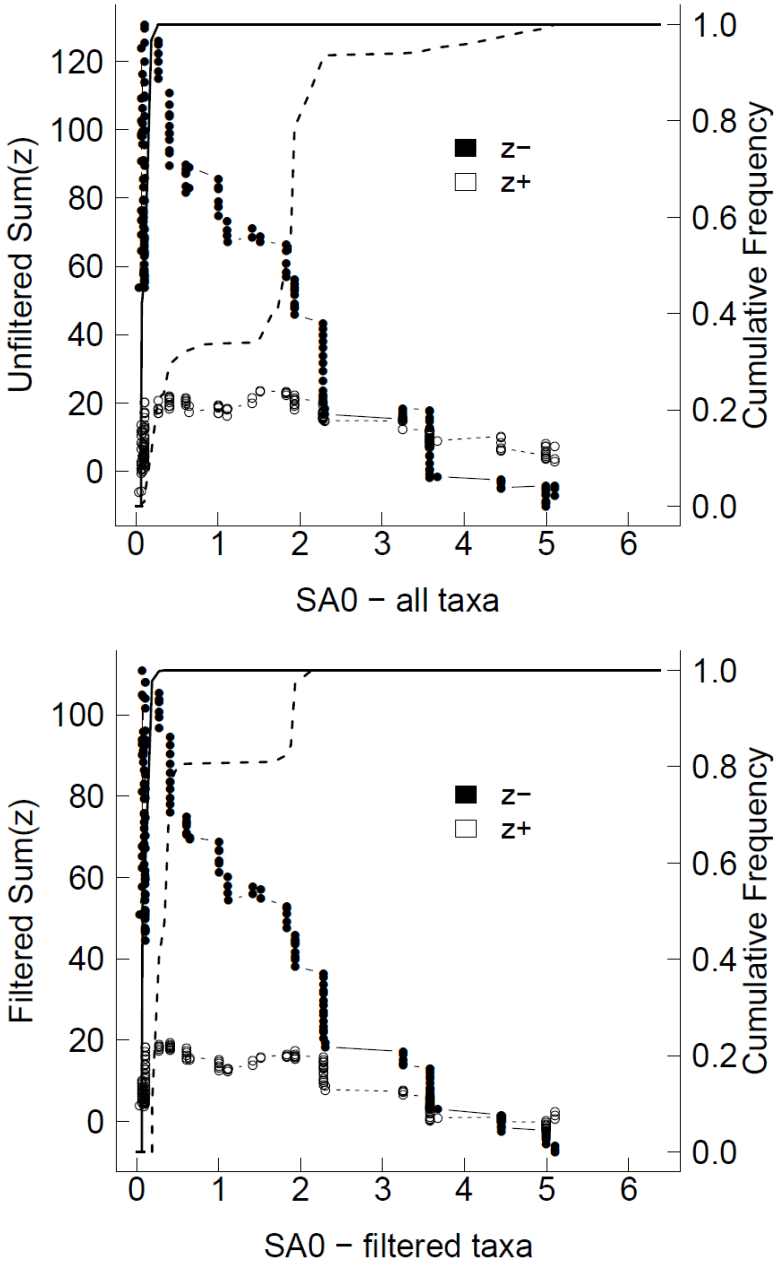

Figure 36. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 7.3) within the dataset “N1.aggregated taxa”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 26. TITAN taxon-specific tabular output for the dataset "N1.aggregated taxa". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 20.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Laniceco*	0.05 (0.05 - 0.19)	12	76.01	Yes	0.99	0.98
	Ophiuroi*	0.07 (0.06 - 0.08)	30	70.85	Yes	0.99	1.00
	Caryoph2*	0.06 (0.06 - 0.08)	10	63.75	Yes	1.00	1.00
	Flustraf*	0.06 (0.05 - 0.19)	11	42.93	Yes	1.00	1.00
	Ophiura*	0.09 (0.07 - 0.19)	31	40.59	Yes	1.00	1.00
	Poraniap*	0.07 (0.06 - 0.19)	33	40.52	Yes	0.97	0.98
	Hexacora*	0.07 (0.06 - 0.08)	6	40	Yes	1.00	1.00
	Sertular*	0.06 (0.06 - 0.08)	6	34.5	Yes	1.00	0.98
	Parazoan*	0.06 (0.06 - 0.19)	9	33.34	Yes	1.00	0.99
	Ophiothr*	0.1 (0.09 - 0.11)	30	31.33	Yes	0.98	1.00
	Hymedesm*	0.11 (0.11 - 0.27)	19	26.49	Yes	1.00	1.00
	Serpulid*	0.27 (0.06 - 1.93)	34	25.39	Yes	0.97	1.00
	Parasmit*	0.11 (0.06 - 0.27)	14	21.54	Yes	1.00	1.00
	Scleract*	0.11 (0.11 - 0.27)	11	16.67	Yes	1.00	1.00
	Asterias*	0.09 (0.04 - 0.83)	8	16.39	Yes	1.00	0.98
	Balanoid*	0.11 (0.04 - 1.52)	13	15.05	Yes	1.00	1.00
	Retepore*	0.11 (0.04 - 0.19)	7	10.61	Yes	1.00	0.96
	Palmiske*	0.19 (0.11 - 0.27)	7	10.45	Yes	1.00	0.97
	Spirobra	5.1 (0.06 - 6.18)	153	70.17	Yes	0.78	0.97
	Bryozoa	5.1 (0.06 - 6.18)	141	68.83	Yes	0.72	0.96
	Caryoph1	0.1 (0.1 - 5.05)	61	34.8	Yes	0.83	1.00
	Securifl	0.06 (0.05 - 2.78)	9	27.26	Yes	0.87	0.83
	Globular	0.07 (0.06 - 0.11)	5	18.69	Yes	1.00	0.94
	Calliost	0.11 (0.09 - 1.93)	18	14.93	Yes	0.92	0.86
	Ebalia	0.11 (0.11 - 0.27)	14	14.64	Yes	0.92	0.96
	Munida	0.27 (0.11 - 3.58)	20	13.98	Yes	0.91	0.93
	Leptaste	1.11 (0.09 - 3.58)	26	12.94	No	0.76	0.74
	Ditrupaa	0.1 (0.1 - 1.27)	6	10.95	Yes	0.99	0.88
	Massive	0.11 (0.06 - 5.1)	12	7.4	No	0.69	0.78
	Porifera	0.83 (0.06 - 1)	6	6.52	Yes	1.00	0.81
	Colus	0.83 (0.11 - 1)	5	5.43	Yes	0.97	0.61
	Ascidiac	0.1 (0.06 - 4.99)	5	5.41	No	0.76	0.74
	Urticina	0.11 (0.09 - 2.32)	5	4	No	0.77	0.30

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Hippaste	1.67 (0.08 - 4.99)	6	3.7	No	0.49	0.46
Positive	Encrusti*	0.27 (0.07 - 1.93)	121	57.8	Yes	1.00	1.00
	Arboresc*	0.51 (0.27 - 1.93)	75	50.24	Yes	1.00	1.00
	Hydrozoa	1.52 (0.06 - 4.99)	120	44.19	Yes	0.74	0.75
	Hyalinoe	5.1 (1.11 - 7.27)	5	31.72	Yes	0.99	0.84
	Flabella	0.11 (0.07 - 3.41)	64	28.59	Yes	0.79	0.94
	Echinoid	3.58 (0.1 - 4.45)	29	23.25	Yes	0.92	0.92
	Henricia	4.72 (0.19 - 4.99)	18	21.56	Yes	0.98	0.86
	Echinus	0.08 (0.08 - 4.45)	35	21.08	No	0.61	0.72
	Paguroid	0.08 (0.07 - 5.05)	33	19.88	No	0.85	0.62
	Asteriid	4.45 (0.08 - 4.99)	30	18.99	Yes	0.73	0.75
	Galatheo	2.28 (0.06 - 5.05)	25	14.6	Yes	0.85	0.82
	Terebell	4.45 (0.09 - 4.45)	14	13.55	No	0.55	0.73
	Thuiaria	5.1 (0.09 - 5.1)	5	12.41	No	0.84	0.64

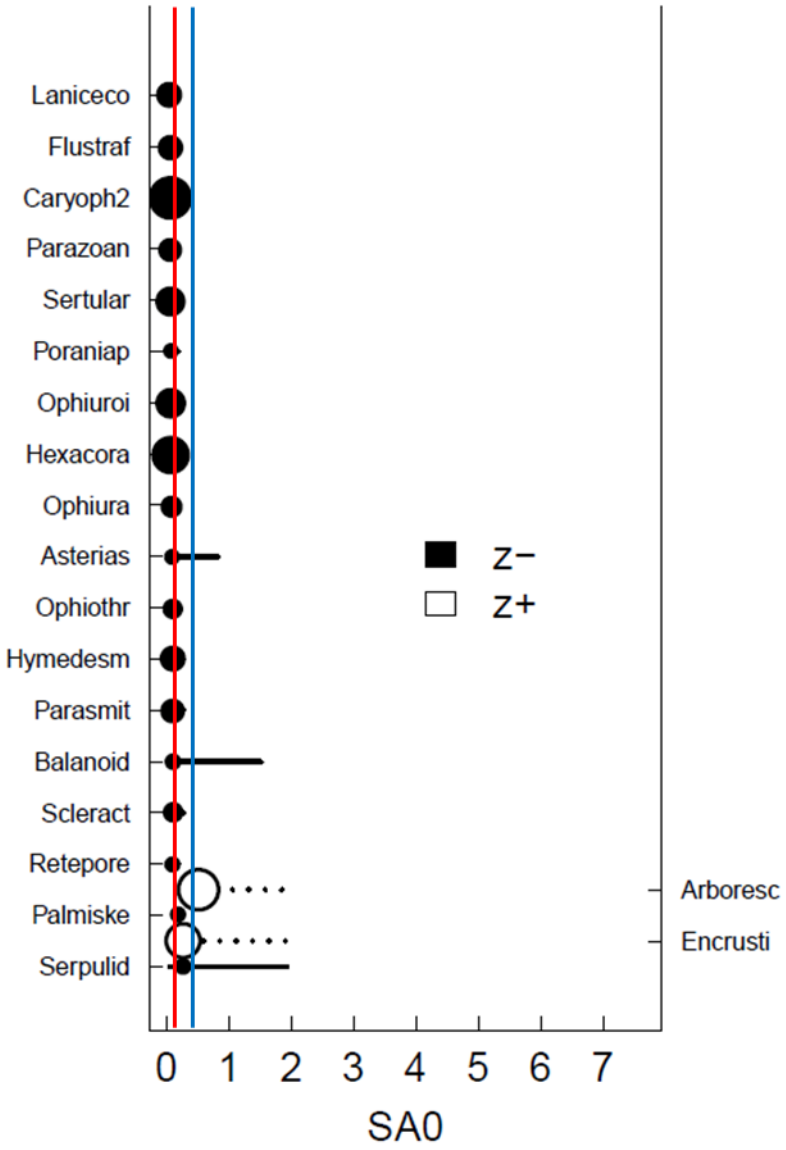

Figure 37. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset "N1.aggregated taxa". Symbols correspond to negative (z-, full circles) and positive (z-, empty circles) indicator taxa, and are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa). Horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Vertical lines represent community change point for taxa responding negatively (red) or positively (blue) to the pressure gradient. Taxa name abbreviations are as per Table 20.

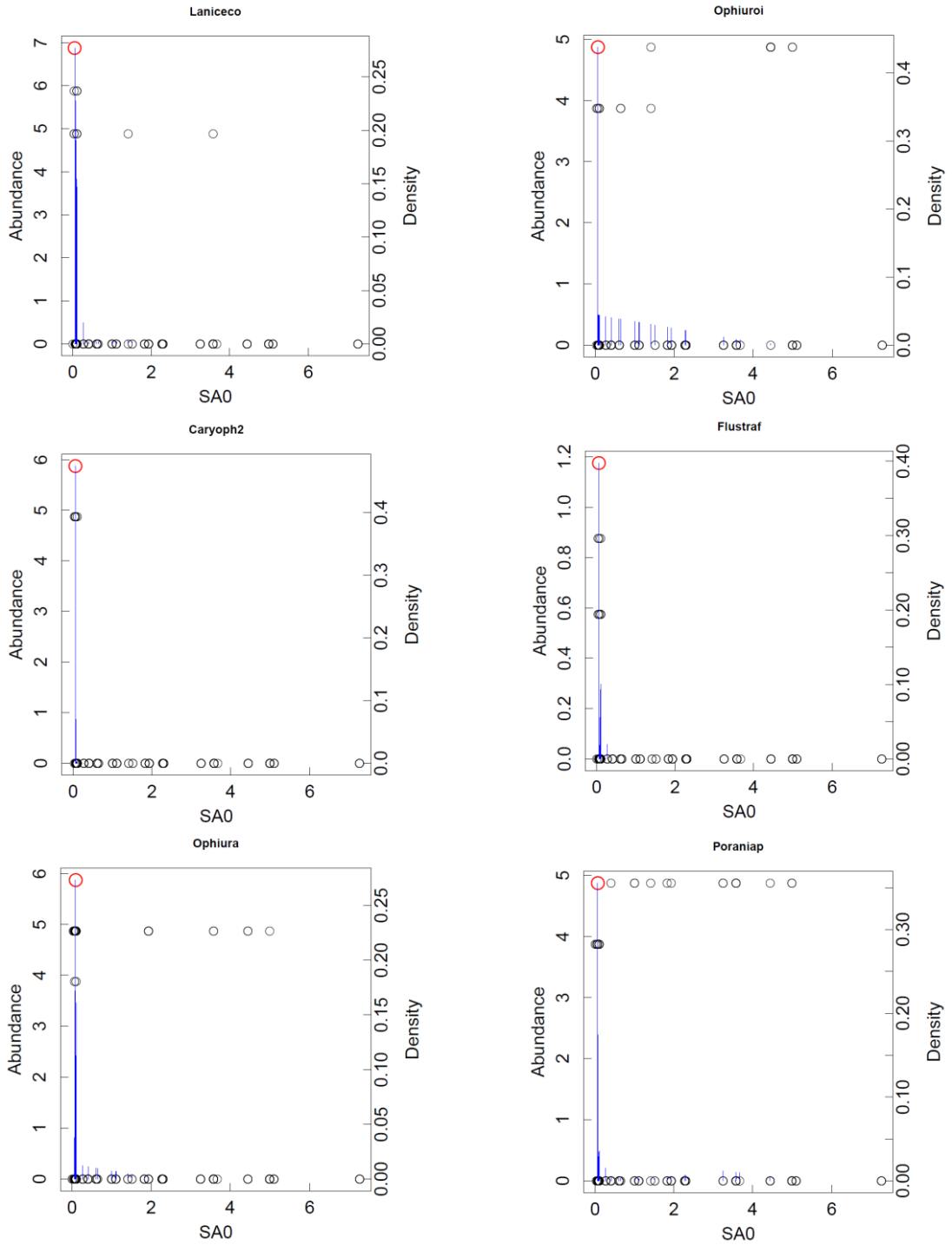

Figure 38. Taxon-specific plots of indicator taxa identified for the dataset “N1.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

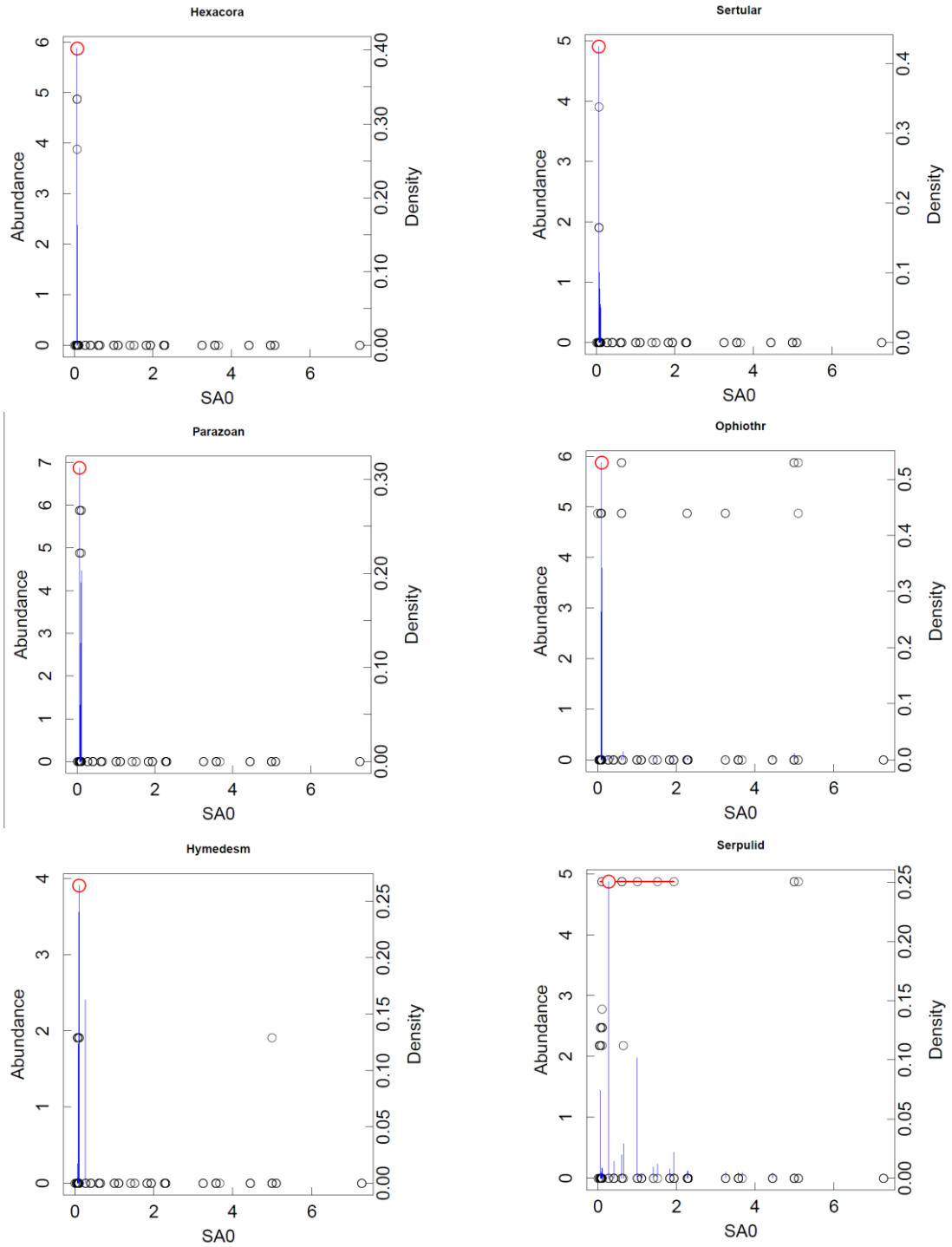

Figure 39. Taxon-specific plots of indicator taxa identified for the dataset “N1.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

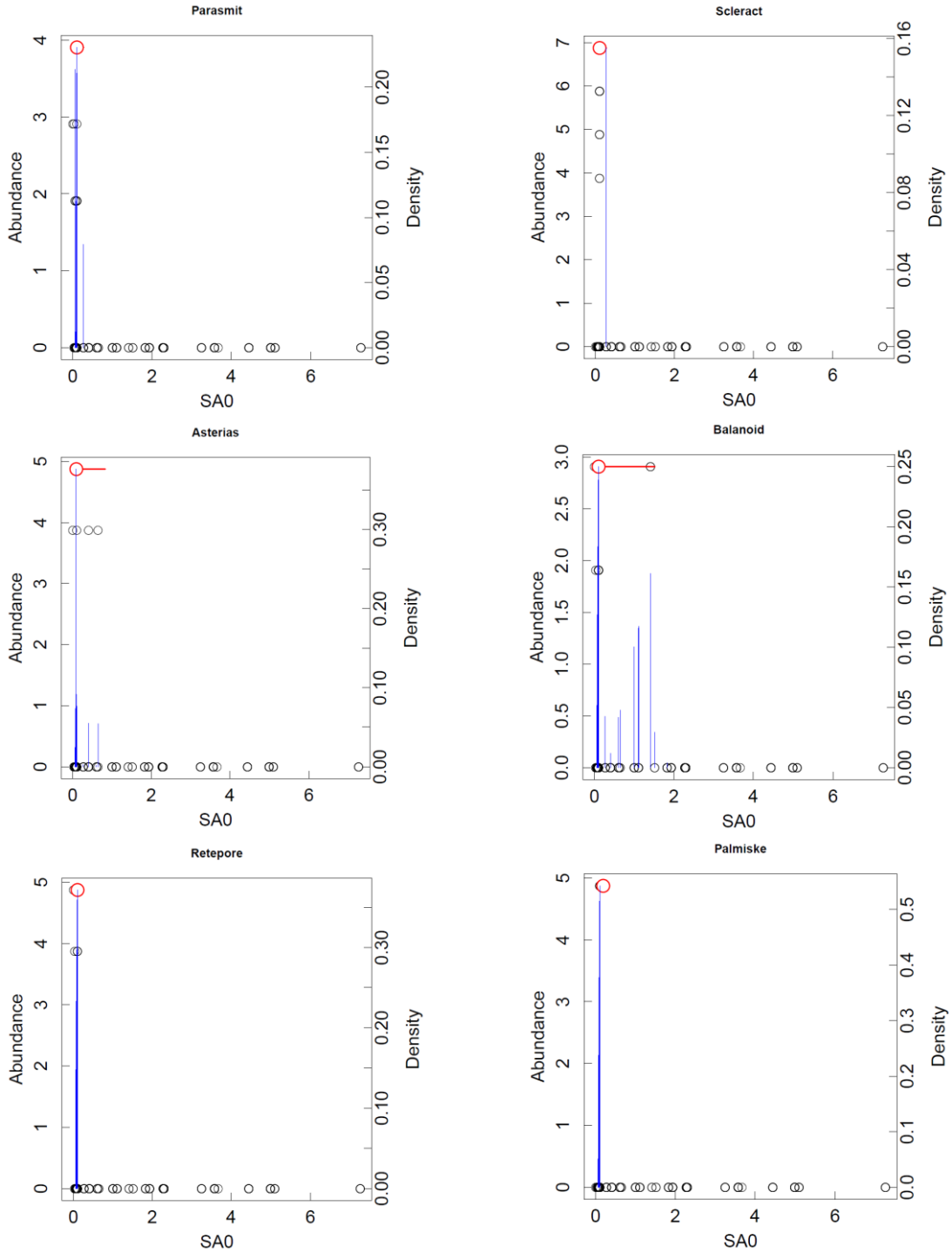

Figure 40. Taxon-specific plots of indicator taxa identified for the dataset “N1.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

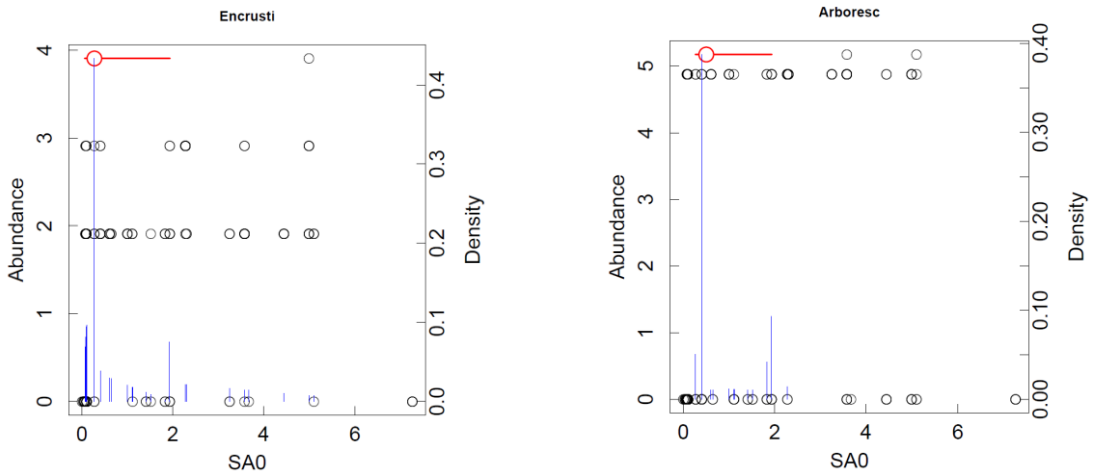

Figure 41. Taxon-specific plots of indicator taxa identified for the dataset “N1.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 7.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

TITAN results for “Aggregated taxa” dataset, stratum N2 - North, shallow (deep circalittoral), moderate energy habitat (with low turbidity and variable rock type)

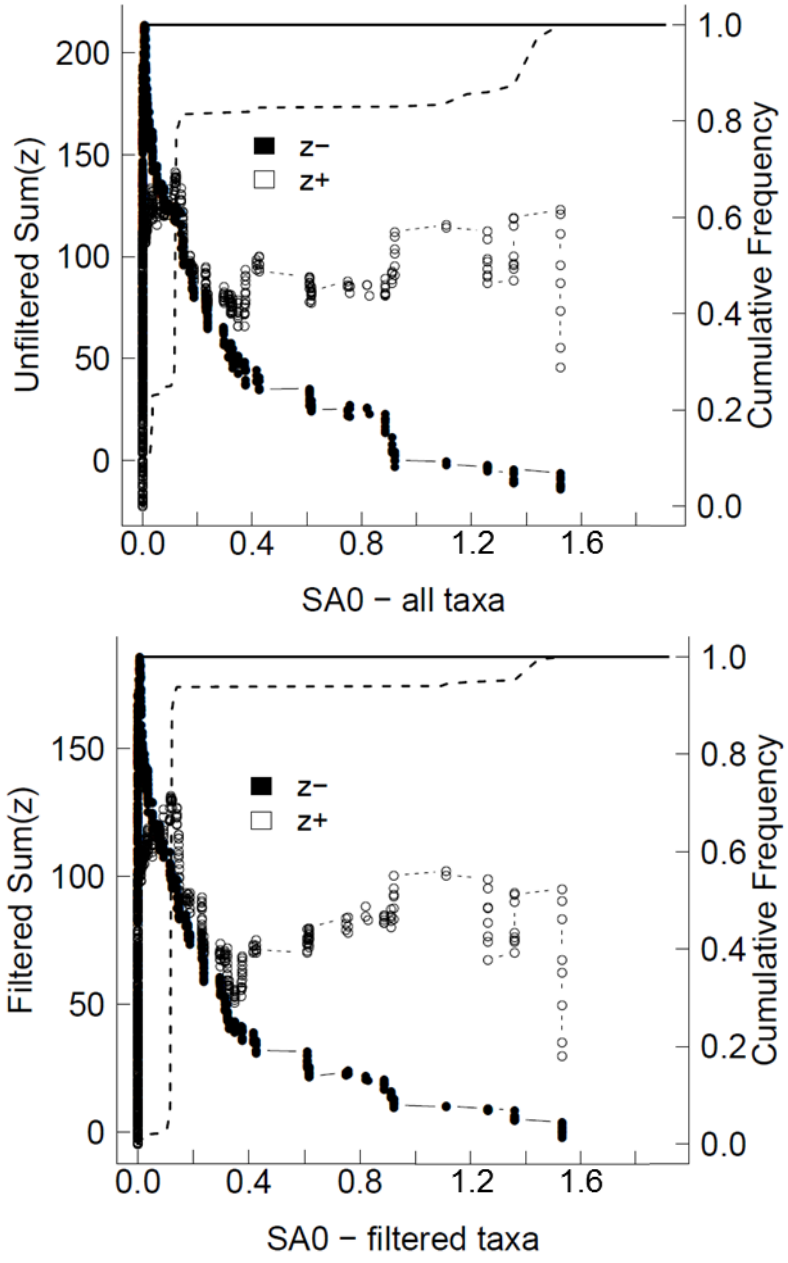

Figure 42. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 2.5) within the dataset “N2.aggregated taxa”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 27. TITAN taxon-specific tabular output for the dataset "N2.aggregated taxa". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 20.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Ophiocom*	0.01 (0 - 0.01)	166	48.19	Yes	1.00	1.00
	Corallin*	0.01 (0.01 - 0.01)	155	47.16	Yes	1.00	1.00
	Cellepor*	0.01 (0 - 0.01)	123	30.61	Yes	1.00	1.00
	Caryoph1*	0.12 (0.04 - 0.14)	216	27.95	Yes	0.96	1.00
	Alcyoniu*	0.01 (0 - 0.01)	91	26.37	Yes	1.00	1.00
	Ophiuroi*	0 (0 - 0.01)	143	26.18	Yes	1.00	1.00
	Smittino*	0.37 (0.35 - 0.38)	136	23.86	Yes	1.00	1.00
	Actiniid*	0 (0 - 0)	45	16.79	Yes	1.00	1.00
	Flustraf*	0.01 (0 - 0.01)	86	16.51	Yes	1.00	1.00
	Crossast*	0 (0 - 0.01)	70	16.17	Yes	1.00	1.00
	Pagurus*	0 (0 - 0)	27	9.13	Yes	1.00	1.00
	Rhodophy*	0.01 (0 - 0.01)	29	6.43	Yes	1.00	0.99
	Tubular*	0 (0 - 0.02)	10	4.16	Yes	1.00	0.99
	Ascidiid*	0.03 (0 - 0.04)	15	4.04	Yes	1.00	1.00
	Flustrin*	0 (0 - 0)	7	2.7	Yes	1.00	0.97
	Spirobra	1.44 (0 - 1.53)	614	59.9	Yes	0.62	1.00
	Buccinid	0 (0 - 0.23)	7	19.14	Yes	0.59	0.33
	Calliost	0.01 (0 - 1.44)	100	18.18	Yes	0.93	1.00
	Antedoni	0 (0 - 0.24)	12	16.37	Yes	0.86	0.66
	Securifl	0.01 (0.01 - 1.45)	96	13.25	Yes	0.92	1.00
	Ascidiac	0 (0 - 0.92)	23	12.03	Yes	0.29	0.78
	Asteriid	0.12 (0 - 1.53)	113	11.94	Yes	0.62	0.95
	Antedon	0 (0 - 0.31)	13	11.71	Yes	0.90	0.73
	Haleciid	0 (0 - 0.32)	13	9.95	Yes	0.87	0.65
	Polyplac	0 (0 - 0.24)	16	8.59	Yes	0.47	0.88
	Thuiaria	0 (0 - 1.36)	7	7.51	No	0.36	0.50
	Echinus	0.12 (0 - 0.62)	56	7.21	Yes	0.53	0.97
	Corynact	0 (0 - 0.12)	5	6.76	Yes	0.84	0.50
	Sertula1	0.33 (0 - 0.35)	34	6.09	Yes	0.84	0.97
	Adamsia	0 (0 - 0.12)	5	5.11	Yes	0.93	0.68
	Omalosec	0 (0 - 0.33)	19	4.92	Yes	0.89	0.79
	Urticina	0.01 (0 - 0.83)	25	4.62	Yes	0.91	0.94
	Flustrid	0.17 (0 - 0.32)	20	3.54	Yes	0.99	0.89

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Anthozoa	0 (0 - 0.35)	9	2.74	Yes	0.73	0.62
	Luidia	0.61 (0 - 0.33)	16	2.65	No	0.42	0.49
	Caryoph2	0.01 (0 - 0.01)	8	2.26	Yes	0.72	0.91
	Alcyonid	0 (0 - 0.31)	9	1.72	No	0.74	0.57
Positive	Scleract*	1.44 (1.36 - 1.53)	35	82.11	Yes	1.00	1.00
	Hymedesm*	1.44 (0.89 - 1.53)	166	65.23	Yes	0.98	1.00
	Parazoan*	1.36 (1.36 - 1.53)	32	61.01	Yes	1.00	1.00
	Munida*	1.53 (0.01 - 1.53)	59	52.61	Yes	0.96	0.97
	Hydrozoa*	0.15 (0 - 0.15)	314	49.91	Yes	1.00	1.00
	Paguroid*	1.53 (0.01 - 1.53)	46	43.9	Yes	0.99	0.99
	Bryozoa*	0.01 (0.01 - 0.52)	294	43.24	Yes	1.00	1.00
	Serpulid*	0.04 (0.01 - 0.32)	319	33.02	Yes	0.97	1.00
	Encrusti*	0.42 (0.01 - 0.43)	153	28.79	Yes	0.99	1.00
	Flabella*	0.43 (0 - 1.36)	142	25.26	Yes	1.00	1.00
	Balanoid*	0.13 (0.12 - 0.86)	118	24.95	Yes	1.00	1.00
	Hexacora*	1.02 (0.23 - 1.19)	15	24.9	Yes	1.00	1.00
	Ophiura*	0.14 (0.04 - 0.15)	123	20.11	Yes	1.00	1.00
	Galatheo*	0.14 (0.04 - 0.23)	106	17.88	Yes	1.00	1.00
	Retepore*	0.12 (0.12 - 1.44)	49	15.33	Yes	1.00	1.00
	Poraniap*	0.12 (0 - 1.53)	96	14.88	Yes	1.00	1.00
	Porella*	0.12 (0.01 - 0.14)	36	10.59	Yes	1.00	1.00
	Actiniar*	0.12 (0.01 - 0.68)	40	8.56	Yes	1.00	1.00
	Ebalia*	0.13 (0.12 - 1.19)	33	8.51	Yes	1.00	1.00
	Nemertes*	0.15 (0.14 - 0.23)	19	6.01	Yes	0.99	0.99
	Terebell*	0.04 (0.03 - 0.04)	22	5.83	Yes	0.97	1.00
	Parasmit	1.44 (0 - 1.53)	219	61.61	Yes	0.74	1.00
	Globular	1.53 (0 - 1.53)	50	27.48	Yes	0.50	0.95
	Ophiothr	0.42 (0.04 - 0.51)	137	23.24	Yes	0.70	1.00
	Inachida	1.53 (0 - 1.53)	7	19.07	Yes	0.85	0.72
	Massive	0.82 (0 - 1.26)	62	16.19	Yes	0.90	0.97
	Gibbula	1.44 (0 - 1.53)	15	13.49	Yes	0.47	1.00
	Arboresc	0.02 (0.01 - 0.43)	86	11.73	Yes	0.92	1.00
	Echinoid	0.38 (0 - 0.61)	59	10.06	Yes	0.82	0.93
	Porifera	0.75 (0 - 0.82)	34	10.05	Yes	0.97	0.95
	Laniceco	1.26 (0 - 1.26)	22	8.95	Yes	0.70	0.83
	Leptaste	0.01 (0.01 - 0.52)	41	6.61	Yes	0.91	1.00
	Trochida	0.62 (0 - 0.61)	19	6.16	Yes	0.94	0.92
	Suberiti	0.92 (0 - 1.53)	7	5.46	Yes	0.74	0.92
	Henricia	0.01 (0 - 0.43)	44	4.95	No	0.59	0.79
	Asterias	0 (0 - 0.62)	24	3.42	No	0.51	0.76
	Pectenma	0.14 (0 - 1.02)	17	3.42	Yes	0.83	0.91
	Hyalinoe	0.01 (0.01 - 1.53)	10	2.86	Yes	0.78	0.95
	Neoloric	0.12 (0 - 0.33)	8	2.32	Yes	0.87	0.84
	Papillat	0.35 (0 - 0.35)	7	2.2	Yes	0.86	0.70

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Ophiopho	0.01 (0.01 - 0.07)	7	2.03	Yes	1.00	0.92
	Chaetopt	0 (0 - 0.24)	12	2	No	0.44	0.52
	Sertula2	0.04 (0 - 0.23)	10	2	Yes	0.67	0.64
	Stomphia	0.05 (0 - 0.33)	8	1.86	Yes	0.78	0.67
	Stichast	0.12 (0 - 1.36)	11	1.84	No	0.60	0.72
	Hippaste	0 (0 - 0.61)	9	1.81	Yes	0.57	0.60
	Sagartii	0.15 (0 - 0.24)	6	1.08	No	0.58	0.45

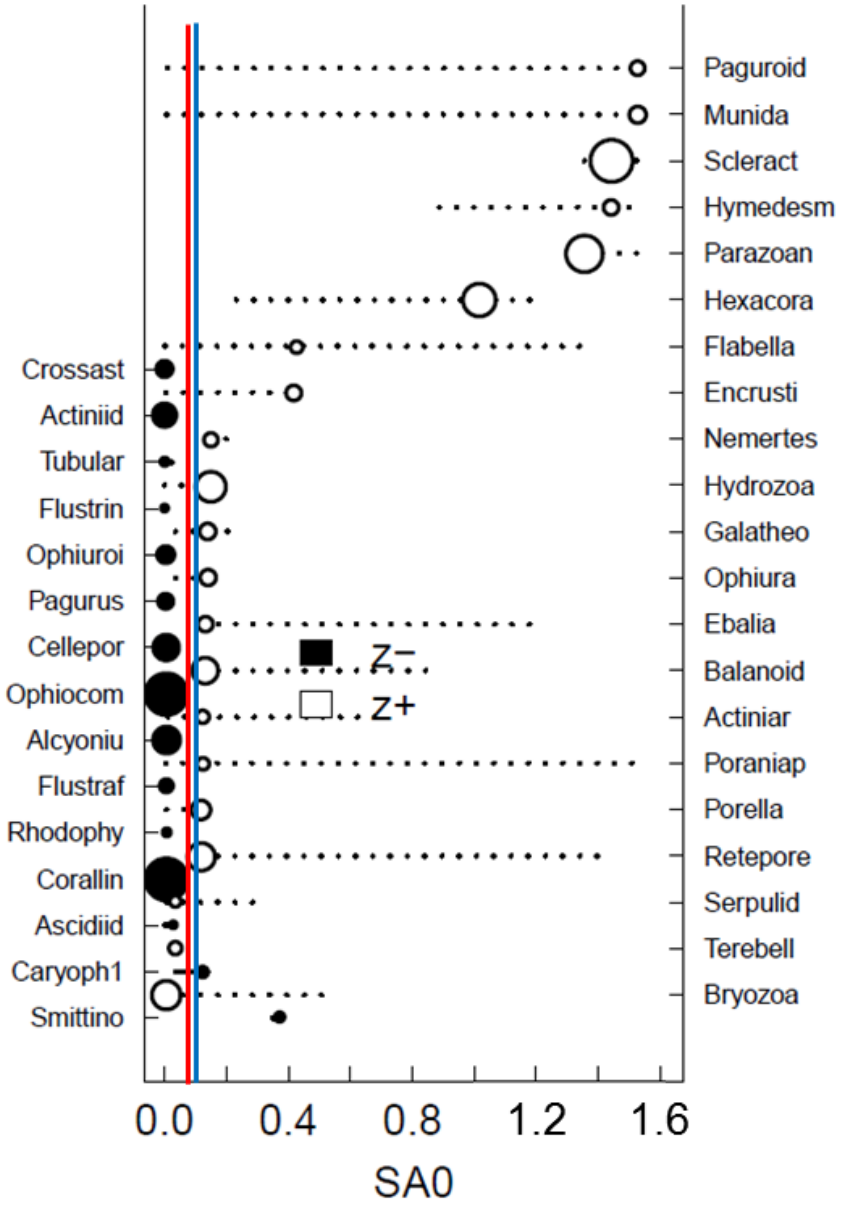

Figure 43. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “N2.aggregated taxa”. Symbols correspond to negative (z-, full circles) and positive (z-, empty circles) indicator taxa, and are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa). Horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Vertical lines represent community change point for taxa responding negatively (red) or positively (blue) to the pressure gradient. Taxa name abbreviations are as per Table 20.

TITAN results for “Aggregated taxa” dataset, stratum S1a - South, Low turbidity, Low energy, Bedrock habitat (in deep circalittoral zone)

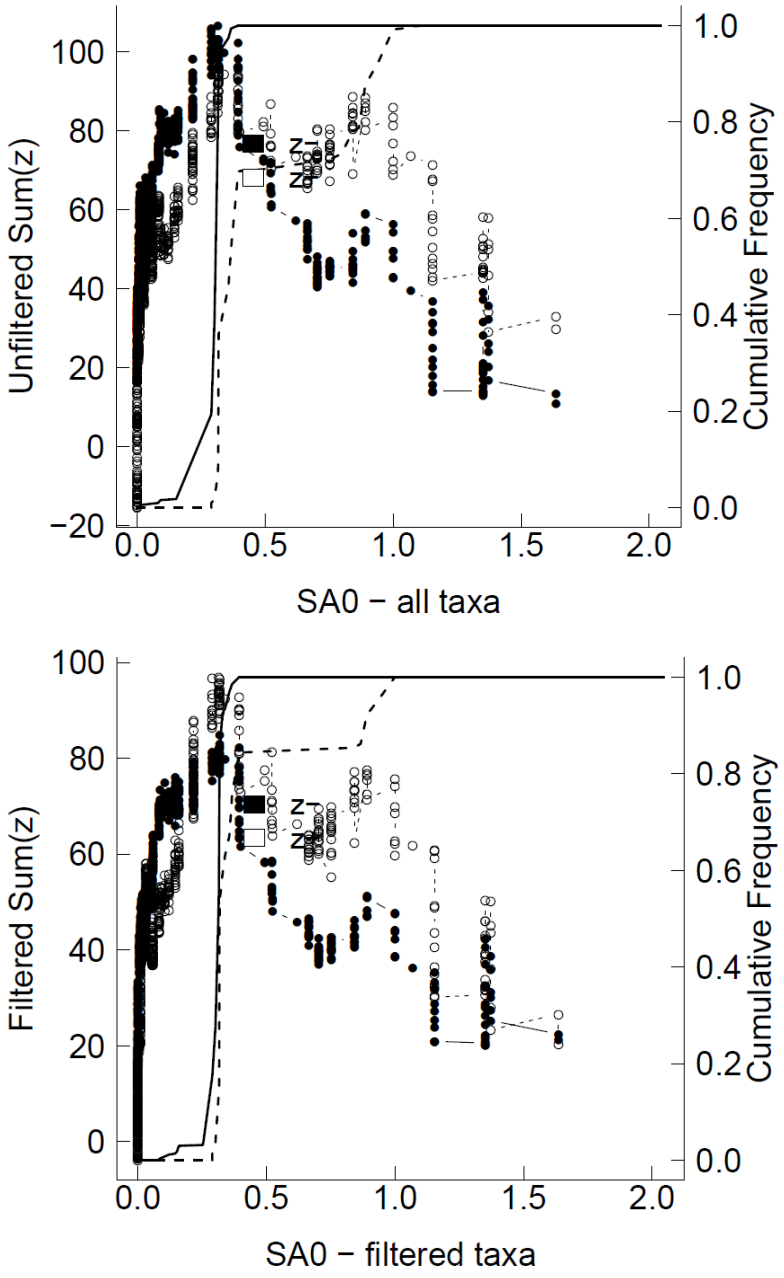

Figure 44. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 – 1.7) within the dataset “S1a.aggregated taxa”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 28. TITAN taxon-specific tabular output for the dataset "S1a.aggregated taxa". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 20.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Hydrozoa*	0.32 (0.29 - 1.5)	698	62.02	Yes	1.00	1.00
	Caryophy*	0.32 (0.02 - 0.39)	607	57.57	Yes	1.00	1.00
	Bryozoa*	0.02 (0.02 - 0.15)	630	54.08	Yes	1.00	1.00
	Porella*	0.95 (0.03 - 1.36)	379	39.89	Yes	0.99	1.00
	Brachiop*	0.29 (0.22 - 0.33)	265	36.51	Yes	1.00	1.00
	Ophiuroi*	0.32 (0.29 - 0.32)	279	35.03	Yes	1.00	1.00
	Alcyonid*	0.02 (0.01 - 0.03)	168	20.97	Yes	1.00	1.00
	Swiftiap*	0.03 (0 - 0.03)	60	11.85	Yes	1.00	1.00
	Sertular*	0.09 (0 - 0.32)	79	10.71	Yes	1.00	1.00
	Repent*	0.05 (0.03 - 0.05)	48	9.2	Yes	1.00	1.00
	Trochida*	0.15 (0 - 0.32)	64	8.83	Yes	0.98	1.00
	Poraniap*	0.05 (0 - 0.3)	59	7.05	Yes	1.00	0.99
	Ascidiac*	0.08 (0 - 0.22)	56	6.46	Yes	0.96	0.96
	Calliost*	0.08 (0 - 0.32)	49	6.26	Yes	0.99	0.95
	Nudibran	0 (0 - 0.05)	17	38.12	Yes	1.00	0.93
	Serpulid	0.22 (0.02 - 0.32)	328	32.59	Yes	0.91	1.00
	Flabella	0.95 (0 - 1)	164	19.05	Yes	0.81	0.93
	Haleciid	0 (0 - 0.84)	10	18.88	No	0.88	0.77
	Antedon	0.01 (0.01 - 0.67)	128	16.96	Yes	0.69	1.00
	Arboresc	0 (0 - 0.73)	49	15.25	No	0.46	0.81
	Globular	0 (0 - 0.84)	9	13.33	No	0.63	0.79
	Massive	0 (0 - 1.11)	11	12.91	No	0.25	0.77
	Salmacin	0 (0 - 0.15)	18	12.5	Yes	0.98	0.93
	Nemertes	0.32 (0 - 0.33)	111	12.18	Yes	0.92	0.97
	Crinoide	0.03 (0.01 - 0.09)	68	7.79	Yes	0.55	0.99
	Gracilec	0 (0 - 0.22)	5	7.2	No	0.67	0.38
	Echinus	0.32 (0 - 1.35)	55	5.74	No	0.51	0.76
	Echinoid	0.01 (0 - 1.35)	32	5.15	Yes	0.65	0.86
	Bugulida	0 (0 - 0.75)	6	3.74	Yes	0.91	0.94
	Palmiske	0.32 (0 - 0.32)	19	3.12	Yes	0.71	0.79
	Diazonav	0.01 (0 - 0.06)	7	2.93	Yes	0.99	0.93
	Stichast	0.01 (0 - 0.22)	11	2.3	No	0.95	0.79
	Ebalia	0.02 (0 - 0.32)	7	1.74	Yes	0.80	0.77
	Cionaint	0.01 (0.01 - 0.84)	6	1.53	No	0.65	0.61

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Terebell	0.03 (0.01 - 0.13)	10	1.52	No	0.59	0.64
	Alcyoniu	0.22 (0 - 0.22)	9	1.52	No	0.67	0.61
	Asterias	0.09 (0 - 0.09)	5	1.04	No	0.83	0.45
Positive	Porifera*	0.84 (0.84 - 1)	31	45.05	Yes	1.00	1.00
	Sabelli1*	1.37 (0.29 - 1.37)	12	31.61	Yes	1.00	0.99
	Ophiocom*	0.02 (0.02 - 0.02)	131	19.89	Yes	0.98	1.00
	Paguroid*	0.32 (0.02 - 0.8)	135	18.46	Yes	1.00	1.00
	Corynact*	0.03 (0.03 - 0.04)	64	15.65	Yes	1.00	1.00
	Spirobra*	0.32 (0.29 - 0.39)	24	14.46	Yes	1.00	1.00
	Ophiacti*	0 (0 - 0.67)	102	13.74	Yes	0.97	1.00
	Ophiothr*	0.02 (0.02 - 0.03)	59	9.78	Yes	1.00	1.00
	Styelida*	1 (0.39 - 1.5)	5	8.55	Yes	1.00	0.99
	Mesacmae*	0.39 (0.32 - 0.39)	9	6.87	Yes	1.00	1.00
	Pectinid*	0.7 (0.12 - 1.15)	7	5.53	Yes	1.00	0.99
	Papillat*	0.05 (0.01 - 1.64)	22	3.67	Yes	0.99	0.98
	Asteriid	1.36 (0 - 1.37)	81	35.55	Yes	0.79	0.99
	Ophiura	0.08 (0.01 - 0.89)	244	20.85	Yes	0.79	1.00
	Lytocarp	1.35 (0 - 1.35)	26	19.24	Yes	0.75	0.99
	Encrusti	1.11 (0.01 - 1.15)	37	10.45	Yes	0.63	1.00
	Retepore	0.75 (0.01 - 1.35)	43	8.53	Yes	0.81	0.98
	Pentapor	1.03 (0 - 1.64)	11	6.96	Yes	0.84	0.97
	Actiniar	0.15 (0.01 - 0.75)	46	5.86	Yes	0.96	0.92
	Munida	0.22 (0 - 1.36)	28	4.77	Yes	0.70	0.93
	Polyplac	0.06 (0 - 0.75)	48	4.74	No	0.52	0.78
	Plumular	0.67 (0.01 - 0.7)	16	4.52	Yes	0.89	0.92
	Crossast	1.15 (0 - 1.15)	5	2.02	No	0.55	0.66
	Diphasia	0.02 (0.02 - 0.89)	6	1.27	Yes	0.61	0.60
	Sabella	0.09 (0.02 - 1.35)	5	1.23	No	0.92	0.67

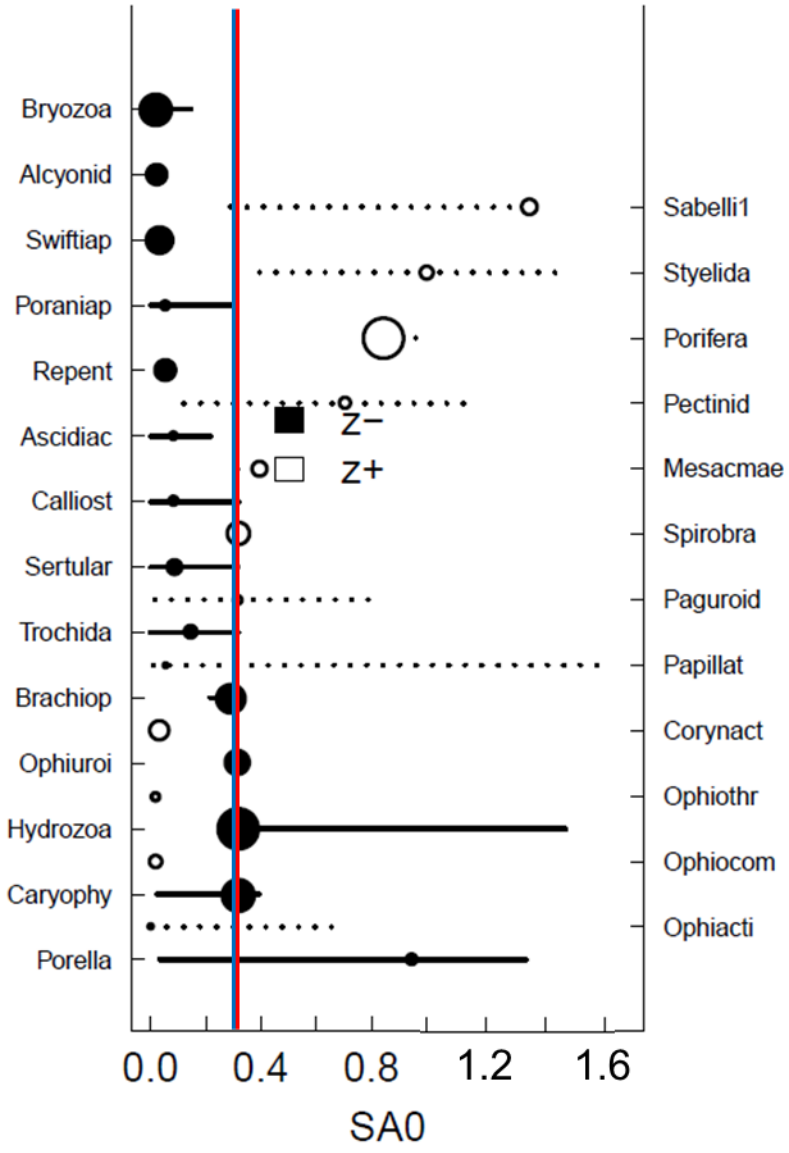

Figure 45. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “S1a.aggregated taxa”. Black symbols correspond to negative (z-) indicator taxa (no positive indicator taxa were found in stratum). Symbols are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa), and horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. The red vertical line represents community change point for taxa responding negatively to the pressure gradient. Taxa name abbreviations are as per Table 20.

TITAN results for “Conspicuous taxa” dataset, stratum N1 - North, shallow (deep circalittoral), low energy habitat (with low turbidity and variable rock type

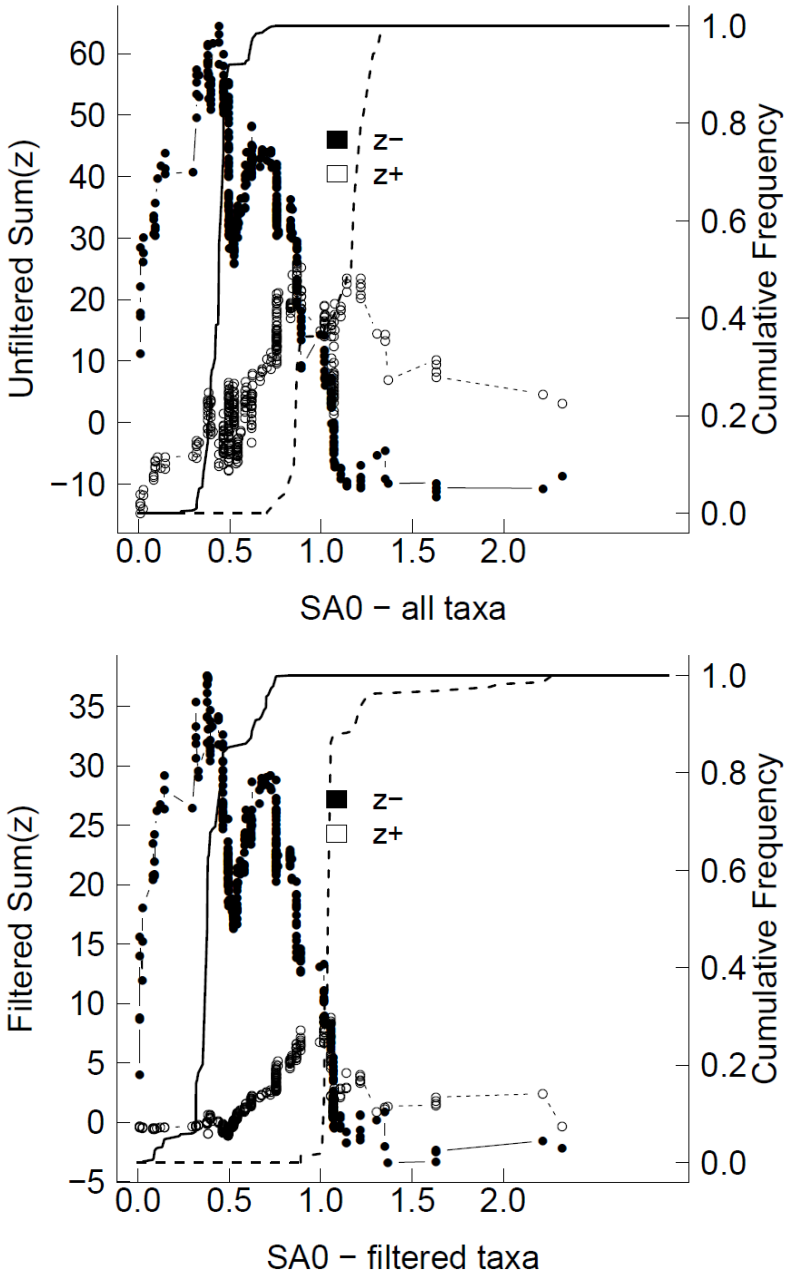

Figure 46. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 3.4) within the dataset “S2.aggregated taxa”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 29. TITAN taxon-specific tabular output for the dataset "S2.aggregated taxa". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 20.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Hydrozoa*	0.64 (0.59 - 1.35)	400	51.46	Yes	0.99	0.99
	Brachiop*	0.49 (0.38 - 0.64)	109	31.68	Yes	1.00	1.00
	Swiftiap*	0.13 (0.01 - 0.33)	5	23.81	Yes	1.00	1.00
	Sertular*	0.32 (0.09 - 0.38)	5	17.86	Yes	0.99	0.99
	Palmiske*	0.76 (0.64 - 0.83)	46	12.85	Yes	0.96	1.00
	Holothur*	0.59 (0.44 - 0.83)	28	9.02	Yes	0.97	1.00
	Edwardsi*	0.76 (0.64 - 0.76)	22	8.12	Yes	1.00	1.00
	Massive*	0.49 (0.38 - 0.76)	14	6.34	Yes	1.00	0.99
	Bryozoa	0.38 (0.32 - 3.27)	358	51.62	Yes	0.75	0.94
	Porella	0.11 (0.05 - 1.63)	232	50.56	Yes	0.87	1.00
	Serpulid	0.49 (0.01 - 1.33)	246	40	Yes	0.72	0.99
	Asteriid	0.59 (0.12 - 1.5)	108	19.18	Yes	0.71	0.97
	Antedon	0.02 (0.01 - 1.06)	27	17.67	Yes	0.69	0.78
	Nemertes	0.71 (0.49 - 1.22)	76	15.31	Yes	0.70	0.99
	Munida	0.76 (0.11 - 0.83)	75	14.82	Yes	0.84	0.80
	Parazoan	0.42 (0.4 - 2.22)	9	14.3	Yes	0.93	1.00
	Trochida	0.32 (0.1 - 0.76)	12	12.92	Yes	0.95	0.86
	Ophiuroi	0.59 (0.5 - 0.87)	42	11.09	Yes	0.89	0.98
	Aglaophe	0.87 (0.52 - 0.89)	28	8.97	Yes	0.77	1.00
	Stichast	0.47 (0.4 - 1.49)	35	8.96	Yes	0.75	0.76
	Poraniap	0.38 (0.38 - 2.8)	22	8.83	Yes	0.63	0.84
	Papillat	0.69 (0.49 - 1.18)	25	8.3	Yes	0.85	1.00
	Globular	0.59 (0.47 - 1.09)	20	6.87	Yes	0.89	0.97
	Ophiothr	0.38 (0.38 - 0.84)	8	6.35	Yes	0.87	0.67
	Ophiocom	0.47 (0.3 - 1.33)	7	5.2	Yes	0.72	0.83
	Echinoid	0.38 (0.33 - 1.36)	5	5.17	Yes	0.58	0.72
	Atrinafr	0.47 (0.38 - 1.63)	12	4.95	No	0.42	0.87
	Galatheo	0.42 (0.03 - 0.54)	5	4.94	Yes	1.00	0.92
	Encrusti	0.49 (0.47 - 0.62)	8	4.43	Yes	0.96	0.80
	Calliost	0.52 (0.49 - 0.83)	10	4.08	Yes	0.90	0.73
	Bolocera	0.83 (0.49 - 1.02)	11	2.67	No	0.64	0.45
	Pectinid	0.52 (0.09 - 0.76)	5	2.19	No	0.93	0.59
Positive	Sabellid*	1.06 (0.87 - 1.26)	9	10.35	Yes	0.95	0.99
	Caryophy	0.94 (0.47 - 1.07)	315	46.03	Yes	0.68	0.98

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Paguroid	1.22 (0.32 - 1.63)	47	27.19	Yes	0.64	0.98
	Echinus	0.4 (0.38 - 1.63)	76	15.81	Yes	0.80	0.88
	Salmacin	1.35 (0.02 - 1.63)	5	14.71	Yes	0.73	0.89
	Ophiura	0.83 (0.38 - 0.87)	54	14.03	Yes	0.91	0.95
	Crinoide	1.22 (0.32 - 1.5)	7	11.45	Yes	0.67	0.89
	Ascidiac	0.76 (0.01 - 1.04)	28	10.47	Yes	0.64	1.00
	Actiniar	0.76 (0.11 - 1.92)	50	9.52	No	0.69	0.83
	Polyplac	1.14 (0.5 - 1.22)	8	8.19	No	0.87	0.73
	Alcyoniu	1.06 (0.52 - 1.36)	8	5.24	Yes	0.99	0.88
	Ophiacti	0.88 (0.12 - 0.89)	8	4.64	Yes	0.59	0.91
	Nudibran	0.52 (0.49 - 1.07)	20	4.55	No	0.74	0.52
	Mesacmae	0.52 (0.52 - 0.76)	10	3.77	Yes	0.82	0.84
	Flabelli	1.02 (0.39 - 1.36)	6	3.26	No	0.62	0.82
	Hyalinoe	0.52 (0.52 - 0.76)	7	2.67	No	0.85	0.56
	Retepore	0.52 (0.38 - 1.06)	9	2.48	No	0.69	0.54
	Cerianth	0.5 (0.49 - 0.84)	5	1.76	No	0.76	0.30

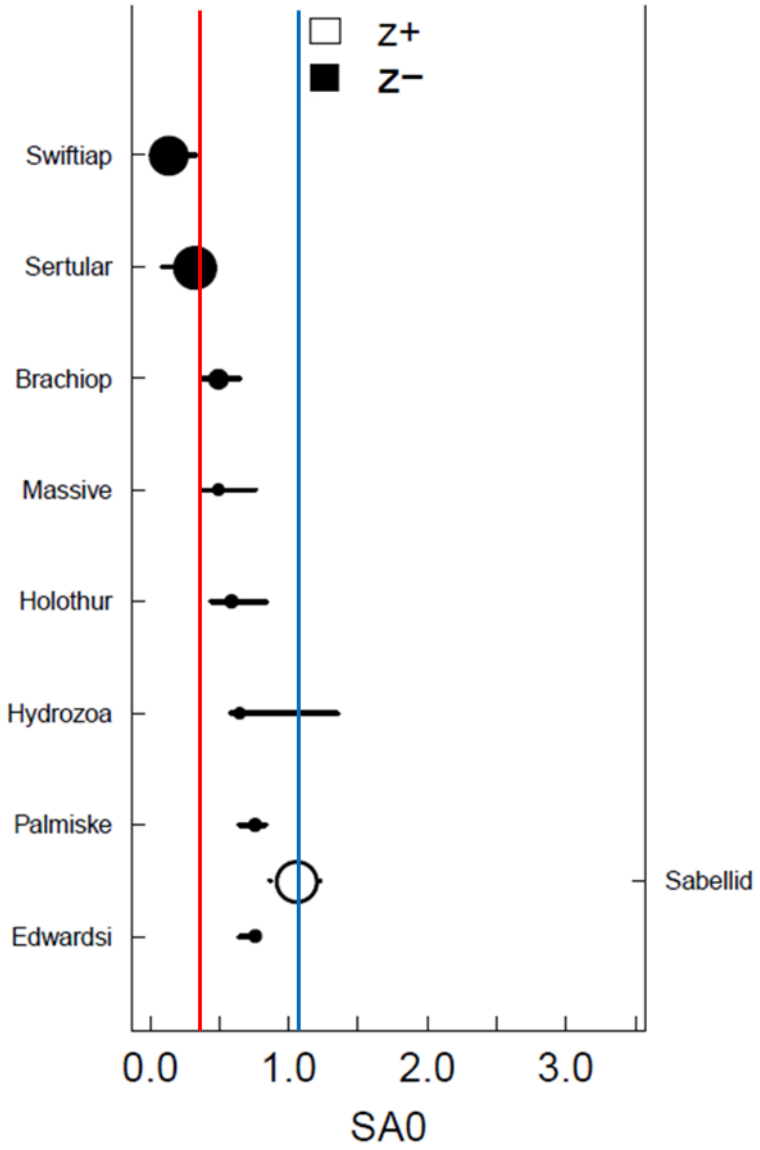

Figure 47. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “S2.aggregated taxa”. Symbols correspond to negative (z-, full circles) and positive (z-, empty circles) indicator taxa, and are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa). Horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Taxa name abbreviations are as per Table 20.

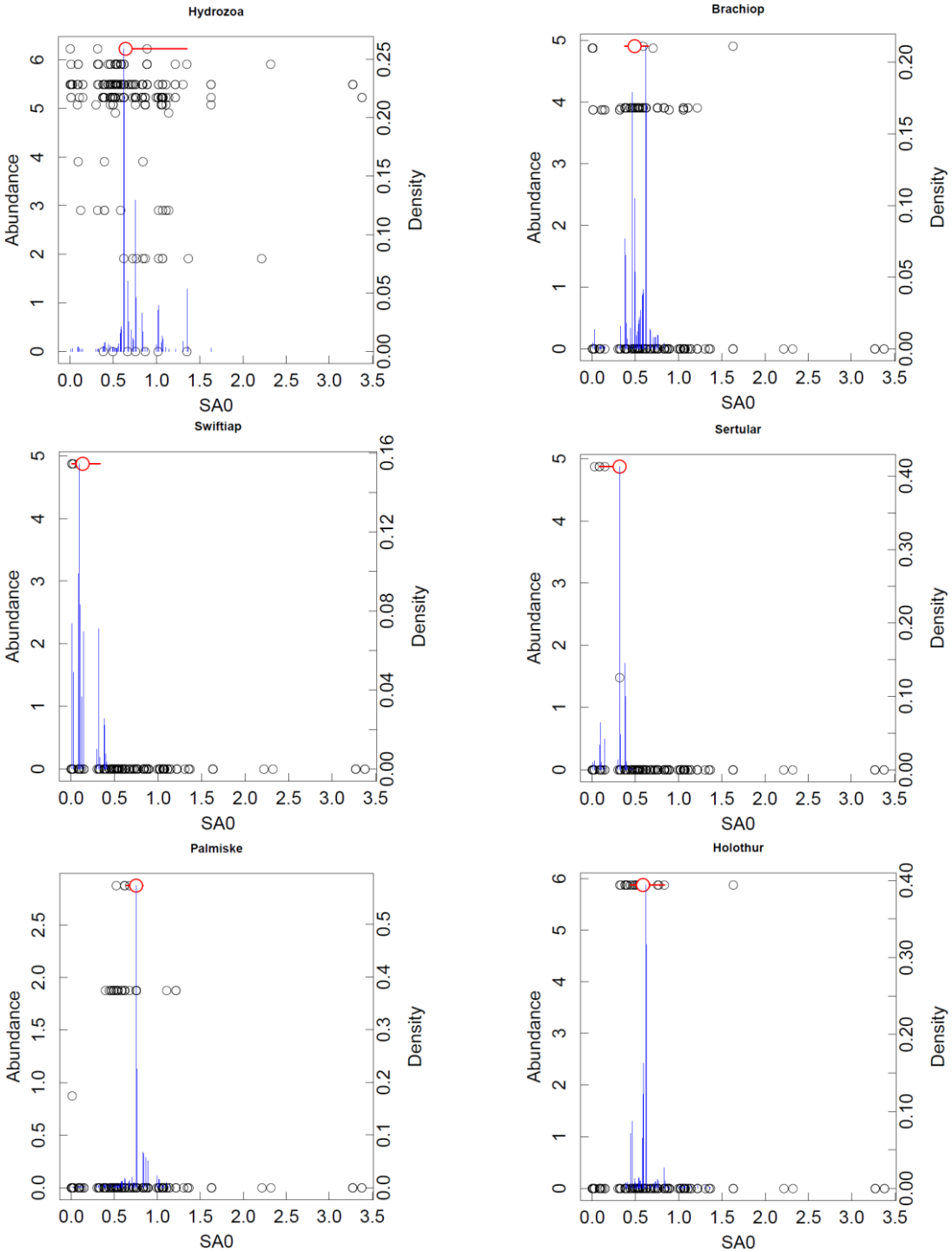

Figure 48. Taxon-specific plots of indicator taxa identified for the dataset “S2.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 3.4). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

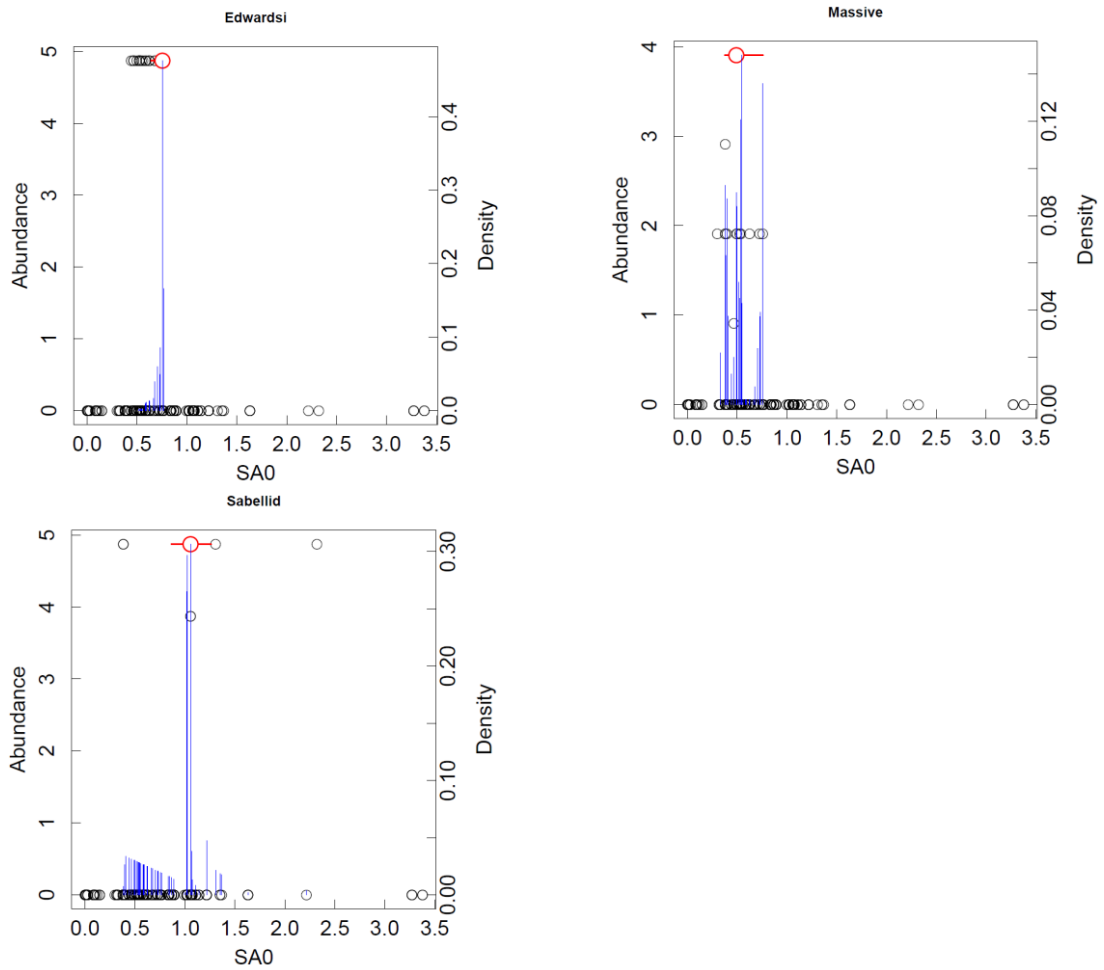

Figure 49. Taxon-specific plots of indicator taxa identified for the dataset “S2.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 3.4). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

TITAN results for “Aggregated taxa” dataset, stratum S3 - South, Low energy, Cobble habitat (in deep circalittoral zone and with low turbidity)

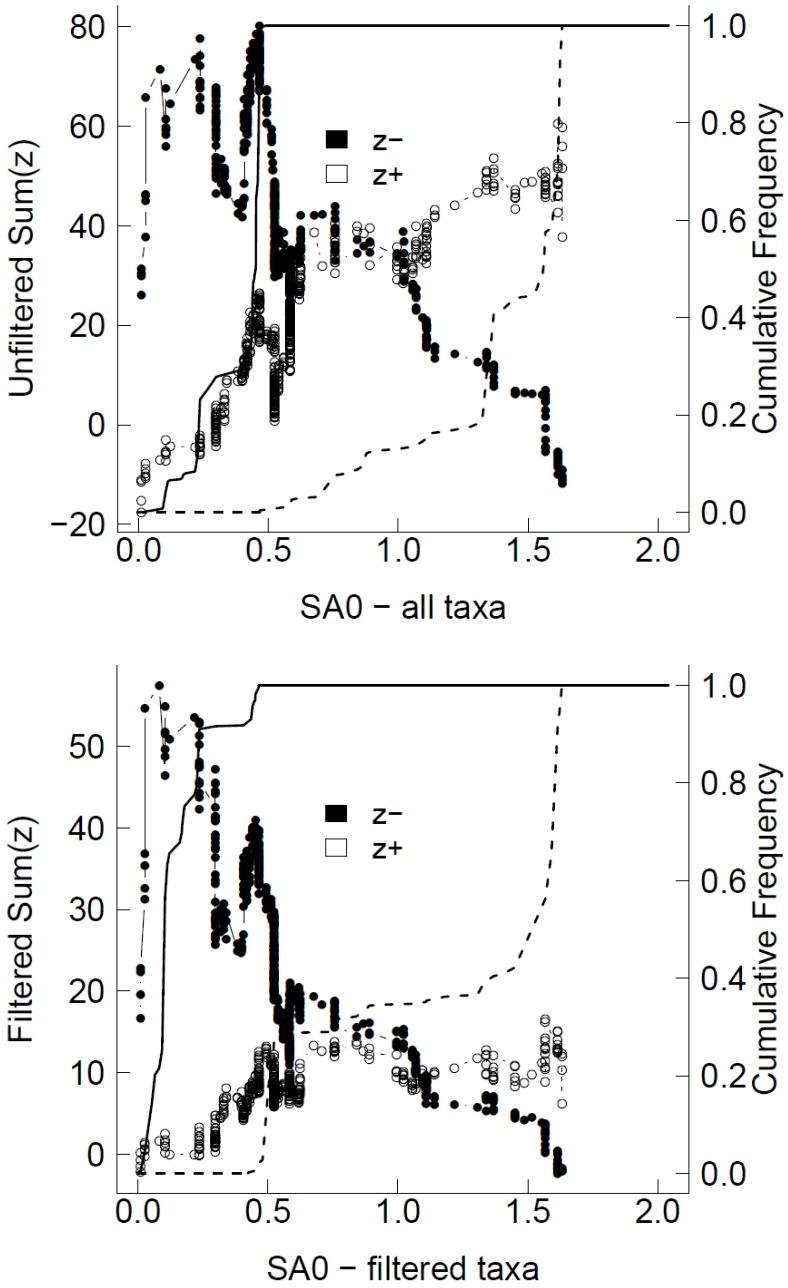

Figure 50. TITAN sum(z-) (taxa with a negative response) and sum(z+) (taxa with a positive response) values corresponding to all candidate change points along the pressure gradient (SA0 0 to 2.3) within the dataset “S3.aggregated taxa”. The top plot is based on all the taxa, the bottom plot only on the filtered taxa (i.e. taxa meeting purity and reliability criteria). The community change points for positive and negative responses are located where sum(z-) or sum(z+) peak, respectively (i.e. there is higher synchronisation in the change between species with a positive or negative response). Continuous and dashed vertical lines represent cumulative frequency distribution of change points among 500 bootstrap replicates for sum (z-) and sum(z+), respectively.

Table 30. TITAN taxon-specific tabular output for the dataset "S3.aggregated taxa". Taxa in the dataset are divided based on the direction of response to the pressure gradient (negative or positive, i.e. decreasing or increasing in frequency and abundance with the gradient, respectively). For each taxon, the analysis results include: change point (and 90% interquartile range); frequency (total number of occurrences in the dataset); IndVal (indicator value, on a range 0 to 100%, expressing the magnitude of change in the taxon frequency and abundance at the change point); "better than random" (expressing the results of the permutation analysis, with Yes identifying cases where the probability of obtaining an equal or larger IndVal score from random data is low, less than 0.05); purity (ranging 0 to 1, representing the consistency in the direction of change among 500 bootstrap resampling); reliability (ranging 0 to 1, representing the consistency in the magnitude of change among 500 bootstrap resampling). Taxa with asterisk (*) and shaded green, meet the purity and reliability criteria (both parameters greater than 0.95), and therefore have been selected as candidate indicator taxa for this stratum. Taxa name abbreviations are as per Table 20.

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
Negative	Swiftiap*	0.09 (0.05 - 0.24)	8	57.14	Yes	1.00	1.00
	Porella*	0.24 (0.05 - 0.52)	214	56.51	Yes	1.00	1.00
	Brachiop*	0.69 (0.41 - 0.76)	214	30.99	Yes	1.00	1.00
	Sertular*	0.09 (0.01 - 0.24)	5	28.52	Yes	0.99	0.98
	Globular*	0.59 (0.58 - 0.62)	141	26.09	Yes	0.96	1.00
	Ophiothr*	0.45 (0.42 - 0.47)	24	9.88	Yes	0.98	1.00
	Nudibran*	0.44 (0.43 - 0.62)	22	6.76	Yes	1.00	0.98
	Massive*	0.52 (0.34 - 1.01)	27	5.27	Yes	0.99	0.95
	Buccinid*	0.41 (0.1 - 0.47)	6	5.07	Yes	1.00	0.98
	Ophiocom*	0.58 (0.45 - 0.59)	20	4.71	Yes	1.00	1.00
	Hydrozoa	0.89 (0.45 - 1.11)	593	55.39	Yes	0.90	1.00
	Serpulid	0.62 (0.17 - 0.62)	430	45.75	Yes	0.93	1.00
	Ophiuroi	0.01 (0.01 - 1)	119	45.19	No	0.82	0.83
	Asteriid	0.47 (0.45 - 1.61)	188	26.3	Yes	0.83	1.00
	Ophiura	0.47 (0.47 - 1.61)	131	19.07	Yes	0.50	1.00
	Calliost	0.05 (0.01 - 0.76)	7	14.57	Yes	0.73	0.86
	Amphiura	0.47 (0.43 - 1.62)	53	14.54	Yes	0.62	1.00
	Nemertes	0.76 (0.24 - 1.63)	96	13.66	Yes	0.81	0.94
	Diphasia	0.24 (0.1 - 0.59)	6	12.54	Yes	0.84	0.94
	Papillat	0.3 (0.23 - 1.63)	33	11.3	Yes	0.51	1.00
	Poraniap	0.17 (0.03 - 1.57)	31	10.65	No	0.89	0.82
	Holothur	0.49 (0.45 - 0.58)	67	10.6	Yes	0.92	0.96
	Aglaophe	0.24 (0.11 - 0.62)	27	10.03	Yes	0.48	0.99
	Echinus	0.94 (0.47 - 0.99)	44	8.91	Yes	0.69	1.00
	Echinoid	0.44 (0.42 - 1.61)	30	7.97	Yes	0.68	1.00
	Antedon	0.23 (0.1 - 1.1)	15	7.34	No	0.62	0.82
	Ascidiac	0.24 (0.24 - 0.62)	7	7.05	Yes	0.67	0.80
	Salmacin	0.09 (0.09 - 1.57)	5	6.62	Yes	0.64	0.80
	Bolocera	0.41 (0.3 - 1.63)	20	5.7	Yes	0.76	0.92
	Psolus	0.24 (0.24 - 1.57)	7	5.47	Yes	0.74	0.86
	Pectenma	0.24 (0.24 - 1.61)	17	5.46	No	0.73	0.71
	Polyplac	0.43 (0.01 - 0.65)	24	5.25	Yes	0.95	0.89
	Parazoan	0.42 (0.41 - 0.99)	11	4.01	Yes	0.55	0.99
	Encrusti	0.52 (0.01 - 0.54)	14	3.76	Yes	0.99	0.93

Response	Taxon/Form	Change point (90% interq. range)	freq	IndVal	better than random	purity	reliability
	Inachida	0.47 (0.24 - 1.61)	7	3.49	Yes	0.78	0.95
	Cerianth	0.3 (0.3 - 0.89)	6	3.09	Yes	0.74	0.48
	Trochida	0.47 (0.1 - 0.62)	5	1.76	Yes	0.89	0.72
	Flabelli	0.45 (0.41 - 1.37)	6	1.42	No	0.57	0.58
	Plumular	0.58 (0.33 - 0.58)	5	1.29	Yes	0.70	0.34
Positive	Caryophy*	1.57 (0.58 - 1.61)	371	60.63	Yes	0.99	1.00
	Actiniar*	1.61 (0.47 - 1.63)	78	40.19	Yes	1.00	1.00
	Palmiske*	0.47 (0.45 - 0.52)	85	15.87	Yes	0.98	1.00
	Munida*	0.49 (0.49 - 1.61)	75	11.7	Yes	1.00	1.00
	Spirobra*	1.34 (0.76 - 1.61)	10	9.16	Yes	0.96	0.97
	Paguroid	1.62 (0.43 - 1.63)	124	51.22	Yes	0.66	1.00
	Bryozoa	1.18 (0.01 - 1.34)	532	50.71	Yes	0.74	0.98
	Galatheo	1.63 (0.41 - 1.63)	21	40	Yes	0.57	1.00
	Atrinafr	1.63 (0.52 - 1.63)	18	37.46	Yes	0.96	0.84
	Pectinid	1.63 (0.43 - 1.63)	10	27.27	Yes	0.76	0.96
	Sabellid	1.63 (0.3 - 1.63)	9	23.9	Yes	0.86	0.97
	Capneasa	1.63 (0.41 - 1.98)	11	18.44	No	0.66	0.61
	Crinoide	1.63 (0.42 - 1.63)	6	15.86	No	0.73	0.82
	Sabella	1.63 (0.4 - 1.63)	7	15.71	Yes	0.76	0.67
	Edwardsi	0.44 (0.43 - 0.62)	61	12.55	Yes	0.77	1.00
	Retepore	1.57 (0.01 - 1.63)	29	10.65	Yes	0.64	0.90
	Mesacmae	1.07 (0.4 - 1.37)	43	10.36	Yes	0.84	0.95
	Ophiacti	0.8 (0.24 - 0.87)	15	6.2	Yes	0.83	1.00
	Ceriallo	1.08 (0.76 - 1.57)	5	5.08	Yes	0.96	0.93
	Stichast	0.56 (0.4 - 0.58)	31	4.92	Yes	0.57	0.89
	Alcyoniu	0.52 (0.41 - 1.06)	25	3.83	No	0.70	0.67
	Hyalinoe	0.62 (0.41 - 0.76)	18	3.69	Yes	0.94	0.79
	Luidia	1.11 (0.47 - 1.57)	7	2.66	No	0.92	0.69

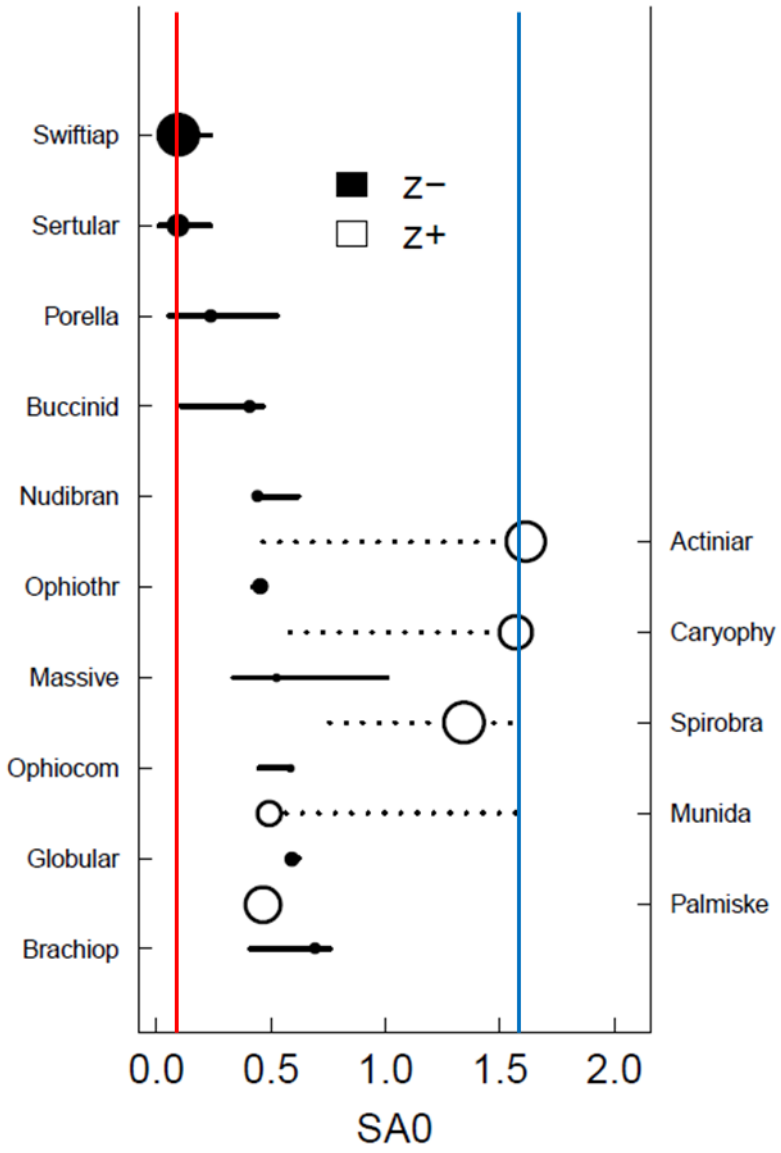

Figure 51. Change points of indicator taxa (i.e. meeting purity and reliability criteria) as identified in the TITAN for the dataset “S3.aggregated taxa”. Symbols correspond to negative (z-, full circles) and positive (z-, empty circles) indicator taxa, and are sized in proportion to z scores (i.e. rescaled IndVal scores to allow comparability between taxa). Horizontal lines overlapping each symbol represent the 90% interquartile range among 500 bootstrap replicates. Vertical lines represent community change point for taxa responding negatively (red) or positively (blue) to the pressure gradient. Taxa name abbreviations are as per Table 20.

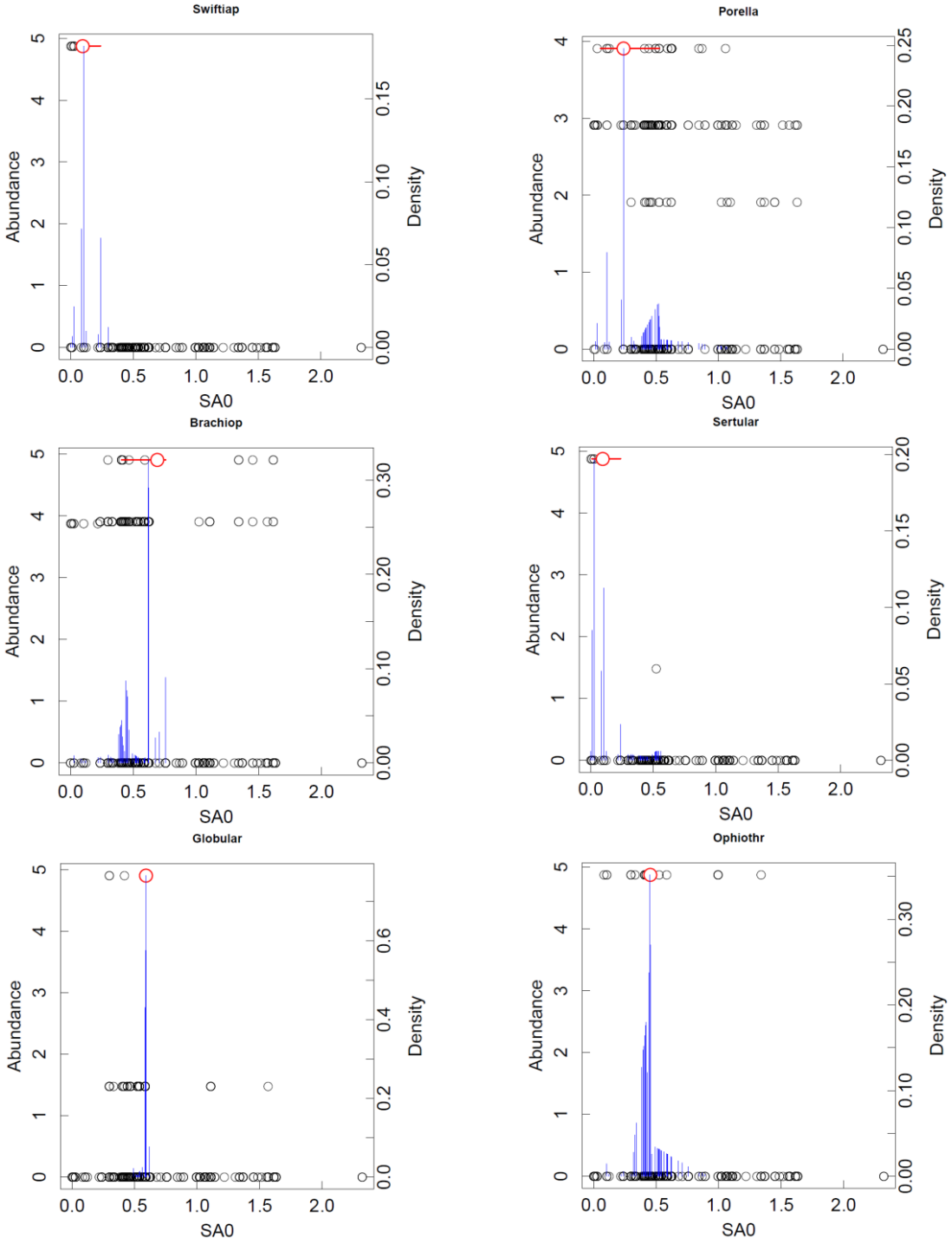

Figure 52. Taxon-specific plots of indicator taxa identified for the dataset “S3.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 2.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

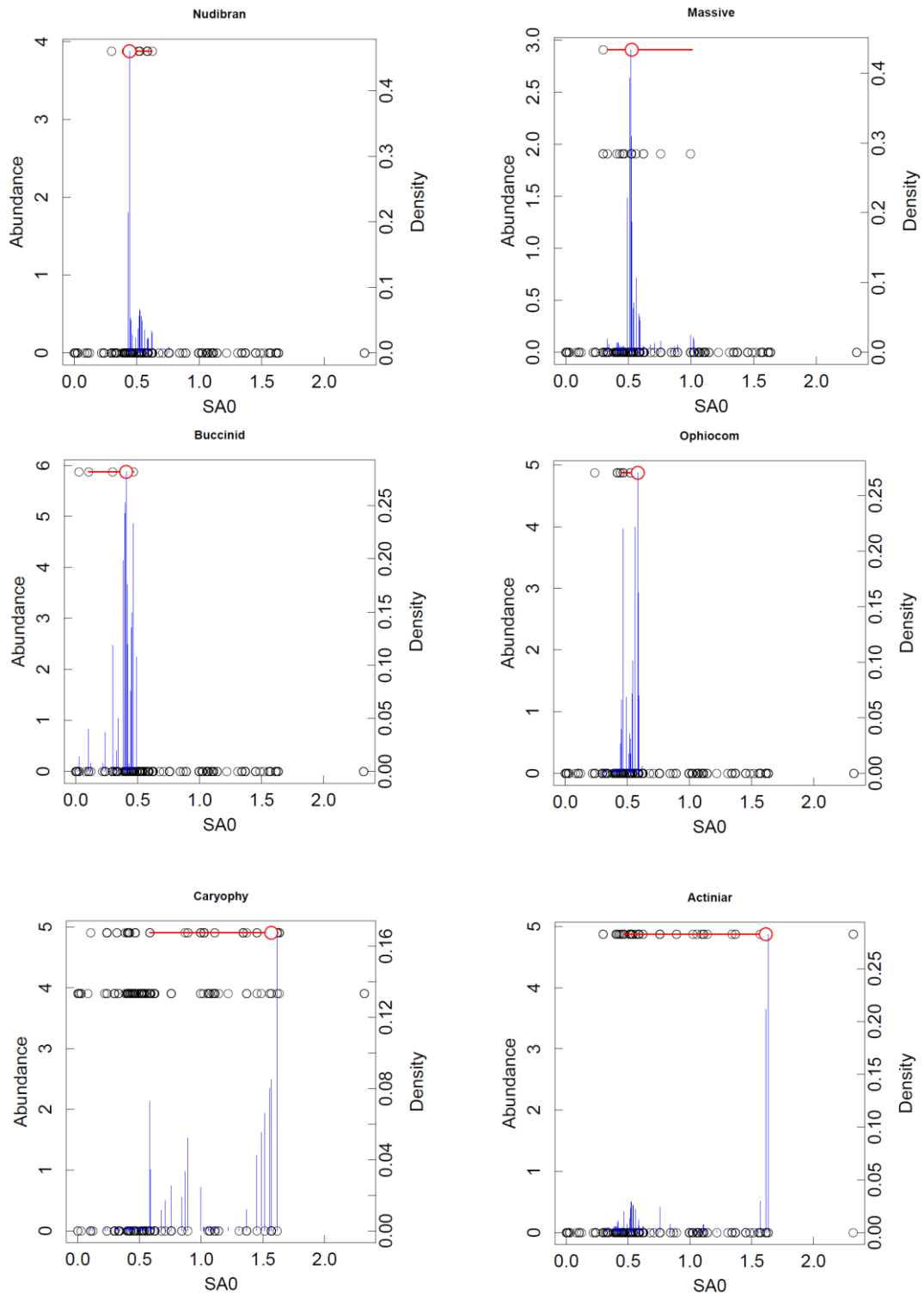

Figure 53. Taxon-specific plots of indicator taxa identified for the dataset “S3.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 2.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

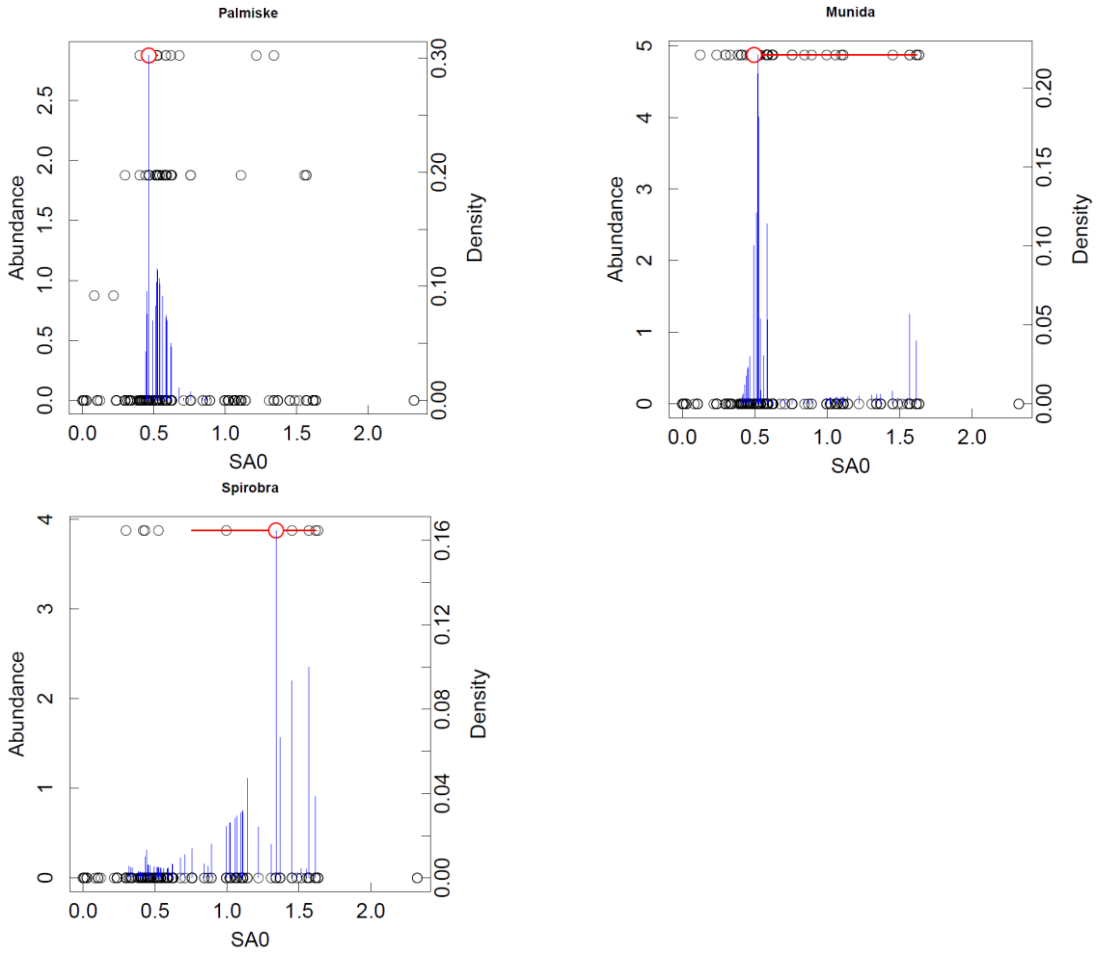

Figure 54. Taxon-specific plots of indicator taxa identified for the dataset “S3.aggregated taxa”. Black circles represent taxon-specific abundance indicator (as derived from SACFOR data) along the pressure gradient (SA0 0 to 2.3). Red circle near the top of the plot represents the observed change point, and horizontal red line overlapping the symbol represent the 90% interquartile range among 500 bootstrap replicates. The blue histogram shows the probability density function of change point locations across all bootstrap replicates.

Appendix 7 – Indicator Taxa Benchmark Abundances

These benchmarks qualify the mean abundance for the indicator taxa (based on the logged abundance index derived from transformation of SACFOR data) to be used as reference for conditions below and above the community change point.

Table 31. Benchmarks for indicator taxa identified for stratum N1. Results are distinguished by the dataset analysed (consp, conspicuous taxa; aggrt, aggregated taxa) and by the part of the pressure gradient below and above the observed community change point, and include: n – total number of samples; Freq – frequency of occurrence of the taxon; Freq% – percentage frequency; Mean – mean value of the logged abundance indicator. Taxa name abbreviations are as per Table 19 and Table 20.

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Arboresc	consp	84	13	15%	0.754	99	62	63%	3.059
	aggrt	84	13	15%	0.754	99	62	63%	3.059
Asterias	consp	15	1	7%	0.258	168	7	4%	0.185
	aggrt	15	1	7%	0.258	168	7	4%	0.185
Balanoid	consp	15	2	13%	0.321	168	11	7%	0.137
	aggrt	15	2	13%	0.321	168	11	7%	0.137
Caryoph2	consp	15	9	60%	3.192	168	1	1%	0.029
	aggrt	15	9	60%	3.192	168	1	1%	0.029
Encrusti	consp	84	40	48%	0.979	99	81	82%	1.793
	aggrt	84	40	48%	0.979	99	81	82%	1.793
Flustraf	consp	15	6	40%	0.310	168	5	3%	0.019
	aggrt	15	6	40%	0.310	168	5	3%	0.019
Hexacora	consp	15	6	40%	2.017	168	0	0%	0.000
	aggrt	15	6	40%	2.017	168	0	0%	0.000
Hymedesm	consp	15	5	33%	0.636	168	14	8%	0.171
	aggrt	15	5	33%	0.636	168	14	8%	0.171
Laniceco	consp	15	4	27%	1.500	168	8	5%	0.250
	aggrt	15	4	27%	1.500	168	8	5%	0.250
Ophiothr	consp	15	1	7%	0.325	168	29	17%	0.931
	aggrt	15	1	7%	0.325	168	29	17%	0.931
Ophialb	consp	15	8	53%	2.600	168	11	7%	0.325
Ophiura	aggrt	15	8	53%	2.600	168	23	14%	0.673
Ophiuroi	consp	15	12	80%	3.767	168	18	11%	0.487
	aggrt	15	12	80%	3.767	168	18	11%	0.487
Palmiske	consp	15	0	0%	0.000	168	7	4%	0.203
	aggrt	15	0	0%	0.000	168	7	4%	0.203
Parasmit	consp	15	6	40%	1.029	168	8	5%	0.109
	aggrt	15	6	40%	1.029	168	8	5%	0.109
Parazoan	consp	15	5	33%	1.825	168	4	2%	0.140
	aggrt	15	5	33%	1.825	168	4	2%	0.140
Poraniap	consp	15	8	53%	2.200	168	25	15%	0.696
	aggrt	15	8	53%	2.200	168	25	15%	0.696
Retepore	consp	15	2	13%	0.583	168	5	3%	0.127
	aggrt	15	2	13%	0.583	168	5	3%	0.127

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Scleract	consp	15	0	0%	0.000	168	11	7%	0.349
	aggrt	15	0	0%	0.000	168	11	7%	0.349
Serpulid	consp	15	7	47%	1.076	168	27	16%	0.582
	aggrt	15	7	47%	1.076	168	27	16%	0.582
Sertular	consp	15	5	33%	0.769	168	1	1%	0.029
	aggrt	15	5	33%	0.769	168	1	1%	0.029

Table 32. Benchmarks for indicator taxa identified for stratum N2. Results are distinguished by the dataset analysed (consp, conspicuous taxa; aggrt, aggregated taxa) and by the part of the pressure gradient below and above the observed community change point, and include: n, total number of samples; Freq, frequency of occurrence of the taxon; Freq%, percentage frequency; Mean, mean value of the logged abundance indicator. Taxa name abbreviations are as per Table 19 and Table 20.

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Actiniar	consp	438	15	3%	0.137	235	25	11%	0.455
	aggrt	438	15	3%	0.137	235	25	11%	0.455
Actiniid	consp	298	44	15%	0.510	375	1	0%	0.010
	aggrt	313	44	14%	0.486	360	1	0%	0.011
Alcyoniu*	consp	298	79	27%	1.118	375	12	3%	0.058
Alcyoniu*	aggrt	313	85	27%	1.091	360	6	2%	0.037
Ascidiid	consp	298	12	4%	0.163	375	3	1%	0.036
	aggrt	313	13	4%	0.171	360	2	1%	0.024
Balanoid	consp	438	47	11%	0.205	235	71	30%	0.665
	aggrt	438	47	11%	0.205	235	71	30%	0.665
Bryozoa	consp	438	172	39%	1.303	235	122	52%	1.985
	aggrt	438	172	39%	1.303	235	122	52%	1.985
Caryoph1	aggrt	313	126	40%	2.177	360	90	25%	1.397
Cellepor	consp	298	101	34%	0.643	375	22	6%	0.069
	aggrt	313	101	32%	0.612	360	22	6%	0.072
Corallin	consp	298	138	46%	1.739	375	17	5%	0.150
	aggrt	313	150	48%	1.802	360	5	1%	0.029
Crossast	consp	298	57	19%	0.771	375	13	3%	0.140
	aggrt	313	57	18%	0.734	360	13	4%	0.145
Ebalia	consp	438	10	2%	0.120	235	23	10%	0.507
	aggrt	438	10	2%	0.120	235	23	10%	0.507
Encrusti	consp	438	102	23%	0.549	235	51	22%	0.512
	aggrt	438	102	23%	0.549	235	51	22%	0.512
Flabella	consp	438	93	21%	1.007	235	49	21%	0.966
	aggrt	438	93	21%	1.007	235	49	21%	0.966
Flustraf	consp	298	64	21%	0.153	375	22	6%	0.045
	aggrt	313	64	20%	0.145	360	22	6%	0.047
Flustrin	consp	298	7	2%	0.045	375	0	0%	0.000
	aggrt	313	7	2%	0.043	360	0	0%	0.000

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Galatheo	consp	438	50	11%	0.493	235	56	24%	1.077
	aggrt	438	50	11%	0.493	235	56	24%	1.077
Hexacora	consp	438	0	0%	0.000	235	15	6%	0.328
	aggrt	438	0	0%	0.000	235	15	6%	0.328
Hydrozoa	consp	438	149	34%	0.931	235	165	70%	2.300
	aggrt	438	149	34%	0.931	235	165	70%	2.300
Hymedesm	consp	438	106	24%	0.505	235	60	26%	0.495
	aggrt	438	106	24%	0.505	235	60	26%	0.495
Munida	consp	438	37	8%	0.391	235	22	9%	0.422
	aggrt	438	37	8%	0.391	235	22	9%	0.422
Nemertes	consp	438	5	1%	0.049	235	14	6%	0.244
	aggrt	438	5	1%	0.049	235	14	6%	0.244
Ophiocom	consp	298	153	51%	2.872	375	13	3%	0.188
	aggrt	313	154	49%	2.750	360	12	3%	0.182
Ophiualb	consp	438	49	11%	0.548	235	63	27%	1.311
Ophiura	aggrt	438	58	13%	0.646	235	65	28%	1.353
Ophiuroi	consp	298	96	32%	1.742	375	47	13%	0.582
	aggrt	313	99	32%	1.705	360	44	12%	0.565
Paguroid	consp	438	26	6%	0.278	235	20	9%	0.368
	aggrt	438	26	6%	0.278	235	20	9%	0.368
Pagurus	consp	298	26	9%	0.378	375	1	0%	0.010
	aggrt	313	26	8%	0.360	360	1	0%	0.011
Parasmit	consp	298	40	13%	0.256	375	59	16%	0.300
Parazang	consp	438	4	1%	0.051	235	16	7%	0.387
Parazoan	consp	438	3	1%	0.040	235	9	4%	0.221
	aggrt	438	7	2%	0.092	235	25	11%	0.608
Poraniap	consp	438	46	11%	0.434	235	50	21%	0.884
	aggrt	438	46	11%	0.434	235	50	21%	0.884
Porella	aggrt	438	8	2%	0.075	235	28	12%	0.487
Porellac	consp	438	8	2%	0.075	235	28	12%	0.487
Porifera	consp	438	15	3%	0.191	235	19	8%	0.468
Retepore	consp	438	9	2%	0.082	235	40	17%	0.706
	aggrt	438	9	2%	0.082	235	40	17%	0.706
Rhodophy	consp	298	24	8%	0.164	375	5	1%	0.039
	aggrt	313	24	8%	0.156	360	5	1%	0.040
Scleract	consp	438	16	4%	0.142	235	19	8%	0.394
	aggrt	438	16	4%	0.142	235	19	8%	0.394
Serpulid	consp	438	185	42%	1.324	235	134	57%	1.872
	aggrt	438	185	42%	1.324	235	134	57%	1.872
Smittino	consp	298	54	18%	0.362	375	82	22%	0.446
	aggrt	313	54	17%	0.345	360	82	23%	0.465
Terebell	consp	438	18	4%	0.200	235	4	2%	0.083
	aggrt	438	18	4%	0.200	235	4	2%	0.083

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Tubular	consp	298	9	3%	0.137	375	1	0%	0.010
	aggrt	313	9	3%	0.131	360	1	0%	0.011

*Alcyoniu refers *Alcyonium digitatum* in the consp dataset and the genus Alcyonium in the aggrt dataset.

Table 33. Benchmarks for indicator taxa identified for stratum S1a. Results are distinguished by the dataset analysed (consp, conspicuous taxa; aggrt, aggregated taxa) and by the part of the pressure gradient below and above the observed community change point, and include: n, total number of samples; Freq, frequency of occurrence of the taxon; Freq%, percentage frequency; Mean, mean value of the logged abundance indicator. Taxa name abbreviations are as per Table 19 and Table 20.

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Alcyonid	consp	620	147	24%	0.656	147	21	14%	0.377
	aggrt	620	147	24%	0.656	147	21	14%	0.377
Ascidiac	consp	620	51	8%	0.290	147	5	3%	0.132
	aggrt	620	51	8%	0.290	147	5	3%	0.132
Brachiop	consp	620	255	41%	1.674	147	10	7%	0.243
	aggrt	620	255	41%	1.674	147	10	7%	0.243
Bryozoa	consp	620	548	88%	2.413	147	82	56%	1.630
	aggrt	620	548	88%	2.413	147	82	56%	1.630
Calliost	consp	620	45	7%	0.357	147	4	3%	0.133
	aggrt	620	45	7%	0.357	147	4	3%	0.133
Caryophy	consp	620	537	87%	3.794	147	70	48%	2.146
	aggrt	620	537	87%	3.794	147	70	48%	2.146
Corynact	consp	620	61	10%	0.501	147	3	2%	0.073
	aggrt	608	61	10%	0.510	159	3	2%	0.067
Hydrozoa	consp	620	607	98%	5.031	147	91	62%	3.027
	aggrt	620	607	98%	5.031	147	91	62%	3.027
Mesacmae	consp	620	0	0%	0.000	147	9	6%	0.292
	aggrt	608	0	0%	0.000	159	9	6%	0.270
Ophiacti	consp	620	76	12%	0.627	147	26	18%	0.910
	aggrt	608	74	12%	0.623	159	28	18%	0.903
Ophiocom	consp	620	124	20%	0.990	147	7	5%	0.232
	aggrt	608	124	20%	1.009	159	7	4%	0.215
Ophiothr	consp	620	56	9%	0.455	147	3	2%	0.099
	aggrt	608	56	9%	0.464	159	3	2%	0.092
Ophiualb	consp	620	108	17%	0.849	147	24	16%	0.796
Ophiuroi	consp	620	264	43%	2.092	147	15	10%	0.497
	aggrt	620	264	43%	2.092	147	15	10%	0.497
Paguroid	consp	620	94	15%	0.739	147	41	28%	1.258
	aggrt	608	90	15%	0.722	159	45	28%	1.285
Papillat	consp	620	19	3%	0.078	147	3	2%	0.046
	aggrt	608	19	3%	0.079	159	3	2%	0.042
Pectinid	consp	620	1	0%	0.008	147	6	4%	0.172

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
	aggrt	608	1	0%	0.008	159	6	4%	0.159
Poraniap	consp	620	56	9%	0.437	147	3	2%	0.099
	aggrt	620	56	9%	0.437	147	3	2%	0.099
Porella	aggrt	620	325	52%	1.603	147	54	37%	1.115
	consp	620	325	52%	1.603	147	54	37%	1.115
Porifera	consp	620	0	0%	0.000	147	31	21%	0.531
	aggrt	608	0	0%	0.000	159	31	19%	0.491
Repent	consp	620	48	8%	0.046	147	0	0%	0.000
	aggrt	620	48	8%	0.046	147	0	0%	0.000
Sabelli1	consp	620	4	1%	0.031	147	8	5%	0.184
	aggrt	608	3	0%	0.024	159	9	6%	0.200
Sertular	consp	620	78	13%	0.613	147	1	1%	0.033
	aggrt	620	78	13%	0.613	147	1	1%	0.033
Spirobra	aggrt	608	2	0%	0.004	159	22	14%	0.339
Spirotri	consp	620	0	0%	0.000	147	20	14%	0.350
Styelida	consp	620	0	0%	0.000	147	5	3%	0.091
	aggrt	608	0	0%	0.000	159	5	3%	0.084
Swiftiap	consp	620	57	9%	0.451	147	3	2%	0.099
	aggrt	620	57	9%	0.451	147	3	2%	0.099
Trochida	consp	620	61	10%	0.386	147	3	2%	0.079
	aggrt	620	61	10%	0.386	147	3	2%	0.079

Table 34. Benchmarks for indicator taxa identified for stratum S2. Results are distinguished by the dataset analysed (consp – conspicuous taxa; aggrt – aggregated taxa) and by the part of the pressure gradient below and above the observed community change point, and include: n – total number of samples; Freq – frequency of occurrence of the taxon; Freq% – percentage frequency; Mean – mean value of the logged abundance indicator. Taxa name abbreviations are as per Table 19 and Table 20.

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Brachiop	consp	59	28	47%	1.898	348	81	23%	0.920
	aggrt	32	14	44%	1.790	375	95	25%	1.000
Edwardsi	consp	59	1	2%	0.083	348	21	6%	0.294
	aggrt	32	0	0%	0.000	375	22	6%	0.286
Holothur	consp	59	9	15%	0.896	348	19	5%	0.321
	aggrt	32	2	6%	0.367	375	26	7%	0.407
Hydrozoa	consp	59	58	98%	5.150	348	342	98%	5.147
	aggrt	32	32	100%	5.346	375	368	98%	5.131
Massive	consp	59	5	8%	0.179	348	9	3%	0.052
	aggrt	32	1	3%	0.060	375	13	3%	0.071
Palmiske	consp	59	3	5%	0.078	348	43	12%	0.246
	aggrt	32	1	3%	0.027	375	45	12%	0.238
Parazoan	consp	59	8	14%	0.441	348	1	0%	0.008
Sabellid	aggrt	339	2	1%	0.029	68	7	10%	0.472
Sertular	consp	59	5	8%	0.356	348	0	0%	0.000
	aggrt	32	5	16%	0.656	375	0	0%	0.000
Swiftiap	consp	59	5	8%	0.413	348	0	0%	0.000
	aggrt	32	5	16%	0.762	375	0	0%	0.000

Table 35. Benchmarks for indicator taxa identified for stratum S3. Results are distinguished by the dataset analysed (consp – conspicuous taxa; aggrt – aggregated taxa) and by the part of the pressure gradient below and above the observed community change point, and include: n – total number of samples; Freq – frequency of occurrence of the taxon; Freq% – percentage frequency; Mean – mean value of the logged abundance indicator. Taxa name abbreviations are as per Table 19 and Table 20.

Taxon/Form	dataset	Below change point				Above change point			
		n	Freq	Freq%	Mean	n	Freq	Freq%	Mean
Actiniar	consp	213	17	8%	0.389	383	61	16%	0.776
	aggrt	576	71	12%	0.601	20	7	35%	1.706
Brachiop	consp	14	7	50%	1.938	582	207	36%	1.414
	aggrt	14	7	50%	1.938	582	207	36%	1.414
Buccinid	consp	14	1	7%	0.420	582	5	1%	0.050
	aggrt	14	1	7%	0.420	582	5	1%	0.050
Caryophy	consp	213	122	57%	2.421	383	249	65%	2.655
	aggrt	576	352	61%	2.507	20	19	95%	4.412
Globular	consp	14	0	0%	0.000	582	141	24%	0.376
	aggrt	14	0	0%	0.000	582	141	24%	0.376
Massive	consp	14	0	0%	0.000	582	27	5%	0.090
	aggrt	14	0	0%	0.000	582	27	5%	0.090
Munida	consp	213	13	6%	0.298	383	62	16%	0.789
	aggrt	576	70	12%	0.592	20	5	25%	1.219
Nudibran	aggrt	14	0	0%	0.000	582	22	4%	0.146
Ophiocom	consp	14	0	0%	0.000	582	20	3%	0.168
	aggrt	14	0	0%	0.000	582	20	3%	0.168
Ophiothr	consp	14	1	7%	0.348	582	23	4%	0.193
	aggrt	14	1	7%	0.348	582	23	4%	0.193
Palmiske	consp	213	13	6%	0.119	383	72	19%	0.389
	aggrt	576	85	15%	0.303	20	0	0%	0.000
Porella	consp	14	11	79%	2.355	582	203	35%	1.017
	aggrt	14	11	79%	2.355	582	203	35%	1.017
Sertular	consp	14	4	29%	1.393	582	1	0%	0.003
	aggrt	14	4	29%	1.393	582	1	0%	0.003
Spirobra	aggrt	576	8	1%	0.054	20	2	10%	0.388
Swiftiap	consp	14	8	57%	2.786	582	0	0%	0.000
	aggrt	14	8	57%	2.786	582	0	0%	0.000