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1714S Solan Bank Reef SCI Environmental Data Analysis

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Executive summary

An investigation has been carried out into the composition and structure of the epibenthic assemblage inhabiting the Solan Bank Reef SCI. The purpose of the investigation was to describe the epibenthic assemblages inhabiting different habitat types, and to identify any environmental variables that may be influential in any pattern observed in the assemblages. In addition, this investigation sought to test whether subsets of the acquired epibenthic dataset would be suitable to use as a surrogate for the whole assemblage. In particular, sponges classified into morphological categories and anthozoa were of interest, because together they have been proposed as a supporting indicator of biodiversity for the assessment of Good Environmental Status under the Marine Strategy Framework Directive.

Datasets of epibenthic taxa were generated from the processing of underwater video and still photographs taken during a dedicated survey of the site in 2014. Analyses were performed on each dataset separately to retain the possibility of comparing which sampling technique, if any, might be more effective in delivering data that revealed the most informative results. Both datasets revealed similar patterns in epibenthic composition across habitat types, between reef elevation categories and between biotopes. However, some of the limitations imposed by each sampling technique were evident in the results. These limitations have been discussed, and recommendations provided on when each technique might be deployed to best effect.

As expected, a greater number of taxa was present in reef habitat types than in non-reef habitat. The number of taxa between reef types, bedrock and stony reef, was not significantly different, although the taxon composition of the assemblage between reef types could be distinguished. Lists of taxa characterising each habitat type are provided. The most pronounced differences in the number of taxa observed were between extremes of reef elevation, from 0 m to >1 m – >5 m. As the number of taxa available for analyses was reduced (by selecting ever smaller subsets of data), the observed differences were broadly maintained, but the statistical significance of those differences was lost. Epibenthic assemblage composition and structure, as informed by multivariate analyses, was also less variable as fewer taxa were included in the analyses.

Environmental variables found to be most influential on the distribution of the epibenthic assemblage were water depth, sediment composition and water temperature at the seabed. Current velocity and bottom shear stress were also found to be of greater influence on the sponge and anthozoan subset of the assemblage. The latter environmental variables were provided by this study as outputs from a dedicated modelling exercise for the site, after the measured variables during survey were deemed unsuitable for the purposes of the investigation. Similarly, the available information on fishing pressure and how this was used to plan the survey to investigate its effects on the epibenthos was not compatible with assumptions in the analyses that would give a reliable account of its possible effects. Recommendations on how such information could be collected and incorporated into future assessments are provided.

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1   Introduction

The geological seabed feature known as the Solan Bank High is located within the Scottish Continental Shelf Regional Sea, between 20 and 60km from the Scottish mainland, north of Cape Wrath (Figure 1). The bank is characterised by bedrock reef outcrops and stony reef structures interspersed with coarse and mixed sediments, and lies in a range of depth zones from the infralittoral to the deep circalittoral; it is exposed to a range of energy levels, with a resulting wide variety of associated biological communities. Since the bedrock and stony reef structures correspond with the definition of Annex I reef habitat under the European Commission (EC) Habitats Directive, the bank has been recommended by the Scottish Government as a candidate Special Area of Conservation (cSAC), and has been adopted by the EC as the Solan Bank Reef Site of Community Importance (SCI) whilst it awaits designation as a SAC (JNCC 2012).

Location of Solan Bank Reef SCI
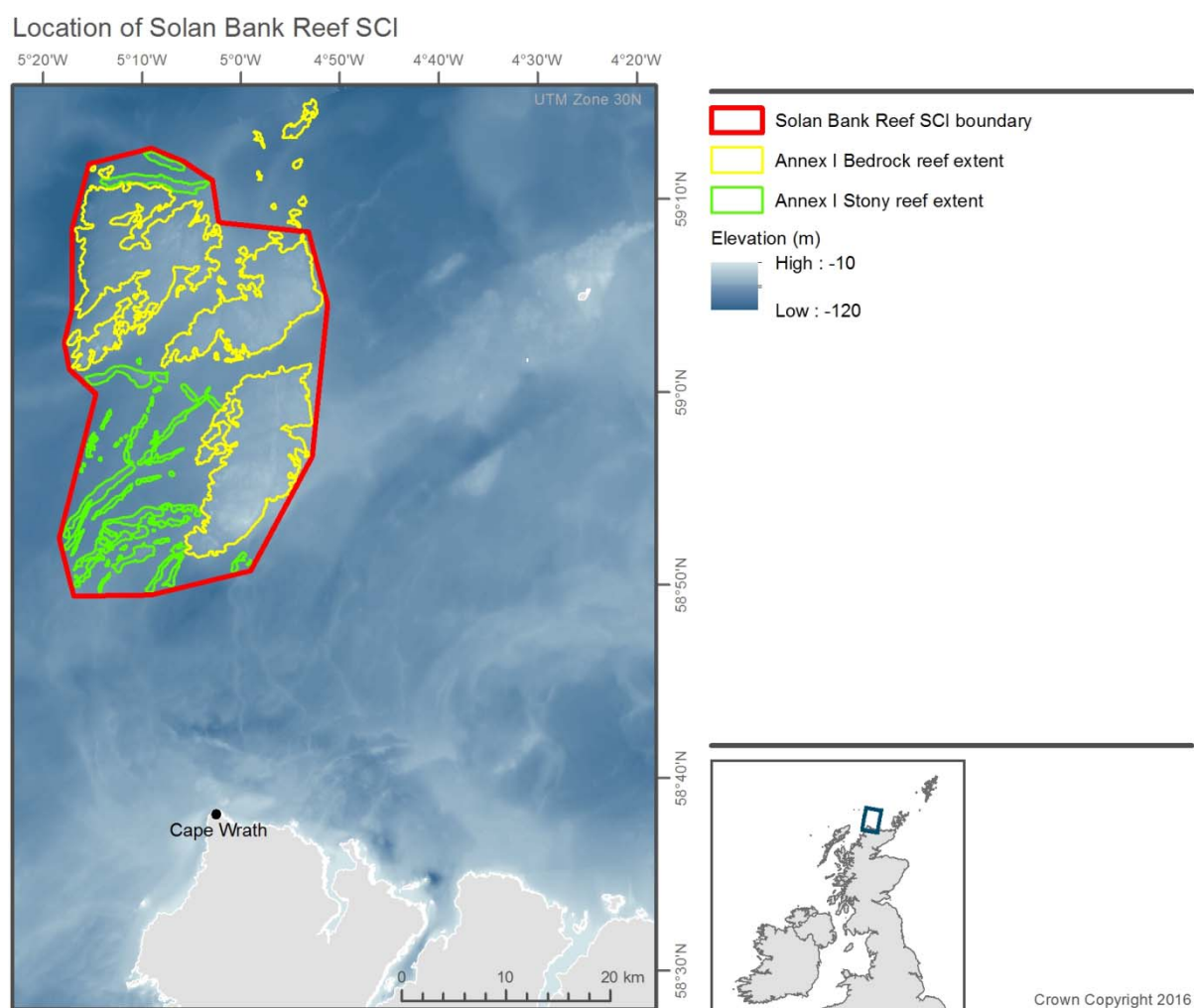
Figure 1. Location of the Solan Bank Reef SCI and extent of Annex I reef features. Elevation layer is from Defra's Digital Elevation Model (Astrium 2011).

Solan Bank Reef SCI contains two types of Annex I reef habitat, namely 'bedrock reef' and 'stony reef'. The exposed bedrock reef provides an underwater landscape of sea cliffs, reaching around 10m in height, as well as smoother, undulating rock features created by moving glacial ice. Stony reef, comprised of boulders and cobbles with a sandy veneer and

likely to be glacial in origin, occurs in ridges to the northwest and southwest of the site. Boulders and cobbles also occur in the larger crevices in the bedrock whilst smaller fissures in the bedrock are infilled with a mixture of coarse sand, shell and gravel. A veneer of sand is present over some flat bedrock surfaces, indicating that sediment movement and scour can be of influence on the resident benthic communities across the site. Most of the site lies within a shallow depth range of 60m to 80m below sea level, with extremes in the southeast (20m) and in the north of the site (>90m) (JNCC 2012).

Unsedimented reef features are largely characterised by encrusting organisms, particularly bryozoans, keel worms and encrusting coralline red algae in brighter shallower areas. Areas of low relief bedrock reef in the circalittoral zone show signs of being affected by sediment scour, with a much lower number of organisms present than in other areas. The number and variety of organisms increases in areas where exposure to scour is lower, and include bryozoans, anemones, corals, sponges, brittlestars, starfish, sea urchins and foliose red algae in shallower areas (Whomersley *et al* 2010).

The Solan Bank Reef SCI has been the subject of several scientific investigations, the most recent dedicated surveys taking place in May 2008 (Whomersley *et al* 2008; 2010) and in October and November 2014 (O'Connor 2014). The purpose of the primarily biological survey conducted in 2014 – undertaken by the Joint Nature Conservation Committee and Marine Scotland Science – was to gather data to enable the testing and evaluation of proposed supporting indicators for the determination of shallow sublittoral rock habitat status (see Haynes *et al* 2014). Developing such indicators forms part of the UK's obligations under the EC Marine Strategy Framework Directive (MSFD) to assess and achieve Good Environmental Status (GES) by 2020. Supporting indicators will ultimately enable the assessment of the MSFD Descriptor 1: Biodiversity, and the maintenance thereof.

The present investigation uses the various datasets collected during the 2014 survey, together with available pre-existing datasets pertinent to the investigation, to characterise the epibenthic assemblages inhabiting the different types of Annex I reef habitat present within the Solan Bank Reef SCI, and to ascertain what physical or environmental factors may be influencing any observed pattern in the epibenthic assemblage. In addition, patterns in the epibenthic assemblage are explored using various subsets of the acquired data, including information on sponge morphology, to test the effectiveness of proposed supporting indicators for the assessment of GES. In doing this, an assessment is made of the suitability of the various datasets collected during the 2014 survey (limitations and advantages) that facilitate the application and development of selected supporting indicators, with a view to recommending which datasets are most useful for future assessments of GES.

2 Sample acquisition and data extraction

The 2014 dedicated survey of the Solan Bank Reef SCI was conducted by experts from JNCC and Marine Scotland Science aboard the *MRV Scotia*. The main purpose of the survey was to gather high resolution underwater video and still images of the epibenthos, together with associated environmental data, for use in the evaluation of proposed supporting indicators for the determination of shallow sublittoral rock habitat status. Details of the survey rationale and methodologies employed are presented in the 1714S Solan Bank Reef SCI Survey Cruise Report (O'Connor 2015). A brief description of the data acquisition methodologies adopted during that survey is presented in Sections 2.1 and 2.2 (below).

Acquired video and photographic samples were processed for the extraction of epibenthic data by Marine Ecological Solutions Ltd. The identity and quantity of organisms was recorded for each sample (video and stills), together with information on seabed substrate, all of which followed standardised protocols for the consistent recording of such data types. Details of the data extraction protocols for video and photographic still samples are presented in the dedicated report produced by the subcontractor (Goudge *et al* 2016). An outline of the methods used for the extraction of epibenthic data from the acquired samples is provided in Section 2.3 (below).

2.1 Survey design

A combination of targeted and random-stratified biological sampling was undertaken to: (i) increase the likelihood of encountering assemblages characterised by sponges, and (ii) to enable a statistically significant assessment of the sponge and associated epibenthic assemblages observed. Sampling stations were stratified by substrate (bedrock reef, stony reef, not reef) and by fishing pressure (high and low fishing activity). Environmental variables, such as water temperature, pressure, salinity, turbidity and chlorophyll concentration, were recorded through the water column at each sampling station, and continuously at the sea surface from the survey platform. Current speed and direction at various depth intervals throughout the water column was also measured at three locations.

2.2 Sample and data acquisition

Underwater video footage and still photographs were captured successfully at 166 sampling stations using drop-frame mounted high-definition cameras. Video footage was recorded continuously throughout each 10-minute transect at approximately 0.3 knots (covering approx. 150m), and still photographs were taken at 10-30sec intervals. Geographic coordinates were recorded throughout each video transect and every time a still photograph was taken. Video footage was of sufficient quality for further processing at 156 transects, and 1,696 out of 1,701 stills acquired from all 166 transects were suitable for processing.

A drop-frame mounted CTD logger, chlorophyll fluorometer and beam transmissometer recorded environmental variables at each sampling station. A vessel-mounted Acoustic Doppler Current Profiler (ADCP) was used to measure seafloor current direction and speed

for a period of >13h at three locations. Full technical specifications and operational methodology for all equipment used is presented in O'Connor (2015). Details on which environmental variables were used in subsequent analyses are given Section 3.4 (below).

2.3   Sample and data processing

Video and still image processing for the extraction of data was conducted in three steps: (i) where necessary, splitting the video footage within a transect into markedly distinct habitat types based on seabed substrate characteristics, (ii) recording the identity and quantity of organisms present within each still photograph, together with substrate composition, and (iii) recording the identity and quantity of organisms observed within each habitat type observed on the video transect. Quality assurance and quality control procedures were applied during the data extraction process, noting where necessary any uncertainty in the quality or reliability of the information being recorded.

In addition to recording the taxonomic identity of observed organisms to the highest possible taxonomic resolution afforded by the sample, sponges were classified further based on their gross morphology following the categories defined by Bell and Barnes (2001; after Boury-Esnault and Rützler (1997)). Gross sponge morphologies were classified and coded as follows: Encrusting (EN), Massive (MA), Globular (GL), Pedunculate (PE), Tubular (TU), Flabellate (FL), Repent (RE), Arborescent (AR) and Papillate (PA) (Figure 2). Post-processing, an additional category of Undefined (UN) was used where gross morphology was indeterminable or where the morphology had not been noted by the sample processor.
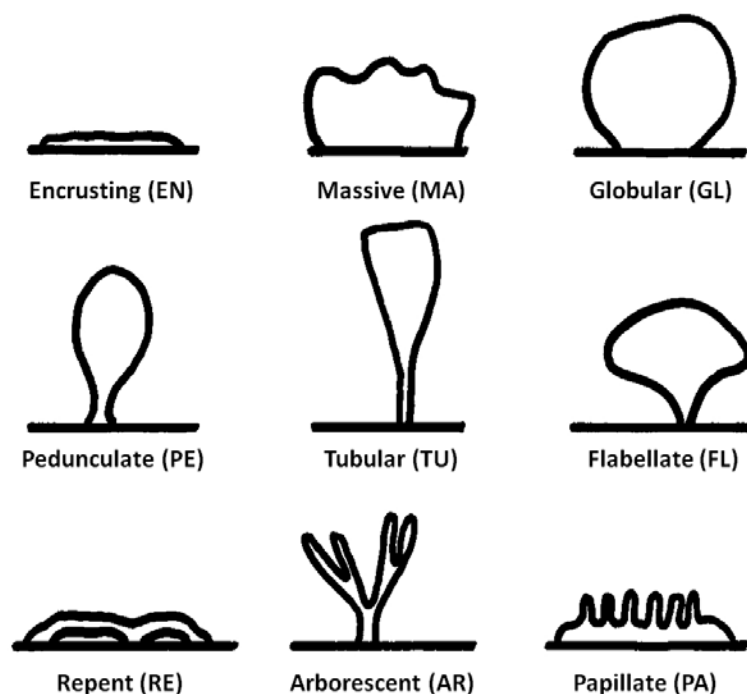
Figure 2. Nine morphological categories into which sponges were classified (from Bell and Barnes, 2001). Unclassified sponge records, or sponges exhibiting an indeterminate morphology were classified as Undefined (UN).

Any evidence of human activity, such as trawl marks or fishing gear, was also recorded. For a detailed description of the sample processing protocol see Goudge *et al* (2016).

3 Data preparation and analysis

Raw epibenthic data extracted from the processing of video footage and still photographs were made available to this investigation as MS Excel spreadsheets, containing taxon-by-sample matrices; individual samples being either photographic stills or distinct habitats identified from video transects. Additional matrices captured the physical attributes of each sample (substrate composition), as well as any other classification applied by the sample processor (e.g. by biotope, reef type, reef elevation, sample quality).

The quantity of each identified taxon within a sample was captured either as the number of individuals or discrete colonies observed (i.e. abundance), or as an indication of percentage cover across the seabed in the field of view. The latter approach is usually applied to gregarious or colonial taxa that cannot easily be discriminated into individuals or counted (e.g. barnacle and hydroid aggregations, encrusting sponges and bryozoans). However, it was noted during the data preparation stage (prior to analyses) that the quantity of several taxa was recorded inconsistently using a combination of both approaches, irrespective of whether the taxa were solitary or colonial. Presumably, this was an unavoidable consequence of having several sample processors working independently on the acquired samples, each making decisions in isolation that most easily overcame any difficulty in quantifying certain taxa in samples of sub-optimum quality. The extent of such inconsistency was such that, to exclude those taxa from subsequent analyses would severely compromise the results of the investigation by significantly reducing the number of taxa available to inform any assessment of biodiversity. Similarly, to select/reject one over another format of taxon quantity (abundance or percentage cover) would also artificially alter the pattern in taxon distribution across the entire site, potentially leading to a skewed picture of epibenthic assemblage composition and distribution. Categorical information on taxon quantity recorded using the SACFOR scale[1] is not considered suitable for quantitative analyses.

Because the merging of abundance data with percentage cover data to a common scale of taxon quantity was, in this instance, practically not possible[2], a decision was made to reduce all taxon quantity data to a record of taxon presence or absence. Such a decision does not come without consequences for the future use of certain analytical tools, however, in light of the inconsistencies encountered in the capture of taxon quantity, the availability of a complete taxon list is considered to outweigh the benefits of conducting taxon abundance-dependent analyses with a considerably and arbitrarily reduced complement of taxa.

Where possible, spatially resolved physical and environmental data were extracted for each sample location from the various formats in which they were made available to this investigation. Complementary physical, environmental and biological data records per

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[1] SACFOR stands for the categories Superabundant, Abundant, Common, Frequent, Occasional and Rare.
[2] Consideration was given to normalising both the abundance and percentage cover records of all taxa (to a relative abundance scale between 0 and 1) by dividing each record of a taxon by the total number/coverage of that taxon across all samples. However, as mentioned, some taxa were recorded both as counts and as percentage cover values, making the summing of values for any one taxon across all samples invalid. In addition, the variation in percentage cover values across some taxa recorded consistently on that scale ranged from 0.01% to >>100%, rendering any range of normalised values grossly unbalanced. Similarly, some abundance values for some taxa were recorded with decimal places (i.e., fractions of individuals), thus casting doubt over the accuracy of the enumeration procedure.

sample have been used in the assessment of correlation between them, to ascertain which environmental variables most greatly influence observed differences in the composition and distribution of the epibenthic assemblage. Further detail on the analyses performed is presented in Section 3.4 and thereafter.

3.1   Data truncation

It is inevitable that all raw taxon recording datasets contain inconsistencies introduced through human error and uncertainty, especially those generated by the collected efforts of several workers. To minimise the influence of such inconsistencies on subsequent ecological analyses, a data truncation exercise is necessary to identify, reduce and neutralise as best as possible such artefacts in the data. Data truncation usually involves the identification of spurious entries into a dataset, by spotting differences or mistakes in the spelling of a taxon's name, instances where taxonomic uncertainty may record the same taxon at different levels in the taxonomic hierarchy or where unorthodox criteria have been used to differentiate taxa, and instances where evidence unusable in analyses, such as taxon fragments, eggs, tubes, tracks or burrows may have been recorded.

A data truncation protocol developed and refined by the author has been applied to both epibenthic data matrices available to the investigation, i.e. the taxon-by-sample matrix extracted from the processing of still photographs, and a similar matrix extracted from the processing of the video footage. A step-by-step guide to the decisions applied during the data truncation process is presented in Appendix 1. The data truncation process reduced the stills-derived raw dataset from 384 entries to 207 accepted taxa, and the video-derived raw dataset from 297 entries to 152 accepted taxa. It is worth noting that the objective of the truncation process is to discard as little information as possible, so any reduction in entries to a dataset is usually a result of the judicious merging of 'conspecific' entries and adding together the recorded abundance values of those merged entries. Only entries that are clearly spurious within an epibenthic dataset are discarded (e.g. fragments, eggs, inert or obviously uninhabited biogenic structures, planktonic taxa).

3.2   Data partitioning

Taxa recorded from stills samples, and those recorded from video samples have been kept separate throughout the analyses, to ascertain whether the same patterns in epibenthic assemblage composition and distribution are evident across both datasets. If the same ecological patterns are detected using both datasets, there may be a case for favouring one approach to data collection over the other in the future, should one be deemed more efficient or less costly or labour-intensive.

As well as conducting all analyses on the full complement of taxa recorded by each sampling technique (stills and video), analyses have been conducted on subsets of taxa (Table 1). The first subset included all epibenthic taxa, but all sponge taxa were reclassified according to their morphology (see Figure 2). A second subset of data excluded sponges all together. A third subset consisted only of sponges classified to the highest possible taxonomic

resolution (after truncation), followed by that same subset reclassified by morphology (Figure 2). A further subset considered all sponge and anthozoan taxa (corals, anemones, sea fans, and sea pens). The final subset consisted of sponge morphology classes and anthozoan taxa. The rationale for analysing different subsets of the data was to compare the utility of selected supporting indicators for detecting natural variation in epibenthic assemblages (Table 2).

Table 1. Comparison of the number of taxa present in different subsets of the datasets extracted from the analysis of photographic stills and from video footage.

Taxon subset	Taxa from photographs	Taxa from video
All taxa	207	152
All taxa, sponge morphs	191	144
All taxa, no sponges	181	135
Sponges & anthozoa	50	31
Sponges	26	17
Sponge morphs & anthozoa	34	23
Sponge morphs	10	9

The original specification of analyses for the present investigation included the calculation of relevant diversity indices and selected supporting indicators, principally Indicator 2 (SpongeMorphAntho). However, given the discrepancies in the recording of taxon quantity from camera-acquired samples (described above), and the unavoidable decision to forfeit taxon quantity data, many diversity indices and indicators that require such data for their calculation could not be used. Nonetheless, the number and variety of taxa per sample remains a powerful and versatile metric with which to analyse and compare epibenthic diversity, assemblage composition and distribution across the study area. The number of taxa within each of the various data subsets can also go some way to informing the calculation of supporting indicators for the assessment of natural variation of epibenthos in shallow sublittoral rock habitats (Table 2).

Table 2. Proposed supporting indicators for the assessment of natural variation in shallow sublittoral rock habitats (from Haynes *et al* 2014).

Indicator	Code	Name	Sensitivity[a]
Indicator 1	SpongeAntho	Sublittoral species composition and abundance of fragile sponge and anthozoan assemblages	5
Indicator 2	SpongeMorphAntho	Morphological diversity of sponge assemblages plus anthozoan species composition and abundance	4
Indicator 3	SpongeMorphAntho-SpongePresAb	Morphological diversity of sponge assemblages plus presence/absence of anthozoan indicator species	3
Indicator 4	SpongeAnthoPresAb	Presence/absence of sponge and anthozoan indicator species	2

[a] Sensitivity score range: 1-5; 5 = high, 1 = low

Data extracted from samples targeted specifically at particular substrate types (e.g. rocky reef, stony reef, not reef) have also been explored in isolation, in an attempt to reduce potential 'noise' in the whole dataset that may obscure any underlying pattern in epibenthic assemblage structure or distribution within each substrate type.

3.3   Univariate analyses

Values of observed number of taxa per sample have been used to compare the mean number of taxa per sample across a number of treatment classes. Treatment classes were either defined prior to the samples being taken (e.g. the stratified sampling boxes targeting different substrate types or degrees of fishing activity), or defined *a posteriori* based on classifications of each sample applied by the sample processors. The various processor-defined treatment classes compared are listed in Table 3. One-way analysis of variance (ANOVA) tests have been performed to determine whether the mean number of taxa values differ significantly between selected treatment classes. Where appropriate, *post-hoc* pairwise comparison tests were performed to ascertain which mean values per treatment class were different from each other. ANOVA and *post-hoc* tests were performed using the Minitab 17 software package. Graphical representations of the results from selected comparisons have been created in MS Excel.

Table 3. Treatment classes into which all samples have been grouped for the purpose of comparison of the epibenthic assemblage across classes.

Annex I reef type[a]	Reef elevation	MNCR biotope[b]
None	N/A	CR.MCR.EcCr
Stony-Low confidence	<64 mm	SS.SCS.CCS
Stony-Medium confidence	64 mm-1 m	SS.SMx.CMx
Stony-High confidence	1.1 m-5 m	CR.MCR.EcCr/SS.SCS.CCS (stills only)
Bedrock-confirmed	5.1 m-10 m	
Bedrock-potential	Unknown	

[a] Confidence levels applied by sample processor (see Goudge et al. (2016) for explanation).
[b] Biotope code key: CR.MCR.EcCr = Echinoderms and crustose communities on moderate energy circalittoral rock; SS.SCS.CCS = Circalittoral coarse sediment; SS.SMx.CMx = Circalittoral mixed sediment; CR.MCR.EcCr/SS.SCS.CCS = a hybrid of constituent biotopes at a small spatial scale.

3.4   Multivariate analyses

Multivariate analyses, which take into account the identity of taxa and their distribution across the dataset, have been conducted on the various data subsets using the Primer 6 software package (Clarke and Gorley 2006). Analysis of similarity tests (ANOSIM; using the Bray-Curtis similarity index) have been performed to ascertain whether there is a significant difference in assemblage composition between the various treatment classes, defined both before and after sample acquisition (see Section 3.3, and Table 3). Where significant differences between treatment classes are observed, the SIMPER routine has been used to identify the taxa which most contributed to the similarity within each class. Clustering techniques (MDS, CLUSTER and SIMPROF routines) have been applied to detect any pattern within the datasets that may not be explained by the classification of the samples into treatment classes. PCA, RELATE and BIOENV/BEST routines have been performed to ascertain the influence of the measured and modelled environmental variables on the epibenthic assemblage. Further detail on the exact specifications of the routines applied, and the significance of their outputs is provided in context under Section 4.

Datasets of environmental variables available to the present investigation for analysis are listed in Table 4.

Table 4. Environmental datasets available to the present investigation.

Metric	Resolution	Source
Substrate composition (% cover)	By still & by video habitat	Image processing - JNCC (2015)
Seabed water temperature (˚C)	By sample site at SOL[a]	CTD - JNCC/MSS (2014)
Seabed chlorophyll concentration (ug/l)	By sample site at SOL[a]	CTD - JNCC/MSS (2014)
Water depth (m)	By sample site at SOL[a]	CTD - JNCC/MSS (2014)
Current direction & speed	3 locations	ADCP - JNCC/MSS (2014)
Slope[b]	By video habitat at centroid	DEM - Astrium (2011)
Bed shear stress (N/m^2)	By video habitat at centroid	Modelled - this investigation
Current velocity (m/s)	By video habitat at centroid	Modelled - this investigation
Exposure to tidal current	By video habitat at centroid	Modelled - this investigation

[a] SOL = start of line/transect
[b] Expressed as Hilliness when combined with exposure to current direction and speed in certain analyses.

3.5   Generation of modelled environmental data layers

Mean and maximum tidal current velocity values at the seabed, bed shear stress and exposure to the tidal current were obtained from a hydrodynamic model built for the study area. The depth-averaged model was built using an unstructured triangular mesh, using the hydrodynamic software Telemac2D (v6p3). The model mesh has a resolution of approximately 1km along the open boundary, whilst in the area of interest a regular triangular grid was used with a resolution of approximately 100m x 200m. Bathymetry for the area was sourced from the Defra Digital Elevation Model (DEM; Astrium 2011). The model was run for 30 days to cover a full spring-neap cycle, with a model spin-up period of five days. The resolution of extracted data layers is 1 arc second (~30m). Bed shear stress was calculated according to the methodology of Soulsby (1997) based on current speed and local sediment characteristics extracted from video and still samples. An index value for exposure to tidal current was calculated based on the orientation of the main slope in relation to the main flood tide current direction (values: 1 = slope is directly facing the current, 0.5 = slope perpendicular to the current and 0 = slope in the direction of current).

4   Results and interpretation

Given the rigorous rationale applied at the survey planning stage of this investigation (see O'Connor 2015), statistical comparisons have been performed between samples grouped into categories defined before any of the samples were taken. These include comparisons between different *targeted* substrate types (habitats) and between areas of high and low fishing activity on bedrock reef (Section 4.1). The benefits and drawbacks of conducting such comparisons are also presented. Further comparisons have been conducted between samples grouped into categories resulting from the processing of the samples, such as *observed* substrate type, reef elevation and recorded biotope (Section 4.2). Correlations between the results observed from the analysis of the various subsets of epibenthic data are investigated (Section 4.3). Epibenthic assemblage structure and composition analyses have been performed, as well as tests to investigate which of the measured physical and environmental variables may have influenced any pattern observed in the epibenthic assemblage (Section 4.4).

4.1   Tests between predefined sample categories

At the survey planning stage, sampling stations were chosen to represent different habitats or different levels of fishing pressure based on available information. Univariate (ANOVA) and multivariate (ANOSIM) tests have been performed on groups of samples belonging to each predefined category.

4.1.1   Target habitat

Three habitats were targeted during the 2014 dedicated survey: bedrock reef, stony reef, not reef. However, practical constraints on the precise positioning of the survey vessel during survey meant that not all intended targets were hit with the sampler, resulting in the pre-survey classification of samples to be inaccurate. To overcome this, all the actual sampling locations have been reclassified based on whether they fall within or outside the polygons representing Annex I bedrock reef and Annex I stony reef (see Figure 1). Those same polygons were used at the survey planning stage to allocate each sample to its target habitat.

Table 5 presents a summary of the results from ANOVA and ANOSIM tests on the various data subsets compared. Where a statistically significant result is attained, the results from pairwise comparisons between different treatment classes are presented in Appendix 2.

Results from the analysis of stills-derived data reveal that significant differences exist in the mean number of taxa per still (including and excluding sponges) between target habitat types. Multivariate analyses of those same data reveal that epibenthic assemblage composition is also different between target habitat types. As the variables in the datasets are reduced (by analysing only sponge and anthozoan taxa or just sponges at different levels of classification), the difference in the mean number of taxa per still across habitats is no longer always evident. Caution must be exercised when interpreting the statistical significance of tests using subsets of data with a limited number of variables (taxa) across

such a large sample size (1,696 stills), as the number of taxa in any one sample is likely to be very low, with a high proportion of zero values, and the variability across samples very high, thus stretching the assumptions of the models on which the statistical tests are based. There is also the added complication that the habitat type into which the sample has been classified (prior to sampling) does not correspond with the substrate actually sampled (due to small-scale heterogeneity within each habitat), further increasing the variability in the number and identity of taxa recorded in any one of the predefined habitat types.

Table 5. Summary of results from univariate and multivariate comparisons between target habitat categories for different subsets of the epibenthic dataset.

Data subset	Univariate		Multivariate	
	ANOVA P-value	Sig.[a]	ANOSIM R-value	Sig.[a]
From stills (n = 1,696)				
All taxa	0.000	✓	0.203	✓
All taxa, sponge morphs	0.000	✓	0.204	✓
All taxa, no sponges	0.000	✓	0.203	✓
Sponges & anthozoa	0.397	✗	0.110	✓
Sponges	0.180	✗	0.015	✗
Sponge morphs & anthozoa	0.621	✗	0.111	✓
Sponge morphs	0.005	✓	0.012	✗
From video segments (n = 278)				
All taxa	0.182	✗	0.220	✓
All taxa, sponge morphs	0.186	✗	0.220	✓
All taxa, no sponges	0.053	✗(✓)	0.268	✓
Sponges & anthozoa	0.000	✓	0.075	✓(✗)
Sponges	0.000	✓	-0.085	✗
Sponge morphs & anthozoa	0.081	✗	0.070	✓(✗)
Sponge morphs	0.000	✓	-0.100	✗

[a] Strict statistical significance (α = 0.05) as reported by test, interpreted significance (i.e. where a strict interpretation of the test result may be ambiguous and an alternative interpretation is probable) is given in parentheses.

Results from the analysis of the data extracted from video samples must also be treated with caution when comparing predefined target habitat categories. The rationale for treating processor-defined video segments as samples, and not whole transects, is to reduce the 'noise' in the data should a transect include more than one habitat type. This makes more sense in later analyses, but here the variability of observed habitats within any one predefined habitat class remains (i.e. a segment of video observed to be sedimentary but taken from a bedrock target habitat is still sedimentary and is likely to host more sediment-dwelling taxa than bedrock, and vice versa). Thus, 'noise' in the dataset remains high, potentially obscuring or distorting any pattern in the data. An additional complication arising from the use of processor-defined video segments as samples is that sample size is not consistent across samples (unlike stills, in which the field of view of the camera remains relatively constant across stills), and there are far fewer video samples representing each habitat type over which such inconsistencies can be 'smoothed out'. There are entire transects which constitute a single sample (equivalent to the highest level of sampling effort per transect), and transects that have been subdivided into several segments based on broad-scale substrate type (effectively reducing the sampling effort per segment/sample in

proportion to the length of the segment – the sampling effort per transect has remained roughly equal across all transects). The resultant inconsistency in sampling effort across samples can lead to a distortion of the pattern observed across target habitats.

Artefacts in the dataset such as those just described may be behind the pattern observed in the analysis of video-derived data (Table 5). When the mean number of all taxa per video sample is compared across target habitat type, no discernible difference is apparent, perhaps because each target habitat includes many of the taxa characteristic of other habitats that have been captured within the small-scale variability of each habitat. After a severe reduction in variables, however (by analysing a combination of sponges, anthozoa and sponge morphs), a significant difference in the mean number of these taxa per sample is observed. Pairwise comparisons (Appendix 2, Section A2.1) indicate that such a difference is evident between reef and not reef target habitats (reef habitats hosting a larger mean number of sponges and anthozoa than non-reef habitat), but not between bedrock and stony reef habitats. Multivariate analyses (ANOSIM) do appear to have identified a difference in assemblage composition between target habitats, but only reliably using the data subsets with the largest number of variables (taxa). Such seemingly contradictory results only serve to underline the caution that must be taken when comparing and interpreting pattern across predefined habitat categories.

4.1.2 Fishing activity

Three treatment classes have been compared, all of which occurring on bedrock reef: Mobile gear-high activity, Static gear-high activity, Mobile and static gear-low activity. Results are presented in Table 6.

Table 6. Summary of results from univariate and multivariate comparisons between fishing activity categories for different subsets of the epibenthic dataset.

	Univariate		Multivariate	
Data subset	ANOVA P-value	Sig.[a]	ANOSIM R-value	Sig.[a]
From stills (n = 1,696)				
All taxa	0.000	✓	0.110	✓
All taxa, sponge morphs	0.000	✓	0.111	✓
All taxa, no sponges	0.000	✓	0.113	✓
Sponges & anthozoa	0.000	✓	0.053	✓(✗)
Sponges	0.000	✓	-0.004	✗
Sponge morphs & anthozoa	0.000	✓	0.054	✓(✗)
Sponge morphs	0.000	✓	-0.005	✗
From video segments (n = 278)				
All taxa	0.082	✗	0.162	✓
All taxa, sponge morphs	0.083	✗	0.168	✓
All taxa, no sponges	0.097	✗	0.179	✓
Sponges & anthozoa	0.014	✓	0.168	✓
Sponges	0.002	✓	-0.036	✗
Sponge morphs & anthozoa	0.003	✓	0.187	✓
Sponge morphs	0.003	✓	-0.030	✗

[a] Strict statistical significance ($\alpha = 0.05$) as reported by test, interpreted significance given in parentheses.

All subsets of the epibenthic dataset extracted from stills appear to show significant differences in the mean number of taxa between fishing activity classes. Subsets of video-derived data containing most taxa do not show a difference in mean number of taxa between treatment classes, but subsets of data representing sponges with and without anthozoa do show a difference in mean number of taxa between classes. According to pairwise comparisons between treatment classes (see Appendix 2, Section A2.2), the greatest mean number of taxa was always recorded in the area classified as having a high activity of mobile fishing gear, and this is always significantly higher than the mean number of taxa recorded from the area classified as having higher activity static fishing gear. The area defined as having a low activity of both mobile and static fishing gears has an intermediate mean number of taxa, and is never significantly different from at least one of the other activity/gear classes. Most multivariate analyses reveal a significant difference in assemblage composition between treatment classes, the exception being sponge and anthozoan assemblages not appearing to be significantly different between both high activity classes (static and mobile gears).

Whilst these results are compelling and somewhat counterintuitive, a large degree of caution must be observed in their interpretation. Each treatment class, defined during survey planning, corresponds with a large, spatially discrete area of bedrock reef with no spatial or temporal overlap with any other treatment class (see O'Connor 2015). It is entirely possible (and highly likely) that the differences in epibenthic assemblage structure and composition revealed by the tests performed are greatly influenced by factors other than fishing activity and intensity. A greater confidence in results from such comparisons might be attained if each treatment class was nested within each of the three discrete bedrock reef blocks (if possible), thus reducing the possibility of spatial autocorrelation, environmental factors and biogeographic factors confounding any observed differences between treatment classes.

4.2   Tests between observed categories

The following comparisons have been performed between samples grouped into treatment classes based on the classification of samples during processing.

4.2.1 Annex I reef type

Samples have been grouped into six treatment classes: None (not reef), Stony-Low confidence, Stony-Medium confidence, Stony-High confidence, Bedrock-confirmed, Bedrock-potential. Results from univariate analyses reveal a significant difference in the mean number of taxa between some Annex I classes using all subsets of both the stills and video derived datasets (Table 7). Pairwise comparisons between treatment classes (Appendix 2, Section 2.3) indicate that the highest mean number of taxa per sample is most often observed in Bedrock-confirmed and Stony-High confidence classes. The lowest mean number of taxa per sample is always observed in the None (not reef) class. Most classes indicative of reef, be it stony or bedrock, are statistically indistinguishable from one another based on the mean number of taxa per sample. The fewer the taxa available for analysis (by working through the various subsets of data), the lesser the difference becomes between reef and non-reef classes.

Table 7. Summary of results from univariate and multivariate comparisons between observed reef categories for different subsets of the epibenthic dataset.

Data subset	Univariate		Multivariate	
	ANOVA P-value	Sig.[a]	ANOSIM R-value	Sig.[a]
From stills (n = 1,696)				
All taxa	0.000	✓	0.091	✓(✗)
All taxa, sponge morphs	0.000	✓	0.095	✓(✗)
All taxa, no sponges	0.000	✓	0.106	✓(✗)
Sponges & anthozoa	0.000	✓	0.003	✗
Sponges	0.030	✓	-0.006	✗
Sponge morphs & anthozoa	0.000	✓	0.005	✗
Sponge morphs	0.019	✓	-0.007	✗
From video segments (n = 278)				
All taxa	0.000	✓	0.125	✓
All taxa, sponge morphs	0.000	✓	0.126	✓
All taxa, no sponges	0.000	✓	0.121	✓
Sponges & anthozoa	0.008	✓	0.032	✓(✗)
Sponges	0.001	✓	0.040	✓(✗)
Sponge morphs & anthozoa	0.007	✓	0.030	✓(✗)
Sponge morphs	0.012	✓	0.036	✓(✗)

[a] Strict statistical significance ($\alpha = 0.05$) as reported by test, interpreted significance given in parentheses.

Figure 3 illustrates the difference in mean number of taxa per sample for each Annex I reef treatment class, using both the total number of taxa and only sponge morphs and anthozoa from the stills and the video datasets. Whilst much of the difference in pattern between treatment classes is maintained by the reduction in the number of taxa used for the comparison, the significance of the difference between classes is lost except for between the most extreme values (i.e. None (not reef) vs bedrock-confirmed). This is evident in both the stills derived dataset and the video derived dataset.

Results from multivariate analyses of stills-derived data are inconclusive, showing no overall difference in the composition of the epibenthic assemblage inhabiting each Annex I reef treatment class. The apparent statistical significance of some results (Table 7) is driven by the large number of samples compared, however, the associated ANOSIM R-values are too small to support any notion of significant differences between classes. Results from the analysis of video-derived data do appear to show a significant difference in assemblage composition between treatment classes when using subsets of the data that include most taxa. Pairwise comparison of treatment classes (Appendix 2, Section A2.3) reveals that the biggest difference in assemblage composition is between the classes Bedrock-confirmed and Bedrock-potential, Bedrock-confirmed and Stony-Medium, and between Bedrock-potential and Stony-Medium. Differences between all other class pairs are less evident, including between the extremes of 'reefiness' None (not reef) and Bedrock-confirmed. It is unclear why this is so, but it is possible that within any stretch of transect designated as a particular reef class, there are pockets of sediment that harbour taxa characteristic of non-reef habitats, thus contributing to the variability and diversity of taxa within the designated reef class. Results from the analysis of the smaller data subsets are less informative.
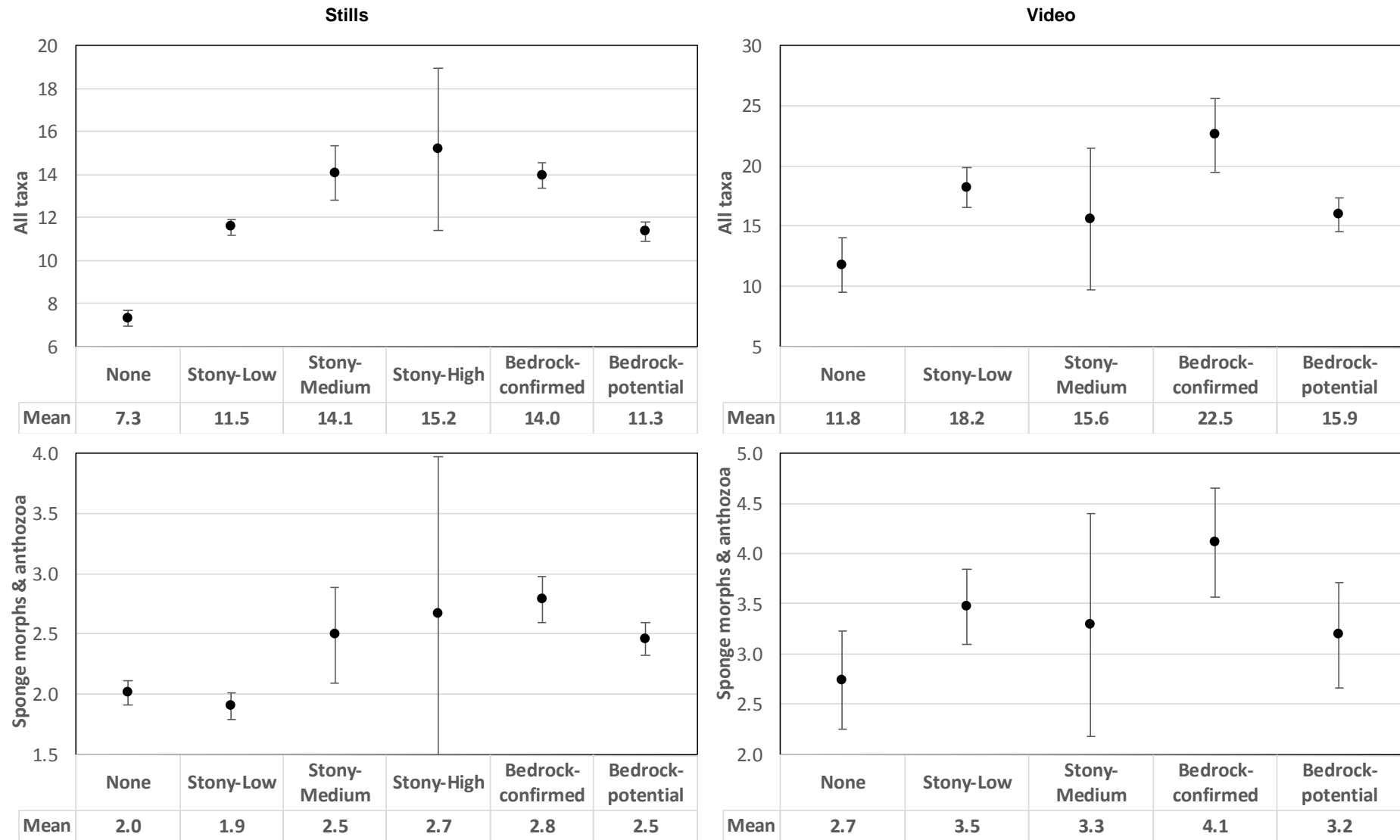
Figure 3. Mean number of taxa per sample (± 95% CI) within each Annex I reef treatment class. All taxa from stills and video samples (top row) and only sponge morphs & anthozoa taxa (bottom row).

The taxa characterising each of the assemblages that represent each treatment class are listed in Appendix 3, ranked by their overall contribution to the similarity within each treatment class. Whilst many taxa thought to be primarily reef or hard substrate dwellers are also found on the 'not reef' class, their contribution to the similarity within each class is generally higher in treatment classes representing reef. Encrusting bryozoa and annelids (Spirobranchus) are well represented in all treatment classes, however, echinoderms such as the common sun star (*Crossaster papposus*), brittle stars (Ophiurida), foliose red algae (Rhodophyta), anemones (*Urticina*), the soft coral known as dead man's fingers (*Alcyonium digitatum*), and most sponge taxa all contribute more highly to the similarity within reef classes than to non-reef habitat.

The distribution of video samples categorised by Annex I reef classes identified during sample processing is illustrated in Figure 4. Despite some overlap in the distribution of the various classes, bedrock reef is confined mostly to the areas delineated as Annex I bedrock reef (see Figure 1). Stony reef is much more widespread, interspersed with bedrock reef and within the areas delineated as Annex I stony reef (see Figure 1).
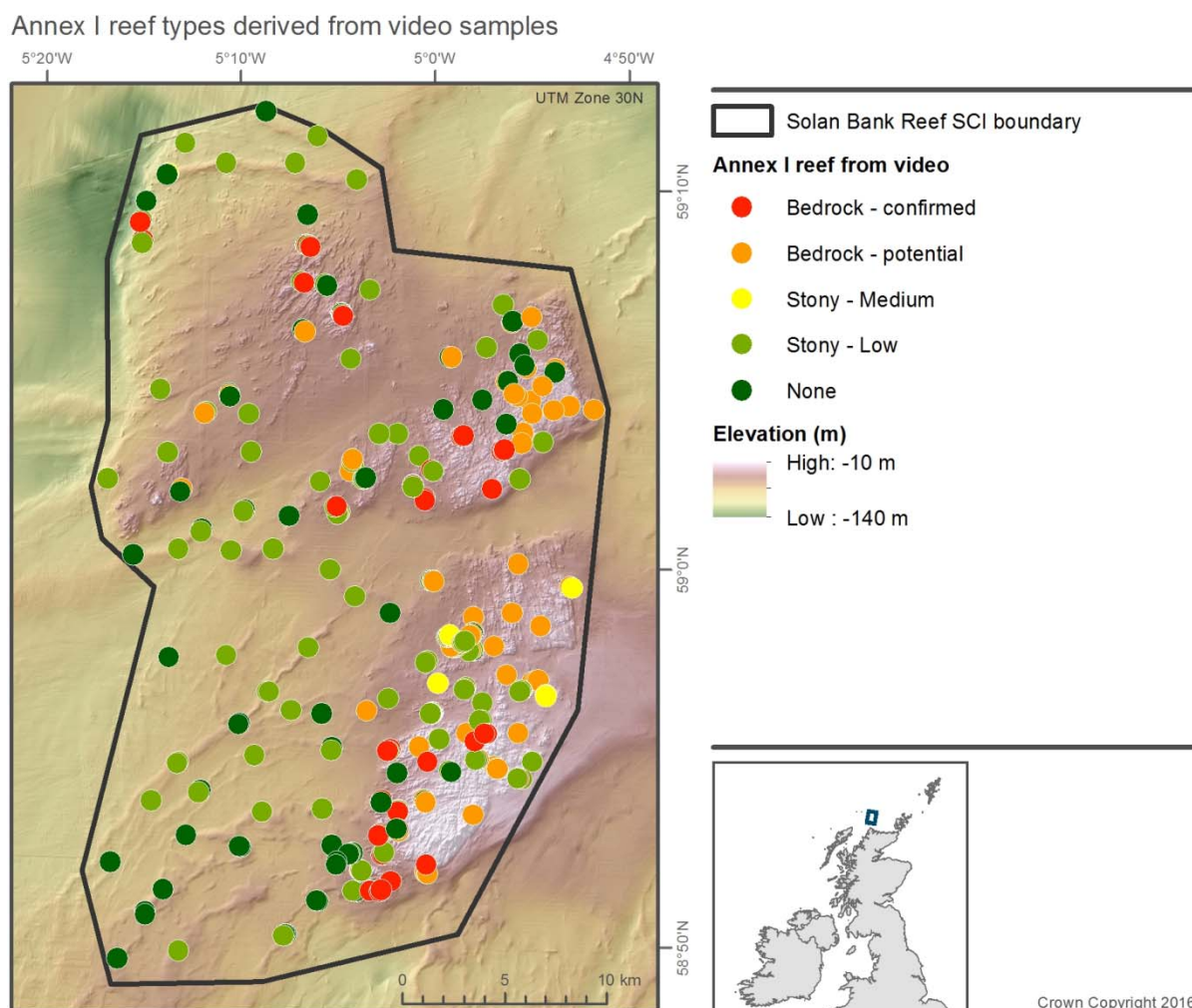
Figure 4. Distribution of Annex I reef types as derived from the analysis of video samples.

4.2.2 Reef elevation

Six treatment classes are compared: N/A (not reef), <64mm, 64mm-1m, 1.1m-5m, 5.1m-10m, unknown. Univariate tests on all subsets of data (except for sponges and their morphs from stills) reveal significant differences in the mean number of taxa per sample between reef elevation classes (Table 8). Comparisons between pairs of classes (see Appendix 2, Section A2.4) show that when most taxa are used, the N/A class (not reef) is significantly different to all the other classes, and any one distinct group of classes with a statistically similar number of taxa shares at least one class with another distinct group of classes. In other words, no reef elevation class (other than 'not reef') is unique or statistically distinct in terms of its mean number of taxa, and this is evident when using most subsets of the dataset. All subsets of data derived from the video samples also show a similar pattern, and not even the N/A (not reef) class appears to have a significantly different mean number of taxa to other classes.

Table 8. Summary of results from univariate and multivariate comparisons between observed reef elevation categories for different subsets of the epibenthic dataset.

Data subset	Univariate		Multivariate	
	ANOVA P-value	Sig.[a]	ANOSIM R-value	Sig.[a]
From stills (n = 1,696)				
All taxa	0.000	✓	0.096	✓(✗)
All taxa, sponge morphs	0.000	✓	0.099	✓(✗)
All taxa, no sponges	0.000	✓	0.112	✓
Sponges & anthozoa	0.000	✓	0.008	✗
Sponges	0.137	✗	-0.010	✗
Sponge morphs & anthozoa	0.000	✓	0.010	✓(✗)
Sponge morphs	0.173	✗	-0.011	✗
From video segments (n = 278)				
All taxa	0.000	✓	0.149	✓
All taxa, sponge morphs	0.000	✓	0.150	✓
All taxa, no sponges	0.000	✓	0.135	✓
Sponges & anthozoa	0.000	✓	0.097	✓(✗)
Sponges	0.000	✓	0.057	✓(✗)
Sponge morphs & anthozoa	0.000	✓	0.098	✓(✗)
Sponge morphs	0.000	✓	0.058	✓(✗)

[a] Strict statistical significance (α = 0.05) as reported by test, interpreted significance given in parentheses.

Figure 5 5 illustrates the differences and similarities of mean taxon number between reef elevation classes using the full complement of taxa and just the sponge morphs and anthozoa subset, from both stills and video samples. In general terms, the higher the elevation of the reef, the higher the mean number of taxa the reef can accommodate, regardless of whether this is significantly different to other elevation classes or not. Such a generalised pattern is also evident when analysing sponge morphs and anthozoa alone. As expected, statistical differentiation between reef elevation classes is compromised as the number of variables is reduced for comparison (from all taxa to sponge morphs and anthozoa, and from stills to video derived data).

Only the results from the multivariate analysis of all stills-derived taxa excluding sponges showed any noteworthy pattern (Table 8). The ANOSIM R-value across all reef elevation classes is relatively low, but comparisons between pairs of classes (Appendix 2, Section A2.4) reveal that the greatest difference in epibenthic assemblage composition is between classes near the extremes of reef elevation (<64mm vs 5.1m – 10m, and unknown vs all reef elevation classes except N/A). This would suggest that the unknown class assemblage is more similar to N/A (not reef) and <64mm assemblage than to any assemblage from any other class of higher elevation, yet it shares some epibenthic taxa with most reef elevation classes. Sponges, however, are not responsible for such differences or similarities. Analyses on video-derived data showed a similar pattern in assemblage composition across reef elevation classes, and similar differences with the N/A (not reef) class, with and without the exclusion of sponges from the analysis.

Taxa characterising each of the reef elevation classes, as revealed by SIMPER routines, are listed in Appendix 3, Section 3.2. As reef elevation increases, the contribution of taxa to the similarity within each elevation class shifts from hydrozoa, encrusting bryozoa and serpulid worms at the lesser elevations, to encrusting red algae (Corallinaceae), sponges of all morphologies, brittle stars (Ophiuroidea), cup corals (*Caryophillia*), jewel anemones (*Corynactis viridis*) and other stalked anemones (*Urticina*, *Stomphia coccinea*), at higher elevations. The combination of taxa contributing the most to the similarity within the unknown reef elevation class most strongly resembles that of the lower elevation classes N/A and <64mm.

Reef elevation, as recorded from the processing of video samples, appears greatest within the areas delineated as Annex I bedrock reef (Figure 6), although much of the reef within those same areas is also under 1m tall. Stony reef samples identified within the area delineated as Annex I stony reef rarely protrude 5m above the surrounding seabed.
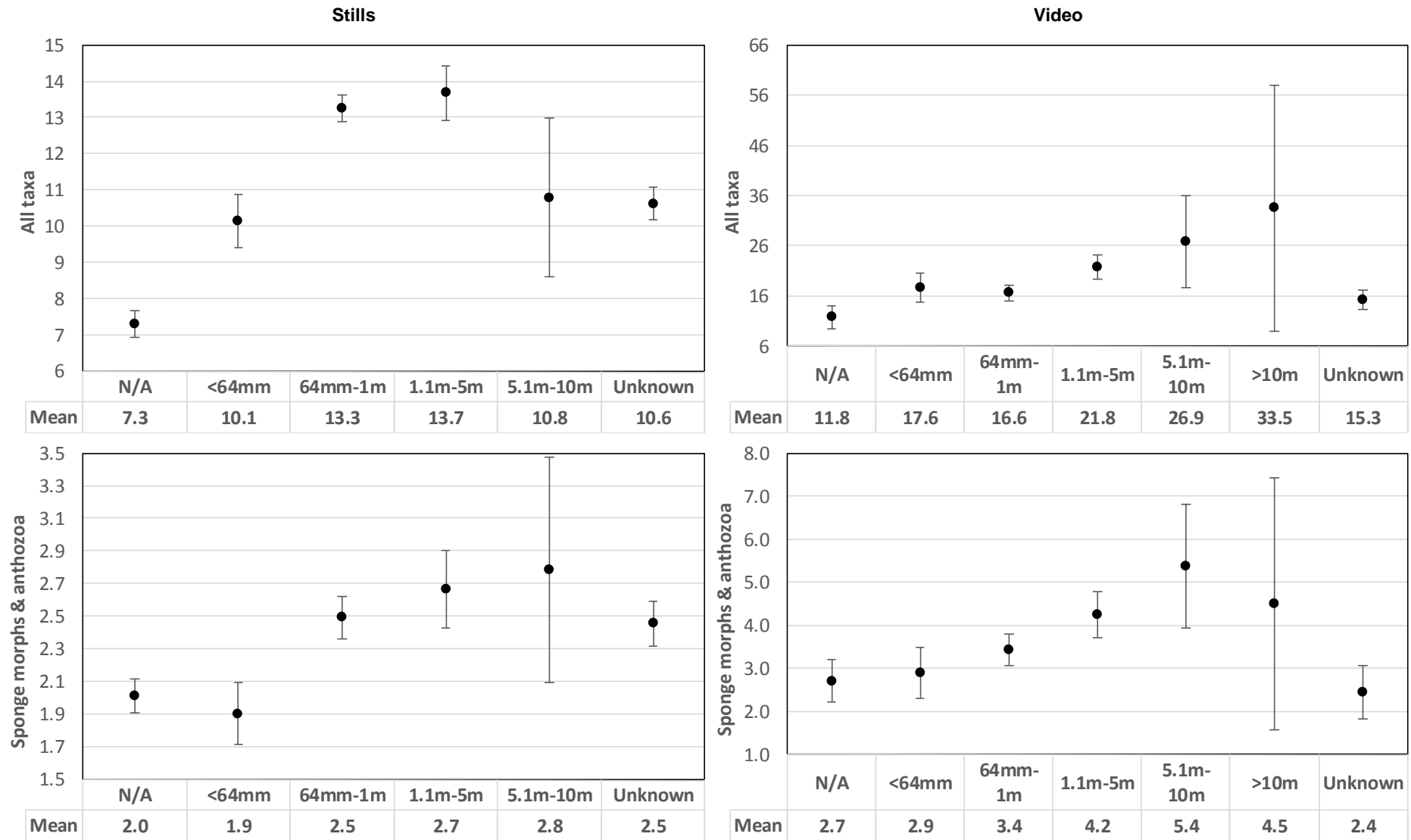
Figure 5. Mean number of taxa per sample (± 95% CI) within each reef elevation treatment class. All taxa from stills and video samples (top row) and only sponge morphs & anthozoa taxa (bottom row).
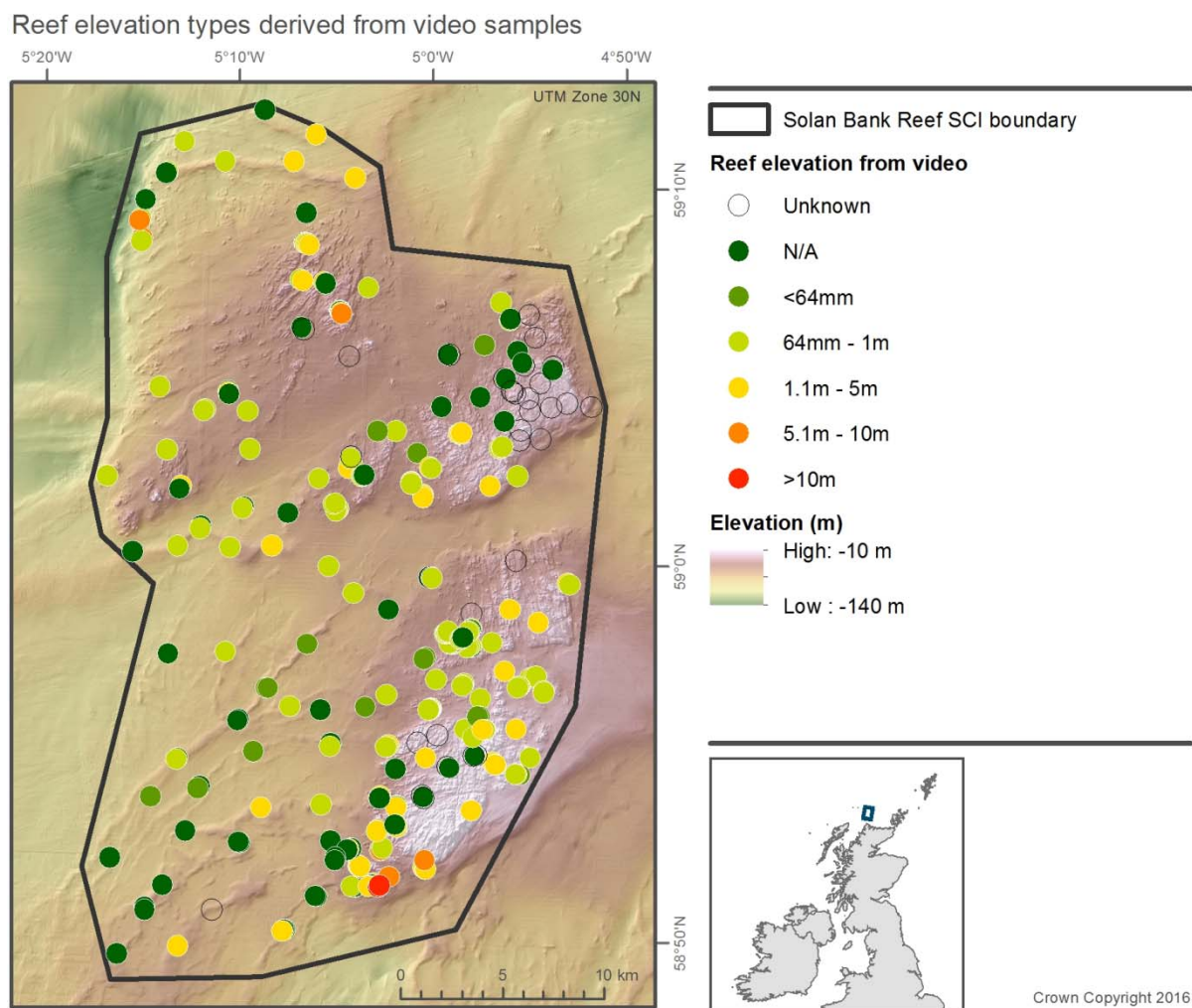
Figure 6. Distribution of reef elevation types as derived from the analysis of video samples.

4.2.3 MNCR biotope

Three (four for stills) treatment classes are compared: CR.MCR.EcCr, SS.SCS.CCS, SS.SMx.CMx, and the hybrid CR.MCR.EcCr/SS.SCS.CCS (stills only). Most univariate and multivariate tests between biotope classes using both still-derived and video-derived datasets reveal significant differences in the mean number of taxa and in assemblage composition between biotopes (Table 9). Only subsets of data with a severely reduced number of taxa do not show any differences between biotopes. In all tests where significant differences are detected, the 'echinoderms and crustose communities on moderate energy circalittoral rock' biotope (CR.MCR.EcCr) harbours the greatest number of taxa per sample (still or video), followed by the 'circalittoral mixed sediment' biotope (SS.SMx.CMx), and the 'circalittoral coarse sediment' biotope (SS.SCS.CCS). The hybrid biotope identified during the processing of stills (CR.MCR.EcCr/SS.SCS.CCS) has a mean number of epibenthic taxa per still most similar to CR.MCR.EcCr. Results from the pairwise comparison of the number of taxa and assemblage composition between biotope classes are presented in Appendix 2, Section A2.5.

Table 9. Summary of results from univariate and multivariate comparisons between observed biotope categories for different subsets of the epibenthic dataset.

Data subset	Univariate		Multivariate	
	ANOVA P-value	Sig.[a]	ANOSIM R-value	Sig.[a]
From stills (n = 1,696)				
All taxa	0.000	✓	0.307	✓
All taxa, sponge morphs	0.000	✓	0.302	✓
All taxa, no sponges	0.000	✓	0.292	✓
Sponges & anthozoa	0.000	✓	0.145	✓
Sponges	0.073	✗	0.102	✓
Sponge morphs & anthozoa	0.000	✓	0.141	✓
Sponge morphs	0.615	✗	0.097	✓(✗)
From video segments (n = 278)				
All taxa	0.000	✓	0.281	✓
All taxa, sponge morphs	0.000	✓	0.282	✓
All taxa, no sponges	0.000	✓	0.280	✓
Sponges & anthozoa	0.102	✗	0.108	✓
Sponges	0.018	✓	0.078	✓(✗)
Sponge morphs & anthozoa	0.263	✗	0.101	✓
Sponge morphs	0.050	✓	0.073	✓(✗)

[a] Strict statistical significance ($\alpha = 0.05$) as reported by test, interpreted significance given in parentheses.

There are limitations to the interpretation of results from the comparison of taxa between biotopes as derived from stills and video samples. The mean number of taxa in each biotope identified from stills appears to be very precise, with little variability (i.e. small 95% CI ranges) within each biotope (Figure 7). Conversely, the variability around the mean number of taxa per biotope identified from video samples is much greater, and the difference in the mean values between biotopes is smaller and not always significant between all pairs of biotopes. This is down to the more limited field of view afforded by a still sample compared with a video sample. Stills might seem easier to classify accurately into biotopes as there is less scope for heterogeneity in substrate type within the limited field of view of a still. However, heterogeneity can sometimes be observed, and without the broader habitat context beyond the field of view, a hybrid biotope is defined, such as CR.MCR.EcCr/ SS.SCS.CCS. Biotopes are, by definition, relatively large areas of seabed, bigger than can be encompassed by a single still image. Therefore, the precision of the data obtained from stills to inform and compare specific biotope characteristics must be treated with caution, as they sample only small-scale attributes of the seabed. Video samples, on the other hand, afford a broader scale of observation of the seabed; a scale more similar in size to that of biotopes. Video samples are, therefore, a more appropriate method of sampling biotopes than stills. The downside of video samples is that biotopes can be heterogeneous at a small spatial scale, so any single biotope identified along a transect is likely to contain small-scale areas of substrate different to the main biotope classification that has been assigned (e.g. an isolated large boulder in an otherwise sandy habitat). Taxa recorded along the length of a video transect include those that are present on the small patches of substrate that are different to the assigned biotope class, thus increasing the variability of taxa within biotopes. Given such limitations, it would be unwise to give too much credence to the finer detail afforded by the analyses performed; only generalised patterns ought to be considered.

Despite such limitations and the caution applied to comparisons between the mean number of taxa per biotope, differences in assemblage composition between biotopes identified from video samples are evident even when using a much reduced list of taxa (i.e. sponge morphs and anthozoa); the sponge morph and anthozoan assemblage from the CR.MCR.EcCr biotope is significantly different to that from the SS.SCS.CCS biotope (Appendix 2, Section A2.5). Each of these two biotopes shares most of the sponge morphs and anthozoan taxa identified (Appendix 3, Section A3.3), but a different combination of taxa contributes more to the similarity within one biotope than within another. While it may seem surprising that a sedimentary biotope should harbour several sponge morph and anthozoan taxa that are considered restricted to hard, stable substrates, it is the presence of small-scale patches of such hard substrate within an otherwise sedimentary habitat that contribute to the heterogeneity, variability and taxonomic diversity within a biotope. Many other taxa from the full complement available, both sediment dwelling and rock dwelling, also contribute to the difference in assemblage composition between these two biotopes.

The degree of spatial overlap between all three identified biotopes is evident in Figure 8. Samples classified as SS.SMx.CMx are restricted mostly to the margins of the reef structures, whereas samples representing CR.MCR.EcCr and SS.SCS.CCS appear much more interspersed with each other, especially in areas of lower topographic relief.
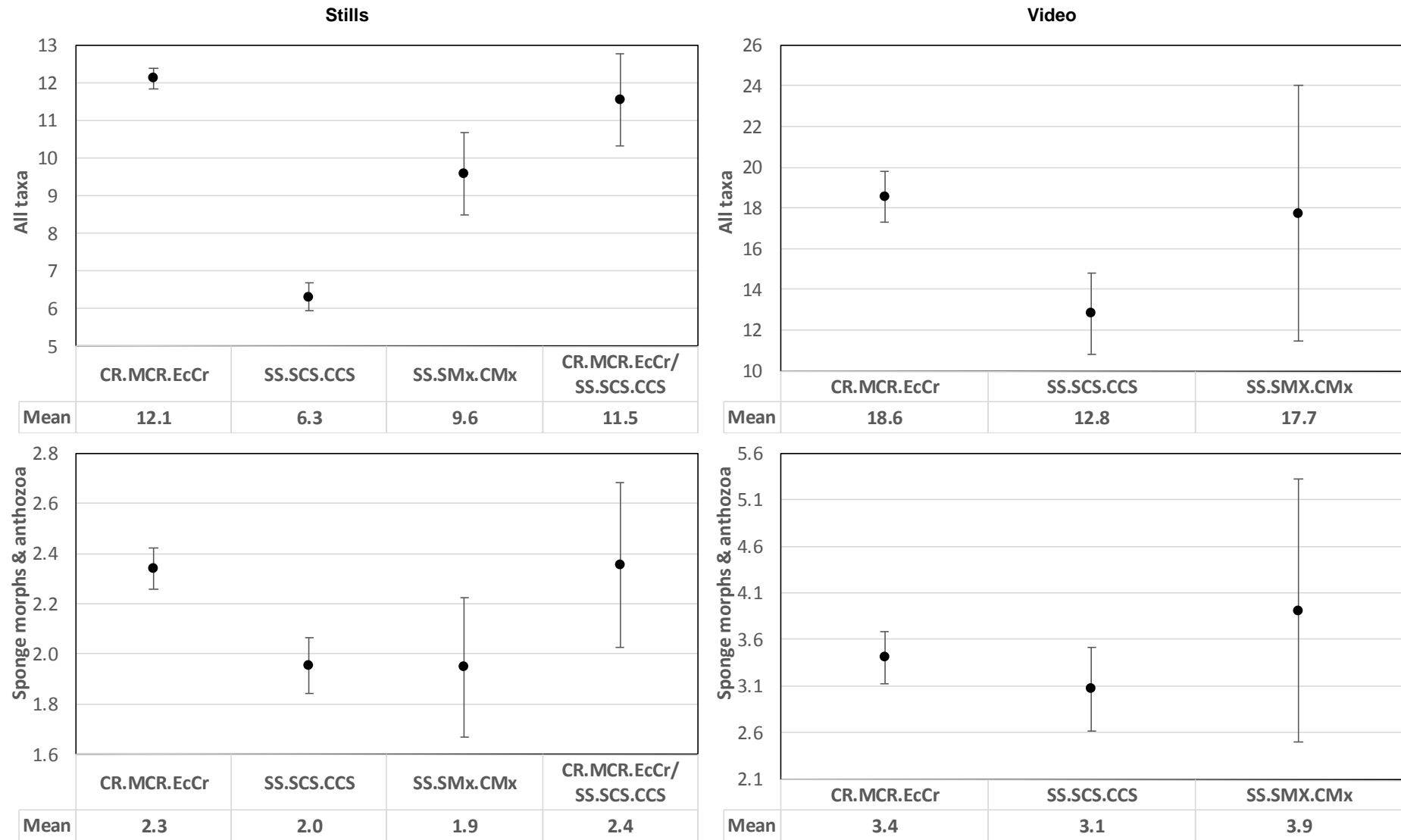
Figure 7. Mean number of taxa per sample (± 95% CI) within each MNCR biotope treatment class. All taxa from stills and video samples (top row) and only sponge morphs & anthozoa taxa (bottom row).
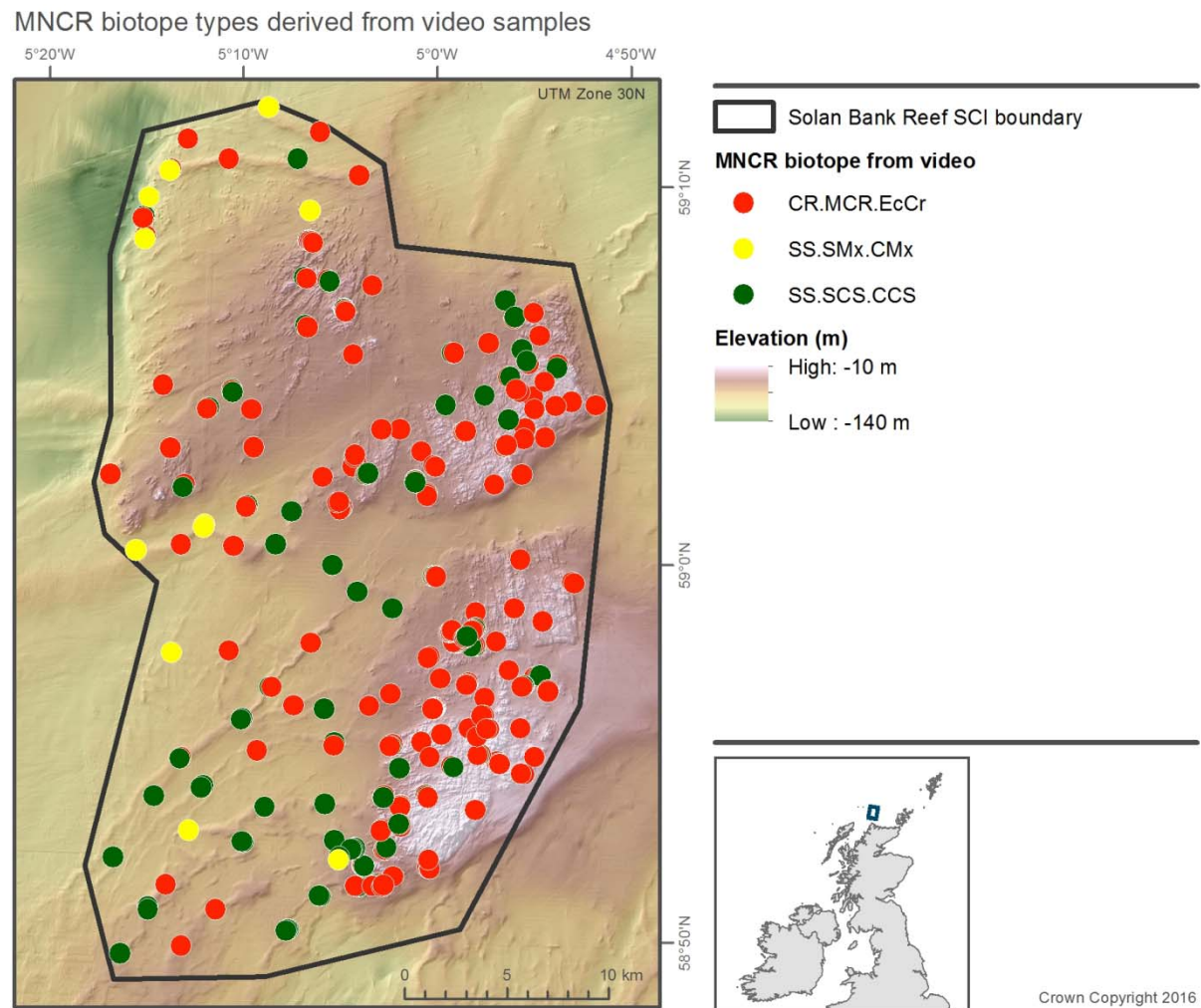
Figure 8. Distribution of MNCR biotope types as derived from the analysis of video samples.

4.3   Environmental factors shaping epibenthic assemblage structure

A PCA plot of all still samples colour-coded by Annex I reef type (Figure 9) illustrates the difference in distribution of groups of samples, as well as the relative contribution of each of the available environmental variables to that distribution. Eigen values for each of the axes plotted in the PCA indicate that substrate type (% sediment or % bedrock) is the principal discriminatory variable between groups of samples, accounting for 42% of the variability amongst samples along the X-axis. A further 28% of the variability amongst samples is explained by differences in chlorophyll concentration (labelled as Bttm_Fluo) along the Y-axis. Water temperature at the seabed (Bttm_Temp) also has a strong influence on the differentiation between groups of samples along the Y-axis. It is important to remember that while such variables explain variability across the samples, they do not necessarily equate with being drivers of pattern within the associated epibenthic assemblage.
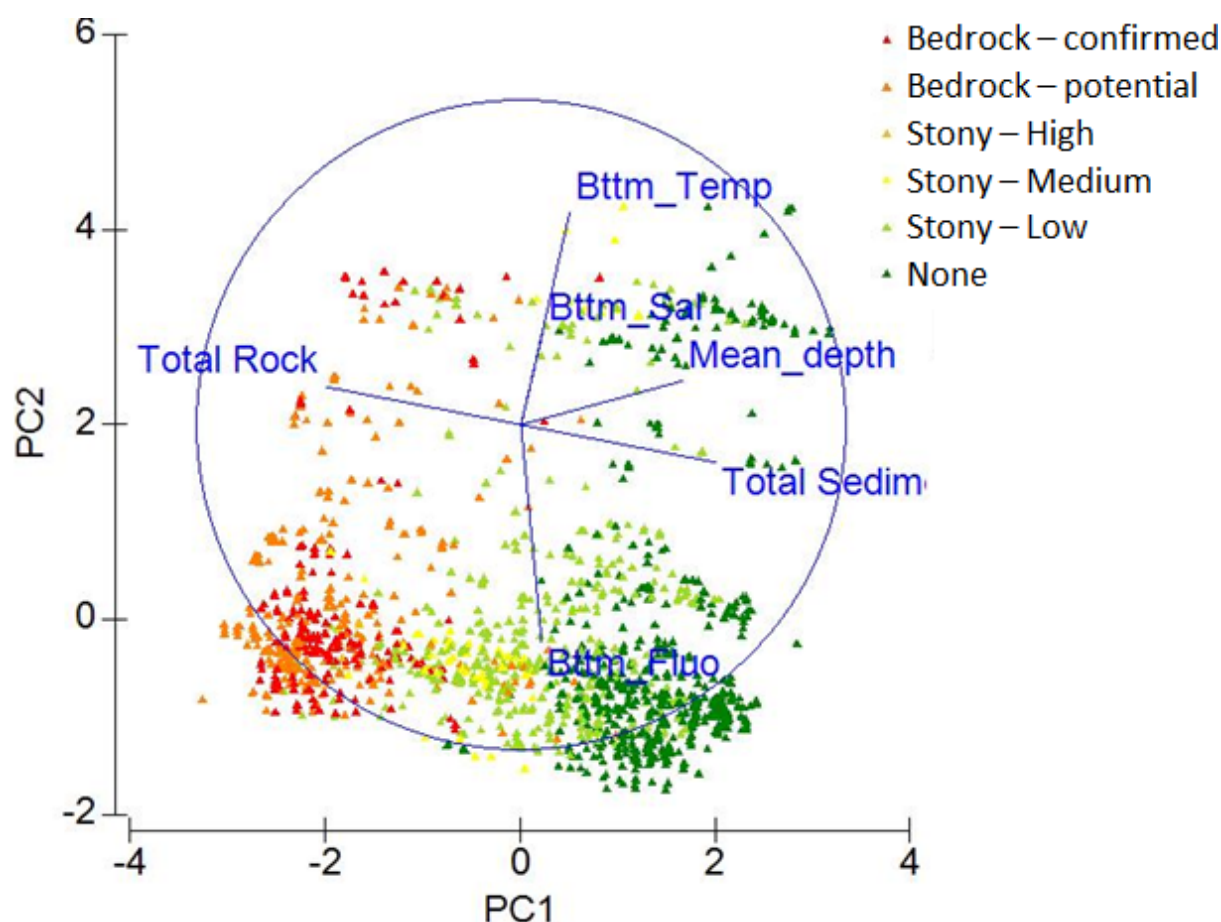
Figure 9. PCA plot of environmental variables recorded from still samples, coded by identified Annex I reef type.

Pattern in epibenthic assemblage structure is significantly correlated with the pattern in the variation of environmental variables across the site, although the confidence in that correlation is low (*rho* statistic = 0.180; Table 10). The strongest correlation between epibenthic assemblage structure and pattern in the environmental variables is apparent in the Annex I stony reef assemblage (*rho* statistic = 0.279; Table 10), whereas the weakest correlation between the two sets of variables is in the assemblage representing the 'not reef' habitat (*rho* statistic = 0.074; Table 10).

Table 10. Output from RELATE routines testing the correlation (*rho* value) between environmental and biological data extracted from stills samples representing different habitat types.

Habitat/samples	RELATE sample statistic (*rho*)	Significance
Stills		
All samples	0.180	0.1%
Annex I bedrock reef samples	0.188	0.1%
Annex I stony reef samples	0.279	0.1%
Not reef samples	0.074	0.4%

Of all the measured environmental variables, depth alone has the greatest influence on epibenthic assemblage structure in all habitat types except for 'not reef', where % gravel has the greatest influence (Table 11). Combinations of environmental variables often have a greater influence on the epibenthic assemblage structure than any one variable on its own; for the whole epibenthic assemblage, depth in combination with different elements of

substrate composition exerts the greatest influence on epibenthic assemblage structure. The assemblage subset comprised of sponge morphs and anthozoa is also mostly influenced by depth, except in Annex I stony reef, where bottom temperature has a greater influence (Table 11), and in 'not reef', where % gravel has the greatest influence.

Table 11. Output from BIOENV/BEST routines that determine the environmental variables that most influence epibenthic assemblage structure recorded on still samples.

Habitat/samples	BEST correlation		Variable
	Single var.	Multiple var.	
Stills			
All taxa, all samples	0.238		depth
		0.299	depth, % sediment/% rock
All taxa, bedrock reef	0.288		depth
		0.292	depth, % mud
All taxa, stony reef	0.256		depth
		0.299	depth, % boulders, % sand, % mud, temp.
All taxa, not reef	0.180		% gravel
		0.244	depth, % gravel, % sand
Sponge morph & anth., all samples	0.119		depth
		0.120	depth, % sediment, bottom temp.
Sponge morph & anth., bedrock reef	0.172		depth
		0.215	depth, % pebbles, % sand
Sponge morph & anth., stony reef	0.095		temp.
		0.108	depth, % cobbles, % pebbles, temp.
Sponge morph & anth., not reef	0.135		% gravel
		0.165	depth, % gravel, % sand

The same analyses performed on video-derived data reveal that only 52% of the variation within the environmental variable dataset is explained by axes X (34%) and Y (18%) in the PCA plot (Figure 10). The remaining variation in the dataset is explained along other axes not easily depicted in a two-dimensional plot. Samples are separated along the X-axis mostly by differences in their mean bottom shear stress (labelled as MeanBSS) and mean current velocity (MeanCurVel) values – both sets of which only available for video samples (not stills) due to the spatial resolution of the model used to generate them – whereas differences in measured values of chlorophyll (labelled Fluo.) and temperature (Temp.) are responsible for most of the spread of samples along the Y-axis.

Correlations between epibenthic assemblage structure (from video samples) and the pattern of environmental variables across the site were strongest in Annex I stony reef habitat (*rho* statistic = 0.229), followed by Annex I bedrock reef habitat (*rho* statistic = 0.201; Table 12). The weakest correlation between epibenthic assemblage structure and the pattern in environmental variables is observed in 'not reef' habitat (Table 12).
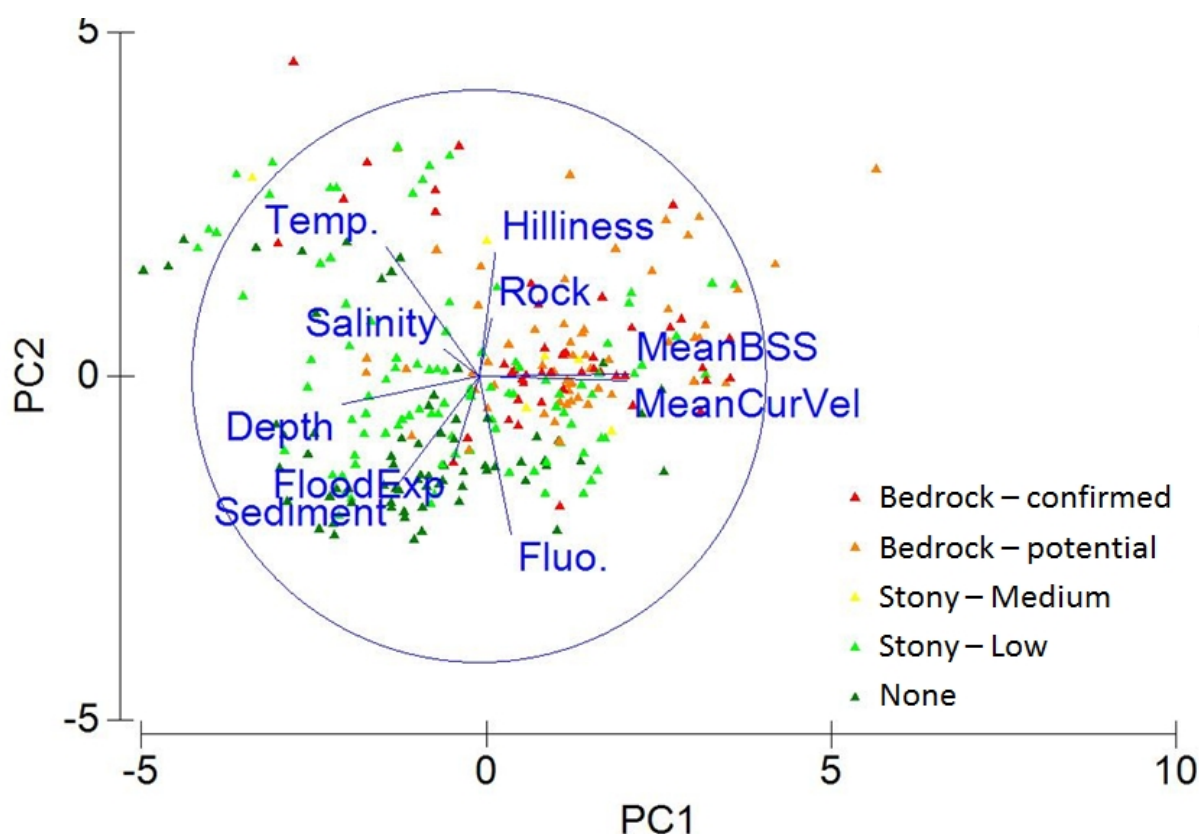
Figure 10. PCA plot of measured and modelled environmental variables from video habitat samples, coded by identified Annex I reef type.

Table 12. Output from RELATE routines testing the correlation (*rho* value) between environmental and biological data extracted from stills and video samples representing different habitat types.

Habitat/samples	RELATE sample statistic (*rho*)	Significance
Video		
All samples	0.174	0.1%
Annex I bedrock reef samples	0.201	0.1%
Annex I stony reef samples	0.229	0.1%
Not reef samples	0.100	0.1%

Across the site as a whole, in Annex I rocky reef habitat only, and in 'not reef' habitat only, depth is the single most influential variable on assemblage structure of all video-derived epibenthos (Table 13). In Annex I stony reef habitat, mean bottom shear stress is the most influential variable on the whole assemblage. Several combinations of environmental variables exert a greater influence on epibenthic assemblage composition, and include % sediment, mean current speed, in addition to those variables with the greatest individual influence. Variation in depth has the greatest influence on the sponge morph and anthozoan assemblage in Annex I bedrock reef and in 'not reef' habitat, whereas mean bottom shear stress is the most influential variable on that same assemblage in Annex I stony reef habitat and across the site as a whole (Table 13). Combinations of physical variables do not always exert a greater influence on the sponge morph and anthozoan assemblage than the most influential physical variable.

Table 13. Output from BIOENV/BEST routines that determine the environmental variables that most influence epibenthic assemblage structure recorded on video samples.

Habitat/samples	BEST correlation Single var.	Multiple var.	Variable
Video			
All taxa, all samples	0.212		depth
		0.287	% sediment, depth
All taxa, bedrock reef	0.181		depth
		0.250	% sediment, mean BSS, depth, temp
All taxa, stony reef	0.306		mean BSS
		0.319	% sed., mean curr.vel., mean BSS, depth
All taxa, not reef	0.090		depth
		0.138	% sediment, mean curr.vel., depth
Sponge morph & anth., all samples	0.145		mean BSS
		0.174	% sed., mean curr.vel., mean BSS, depth
Sponge morph & anth., bedrock reef	0.104		depth
		0.124	% sediment, mean BSS, depth
Sponge morph & anth., stony reef	0.377		mean BSS
		0.377	mean BSS
Sponge morph & anth., not reef	0.214		depth
		0.214	depth

It is worth noting that many of the environmental data types available for analyses are themselves correlated (e.g. mean bottom shear stress and max. bottom shear stress). Where such strong correlations are apparent, the variable in the pair with the greatest range in variability has been chosen for the analyses, and the variable with the least variability of the pair has been excluded.

Lastly, sample cluster routines (CLUSTER, MDS, SIMPROF) on both still-derived and video-derived epibenthic datasets do not reveal any pattern in the assemblage that is not already evident in the results from the analyses performed between the different treatment classes defined. Many (>30) statistically distinct assemblages are identified by the CLUSTER-SIMPROF routines (data not shown), each represented by just a handful of samples, and none with any obvious spatial coherence or affinity with surrounding samples. Such results only serve to highlight the high degree of small-scale variability in the epibenthic assemblage structure, which is to be expected in heterogeneous habitats such as bedrock and stony reefs.

5   Discussion

The present investigation has served to characterise the epibenthic assemblage in the Solan Bank Reef SCI as recorded by two survey techniques – video vs stills samples – and to ascertain which environmental variables most influence assemblage structure in the various habitats present within the site. In addition, this investigation has sought to ascertain whether subsets of the epibenthic dataset that inform the calculation of supporting indicators of biodiversity (see Table 2) carry sufficient information to detect differences in biodiversity across different habitats or between different fishing activity regimes.

To reach a position where analyses on the acquired data could be performed, several data preparation steps were necessary; some inflicting significant yet inevitable limitations to the range of analyses that could be performed. For example, all recorded information on taxon quantity (i.e. abundance or % cover) had to be sacrificed, after inconsistences in the recording of quantity across and within taxa on different scales rendered the assimilation of all records to a common scale impractical. Consequently, any index of biodiversity requiring the relative abundance of taxa for its calculation has been precluded from the investigation. Whilst this may seem like a severe blow to the range of analyses that could be performed to achieve the objectives of the investigation, the limitation of analyses to those that use only data on the presence/absence of taxa has reduced the potential for variation in the results obtained. Biodiversity indices come in many forms, each with its own advantages, disadvantages, and suitability for particular situations. There is not a single biodiversity index that can be used effectively in every situation, and those indices most commonly used are usually chosen because of their popularity in the literature rather than because they are the most appropriate for the objectives of the investigation being performed (Gray 2000). Even if the present investigation hadn't been compromised in its use of taxon abundance information, the choice of biodiversity index – although appropriate for the purposes of this investigation – may have been different to the choice of index by past or future analysts of data from the study site. In addition, the values of biodiversity resulting from the calculation of biodiversity indices cannot be compared across different studies, even if the choice of index is the same. With all of this in mind, it is perhaps fortuitous that only the number and identity of taxa in each sample can be used in analyses for the present investigation. The number and variety of taxa, whilst not devoid of problems in its measurement or limitations in its use (Gaston 1996), is as robust and informative a metric as can be, with little opportunity for different analysts to corrupt or distort the pattern contained within such a dataset. Furthermore, by maintaining and observing the same standards in sampling protocols across sampling events, the number and variety of taxa per sample can be compared over space, time, and between studies. The relative simplicity of measuring and using the number of taxa in analyses is in fact its strength.

Initial comparisons were made between groups of samples classified into categories defined prior to their collection, such as target habitat and fishing activity regime. Results from such comparisons were informative to a degree, but the heterogeneity of the seabed at a small spatial scale, together with logistical limitations of the sampling protocol (i.e. fine-scale vessel and sampler manoeuvrability), meant that several sampling attempts targeting a particular habitat type had in fact sampled a patch of habitat different to the one intended.

Differences in the mean number of taxa per targeted habitat type and per predefined fishing regime were detected, as well as differences in the assemblage composition between such groups. However, it would be unwise to attach too much importance to those results, owing to the difficulty in quantifying the influence of environmental variables and/or spatial autocorrelation of taxa, both potentially affecting any observable difference in epibenthic assemblage composition between spatially discrete areas with different fishing activity/ intensity regimes.

The overriding pattern emerging from almost all analyses performed is the greater number of taxa recorded in reef habitats than in non-reef habitat, and the less perceptible difference in the number of taxa and assemblage composition between bedrock and stony reef habitats. Differences in mean number of taxa per sample and in assemblage composition appeared greatest between the extremes of reef elevation; the greater the elevation (and presumably, the more stable a substrate), the greater the number of taxa recorded. Predictably, epibenthic assemblage composition on stable reef habitat substrates was characterised mostly by sessile, attached, filter-feeding organisms, such as anemones, corals, sponges (particularly, but not excluding non-encrusting morphs), motile aggregations of filter-feeding brittlestars, and autotrophic red algae, all of which benefiting from their increased exposure to nutrients carried by the water currents and decreased exposure to scour from suspended sediments in the lower water column. As well as the obligate dependency of some of those taxa on a hard stable substrate for their attachment, the composition of the epibenthic assemblage across the whole site and within each habitat type was also strongly influenced by depth (or by unmeasured variables that correlate with depth). Deeper samples were less likely to have sampled elevated reef habitat, therefore the average number of taxa per sample tended to be lower in deeper substrates with reduced or no reef features.

By selecting and comparing the results from the analysis of different subsets of data, an assessment can be made on the suitability of each subset as a proxy for detecting the pattern contained within the entire dataset. Naturally, as variables (taxa) in an analysis are reduced (by selective exclusion or reducing their variability to morphs), the power of those analyses to detect a significant difference between groups of samples with reduced variables is diminished. However, for most of the analyses performed on subsets of data, the difference between groups of samples compared was maintained, albeit not always to a statistically significant degree. A higher mean number of sponge morphs and anthozoa in reef habitats than in non-reef habitat was still evident after such a severe reduction in variables from the original whole dataset. However, differences in sponge morph and anthozoan assemblage composition were not detected between reef and non-reef habitats after multivariate analyses of the data, despite those differences being apparent when using the entire dataset. Clearly, the option of reducing the number of variables measured for analyses of habitat/assemblage condition is an attractive one, especially as the speed of assessments could be greatly increased, but consideration must be given to what is required from the data before such a decision is made, especially as a change of requirements could prove costly if the acquired limited data is no longer fit for purpose. It would seem prudent to continue to extract as much information as possible from acquired samples and have the option to not use it, than to restrict the quantity of data extracted from samples up front only

to realise that additional (available but unextracted) data are required at a later date because the available data are insufficient.

The present investigation has sought to determine whether there are any advantages in using data collected by either video samples or still samples for the purposes of assessing epibenthic assemblage composition and structure. Stills offer a greater visual resolution, enabling more features on the seabed to be observed and support greater confidence in the identification of taxa. Conversely, video samples – being moving images – can sometimes blur smaller and more cryptic taxa, or they fail to provide sufficient detail for a confident identification (van Rein *et al* 2012). As mentioned previously (Section 4.2.3), hundreds of still images each sampling a relatively small area of the seabed capture small-scale variability that can either help or hinder broad-scale analyses. Video samples are inherently fewer, but offer a broader perspective on the area investigated, and can assist with the identification of boundaries and transitions between habitats and biotopes in a way that stills cannot. Data extracted from video samples in this study have been adequate to detect generalised differences between different habitat types targeted by the investigation. Should the detection of such differences be the sole purpose of future investigations (e.g. for the monitoring of habitat condition), video samples alone could suffice to inform those investigations. However, should future investigations also aim to assess changes in the distribution of particular taxa (e.g. sensitive, threatened, invasive or non-native species), or seek to create a complete inventory of the biodiversity of an area, stills offer more potential for the identification of taxa to a greater taxonomic resolution.

Most of the environmental variables measured during the dedicated survey of Solan Bank Reef SCI to inform this investigation have been useful in the analysis and determination of which variables exert a greater influence over the epibenthic assemblage. However, one measurement in particular – current speed and direction as measured by ADCP – was not so useful. The acquired ADCP data are in the form of a binned dataset from a bottom tracking instrument which collected data from a controlled but unstructured pass over three chosen locations within the SCI boundary (see O'Connor 2015). Hydrodynamic models, with either structured or unstructured meshes, compute the hydrodynamic conditions (and store results and outputs) at constant positions in space and over an evenly spaced time series in time. To validate a model, it is necessary to compare the measured data against the modelled data. With the ADCP dataset in its current format, this can only be done by picking out data points that can be closely matched to modelled points in both time and space. Because of the unstructured track of the vessel during data collection, this matching process can only be done manually, which is time consuming and can only produce random points for comparison. Such random points are not suitable for a systematic model validation exercise. ADCP data would be more useful if collected at a stationary point (e.g. from a lander) positioned at the location of one of node positions of the model. This would allow a time series to be derived in time and space. The bottom tracking instrument used in cruise mode (as was done) would have been better employed by steaming along a fixed transect over the area (ideally over a set of nodes) repeatedly over the course of a flood/ebb tide. Data recorded by this approach would be more useable for cross-referencing against a model.

Despite the limitations of the acquired ADCP data, modelled environmental variables produced by the present investigation (and supplied to JNCC as data layers) were a useful addition to the range of variables available for analysis. Of those modelled environmental variables, bottom shear stress proved to be most influential in the distribution of the sponge morph and anthozoan assemblage on stony reef in particular, and across the site as a whole. Other patterns in the composition of the entire epibenthic assemblage were more greatly influenced by measured environmental variables, such as depth, temperature and substrate composition.

It is worth noting that in the course of this report being finalised, the Scottish Shelf Model was published by the Scottish Government[3]. Whilst it was published too late to be incorporated into the analyses presented here, it may assist in future assessments of hydrodynamic conditions on benthic assemblages.

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[3] URL: http://www.gov.scot/Publications/2016/03/8542

6   Conclusion and recommendations

The present investigation has succeeded in characterising the epibenthic assemblage inhabiting different habitat types present within the Solan Bank Reef SCI. The various methods of sample and data acquisition have been summarised and reviewed, and results from their analysis presented. The broad-scale differences in epibenthic assemblage structure and composition that exist between different habitat types have been detected using datasets acquired using different but complementary survey techniques. Overall, the mean number of taxa per sample was greater in habitats described as either bedrock or stony reef than in 'not reef' habitats. Those same differences in assemblage composition between habitats have been detected using subsets of the entire dataset that are being considered as supporting indicators of biodiversity for the assessment of GES under the MSFD. Environmental variables showing the strongest correlation with pattern in the number of taxa across the study site were also similar across subsets of the epibenthic dataset. It would appear, therefore, that the use of a data subset comprising sponge morphs and anthozoa would be a suitable proxy for detecting variation in the whole assemblage between reef and non-reef habitat types. Other advantages and limitations in the use of such data subsets, and in the selection of data types to include in similar assessments have been presented. While individual techniques for sample acquisition might be favoured under specific circumstances, it would be preferable if a combination of techniques continues to be deployed, to overcome the limitations of any technique used in isolation. By doing so, the optimum complement of data that can be analysed is acquired, and the potential for pertinent analyses not conceived at the outset to be conducted is maximised. Consistency in the recording of the quantity of taxa is paramount to minimise the potential for inconsistencies that could invalidate certain analyses.

Correlations between the pattern in the epibenthic assemblage and the pattern in environmental variables have been explored, revealing that substrate type, depth and temperature in isolation and in combination have the greatest influence on overall assemblage structure. Relevant modelled environmental data layers identified and produced under the present investigation were included in the analyses. The distribution of specific elements of the epibenthic assemblage, such as sponges and anthozoa, appear to be strongly affected by current velocity and bottom shear stress. Suggestions for the collection of suitable data on current velocity have been made, and include the use of either static samplers, or structured sampling along predefined transects. Data acquired in this way should be more easily integrated into the validation of existing models, thus ensuring a more accurate representation of the natural environment.

Investigations into human impacts on the targeted epibenthic assemblage were inconclusive. While scant evidence of human activities was observed during the processing of acquired samples (e.g., discarded/lost static fishing gears), none of the results from the analyses performed can be relied upon to express with confidence whether fishing activity or intensity had any effect on the epibenthic assemblage. There are too many confounding factors in the acquired datasets that may have been responsible for any differences in the observed pattern in assemblage composition between areas of differing fishing pressure. The sponge

morphs and anthozoa data subset was similarly compromised. A dedicated survey plan would be necessary to investigate the effects of fishing and to attain a reliable result.

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Appendix 1   Data truncation protocol

A number of decisions applied during the data truncation process are described here, in the hope that by following such decisions, a greater degree of consistency in truncation exercises across different studies may be achieved.

Raw taxon-by-sample matrices can often contain entries that include the same taxa recorded differently, erroneously or differentiated according to unorthodox, subjective criteria, for example:

Species name [as recorded]	Qualifier	Certainty	Size class	Scale
Abietinaria abietina	Yellow		Crust / Meadow	%
Abietinaria abietina			3-15 cm	Count
Sertularella			Turf / Massive	%
Sertularella			3-15 cm	Count
Sertularidae		Uncertain	3-15 cm	Count
Sertulariidae			Turf / Massive	%

Each row is supposed to represent a legitimate taxon to be used in analytical software packages as a unit for the calculation of diversity indices and of similarity amongst groups of samples. An artificially inflated taxon list (i.e., one that has not had spurious entries removed) risks distorting the interpretation of pattern contained within the sampled assemblage. The truncation exercise aims to identify and neutralise such entries to reduce the risk of them supporting an artificial pattern in the assemblage.

To assist in the identification of entries that could potentially represent the same taxon, a taxonomic aggregation matrix is created that lists the taxonomic hierarchy of each entry, such as:

Phylum	Class	Order	Family	Genus	Species name [corrected]
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Abietinaria	Abietinaria abietina
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Abietinaria	Abietinaria abietina
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Sertularella	Sertularella
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Sertularella	Sertularella
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Sertulariidae	Sertulariidae
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Sertulariidae	Sertulariidae

For convenience, the aggregation matrix is restricted to the major ranks in the taxonomic tree. A contrasting colour palate can be used to identify and group rows that could be considered for truncation. Taxa that share an identical name but have been recorded in different ways (as a % or as a count), or taxa that have been differentiated by size, colour, a spelling mistake, or due to lack of detail in the sample image, must be identified and a decision made on a case-by-case basis on how to truncate each entry. Truncation normally means merging any number of similar entries into a single row that unambiguously represents the taxon in question.

It is often the case that to overcome uncertainty and to avoid the introduction of unsupported certainty, some taxa have to be merged to a level in the taxonomic hierarchy that is higher

than the level at which they were identified. In such situations, a compromise must be reached between the level of information lost by discarding recorded detail on a taxon's identity, and the potential for error in analyses, results and interpretation if that detail is retained. For example, after the first round of truncation the table above may look like this:

Phylum	Class	Order	Family	Genus	Species name [corrected]
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Abietinaria	Abietinaria abietina
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Sertularella	Sertularella
Cnidaria	Hydrozoa	Leptothecata	Sertulariidae	Sertulariidae	Sertulariidae

A further truncation step may consider the merging of the genus Sertularella with its parent family Sertulariidae. However, there is no way of knowing whether entries recorded to the level of family represent the genus Sertularella, the other recorded genus in that family Abietinaria, or any other genus in the family. It is highly likely, however, that the unresolved entry does indeed represent a taxon already present in the dataset. To keep Sertulariidae as a distinct entry means keeping a row (taxon) that may unnecessarily inflate the total number of taxa in the matrix. To reduce all entries to their common known denominator (the family) means losing taxonomic resolution in the matrix. To merge the entries recorded at family level with one or both (proportionally) of the named genera/species, means assigning certainty where none was available at the time of sample processing. Looking at the frequency of occurrence of each entry among the samples, as well as any co-occurrence of entries, may assist in deciding which truncation option would be optimal. None of the options available is necessarily wrong, but the consequences of choosing any one option over another must be considered, and any decision taken must be justifiable.

Whichever decision is taken, a number of rules can be applied in the naming of merged entries, to ensure consistency and transparency of approach. Examples of each rule are as follows.

Where there are records of one named species together with records of members of the same genus but the latter not identified to species level, the entries are merged and the resulting entry retains only the name of the genus (i.e., species level information is forfeited).

Annelida	Polychaeta	Sabellida	Serpulidae	Salmacina	Salmacina dysteri
Annelida	Polychaeta	Sabellida	Serpulidae	Salmacina	Salmacina

Is truncated to:

Annelida	Polychaeta	Sabellida	Serpulidae	Salmacina	Salmacina

In this way, the entries identified only to genus are not assigned to a level that is unsupported by the evidence, and the resulting single entry is representative of both original entries, albeit with a little less information, but a loss that will not affect the pattern in the assemblage as a whole.

Where there is more than one named species in a genus together with an entry of the genus unidentified to species level, the loss of information inflicted by merging all entries to genus might be unacceptable. In this case, the entry representing the genus alone, if significantly prevalent across the samples, may have to be retained as a distinct entry. For example:

Cnidaria	Anthozoa	Actiniaria	Actiniidae	Urticina	Urticina
Cnidaria	Anthozoa	Actiniaria	Actiniidae	Urticina	Urticina eques
Cnidaria	Anthozoa	Actiniaria	Actiniidae	Urticina	Urticina felina

Urticina is retained, as it is possible that where it has been observed it is distinct enough for it not to be identified as *U. eques* or *U. felina*, but impossible to be given a species name based on available evidence. Should Urticina be identified in subsequent analyses as being distinctive or characteristic of a group of samples, the epithet SP.INDET can be added to the name before analyses, to denote that there are species within that genus that have been identified beyond genus, but that in this instance it is the unidentified member of that genus that is responsible for any observed pattern. Without it, a reader might infer that all species within the genus Urticina were characteristic of a group of samples, and not just the organisms that were unidentifiable to species. The resulting entries might look like this:

Cnidaria	Anthozoa	Actiniaria	Actiniidae	Urticina	Urticina_SP.INDET
Cnidaria	Anthozoa	Actiniaria	Actiniidae	Urticina	Urticina eques
Cnidaria	Anthozoa	Actiniaria	Actiniidae	Urticina	Urticina felina

The epithet may also be used in other instances where truncation involves merging entries identified to levels higher up in the taxonomic hierarchy. For example, where there are several genera or species within a family together with an unresolved genus for that same family, or if there is an unresolved family within an order containing several named families.

Porifera	Demospongiae	Polymastiida	Polymastiidae	Polymastia	Polymastia boletiformis
Porifera	Demospongiae	Polymastiida	Polymastiidae	Polymastia	Polymastia penicillus
Porifera	Demospongiae	Polymastiida	Polymastiidae	Polymastiidae	Polymastiidae_GEN.INDET

Mollusca	Gastropoda	Littorinimorpha	Littorinimorpha	Littorinimorpha	Littorinimorpha_FAM.INDET
Mollusca	Gastropoda	Littorinimorpha	Rissoidae	Rissoidae	Rissoidae

The INDET epithet is not necessary where the entry is the sole representative of its taxon, as no extra information is imparted by its use. It is only useful when wanting to differentiate the unresolved entry from other entries that may also share its identity (i.e., by belonging to the same rank/taxon).

Finally, any entries recorded at an intermediate level in the taxonomic tree (e.g., infraorder, superfamily, subgenus) should be reclassified as the closest higher rank in the taxonomic hierarchy, and merged with any other pre-existing unresolved members of that rank. For example, the subclass Hexacoralia is reclassified and merged with its closest parent rank, the class Anthozoa, so that:

Cnidaria	Anthozoa	Alcyonacea	Alcyoniidae	Alcyonium	Alcyonium digitatum
Cnidaria	Anthozoa	Hexacorallia	Hexacorallia	Hexacorallia	Hexacorallia
Cnidaria	Anthozoa	Anthozoa	Anthozoa	Anthozoa	Anthozoa

becomes:

Cnidaria	Anthozoa	Alcyonacea	Alcyoniidae	Alcyonium	Alcyonium digitatum
Cnidaria	Anthozoa	Anthozoa	Anthozoa	Anthozoa	Anthozoa_ORD.INDET

Appendix 2   Detailed results from pairwise comparisons between treatment categories

A2.1 Tests between target habitat categories

One-way ANOVA: **All taxa** versus Substrate/Habitat – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	1130	564.81	22.76	0.000
Error	1568	38907	24.81		
Total	1570	40036			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Bedrock reef	1126	11.002	4.847	(10.711, 11.293)	A
Stony reef	240	10.208	5.089	(9.578, 10.839)	A
Not reef	205	8.488	5.552	(7.805, 9.170)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus Substrate/Habitat – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	1052	525.91	22.84	0.000
Error	1568	36108	23.03		
Total	1570	37159			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Bedrock reef	1126	10.672	4.671	(10.392, 10.953)	A
Stony reef	240	9.808	4.897	(9.201, 10.416)	B
Not reef	205	8.268	5.344	(7.611, 8.926)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus Substrate/Habitat – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	1239	619.29	30.93	0.000
Error	1568	31393	20.02		
Total	1570	32632			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Bedrock reef	1126	9.907	4.368	(9.645, 10.168)	A
Stony reef	205	8.850	4.600	(8.283, 9.417)	B
Not reef	240	7.332	4.889	(6.719, 7.945)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus Substrate/Habitat – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	12.02	6.012	5.34	0.005
Error	771	867.93	1.126		
Total	773	879.95			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Not reef	99	1.939	1.346	(1.730, 2.149)	A
Stony reef	131	1.7557	1.0007	(1.5738, 1.9377)	AB
Bedrock reef	544	1.5846	1.0156	(1.4953, 1.6739)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus Substrate/Habitat – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	383.9	191.95	2.97	0.053
Error	275	17761.4	64.59		
Total	277	18145.3			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Bedrock reef	220	14.609	7.788	(13.542, 15.676)	A
Stony reef	37	13.49	9.04	(10.89, 16.09)	AB
Not reef	21	10.24	8.76	(6.79, 13.69)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges and anthozoa** versus Substrate/Habitat – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	92.60	46.301	8.45	0.000
Error	262	1436.06	5.481		
Total	264	1528.66			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Stony reef	35	5.400	2.252	(4.621, 6.179)	A
Not reef	18	5.278	2.718	(4.191, 6.364)	A
Bedrock reef	212	3.882	2.322	(3.565, 4.199)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges** versus Substrate/Habitat – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	167.6	83.808	18.23	0.000
Error	275	1264.1	4.597		
Total	277	1431.8			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Stony reef	37	4.459	2.268	(3.766, 5.153)	A
Not reef	21	3.143	2.651	(2.222, 4.064)	AB
Bedrock reef	220	2.209	2.070	(1.925, 2.494)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges morphs & anthozoa** versus Substrate/Habitat – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Substrate/Habitat	2	83.63	41.817	16.44	0.000
Error	275	699.46	2.544		
Total	277	783.10			

Substrate/Habitat	N	Mean	StDev	95% CI	Grouping[a]
Stony reef	37	3.216	1.601	(2.700, 3.732)	A
Not reef	21	2.429	1.989	(1.743, 3.114)	AB
Bedrock reef	220	1.650	1.553	(1.438, 1.862)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOSIM: **All taxa** versus target Substrate/Habitat – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.163	0.1
Bedrock reef, Not reef	0.272	0.1
Stony reef, Not reef	0.054	0.1

One-way ANOSIM: **All taxa, sponge morphs** versus target Substrate/Habitat – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.168	0.1
Bedrock reef, Not reef	0.269	0.1
Stony reef, Not reef	0.052	0.1

One-way ANOSIM: **All taxa, no sponges** versus target Substrate/Habitat – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.175	0.1
Bedrock reef, Not reef	0.264	0.1
Stony reef, Not reef	0.051	0.1

One-way ANOSIM: **Sponges & anthozoa** versus target Substrate/Habitat – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.086	0.1
Bedrock reef, Not reef	0.142	0.1
Stony reef, Not reef	0.019	0.1

One-way ANOSIM: **Sponge morphs & anthozoa** versus target Substrate/Habitat – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.092	0.1
Bedrock reef, Not reef	0.139	0.1
Stony reef, Not reef	0.017	0.1

One-way ANOSIM: **All taxa** versus target Substrate/Habitat – from **video**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.155	0.2
Bedrock reef, Not reef	0.351	0.1
Stony reef, Not reef	0.142	0.1

One-way ANOSIM: **All taxa, sponge morphs** versus target Substrate/Habitat – from **video**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.157	0.2
Bedrock reef, Not reef	0.350	0.1
Stony reef, Not reef	0.142	1.0

One-way ANOSIM: **All taxa, no sponges** versus target Substrate/Habitat – from **video**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.207	0.1
Bedrock reef, Not reef	0.387	0.1
Stony reef, Not reef	0.133	1.7

One-way ANOSIM: **Sponges & anthozoa** versus target Substrate/Habitat – from **video**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.041	15.3
Bedrock reef, Not reef	0.146	0.8
Stony reef, Not reef	0.141	0.9

One-way ANOSIM: **Sponge morphs & anthozoa** versus target Substrate/Habitat – from **video**

Pairwise tests	R statistic	Sig. level (%)
Bedrock reef, Stony reef	0.043	12.4
Bedrock reef, Not reef	0.135	0.5
Stony reef, Not reef	0.137	0.7

A2.2 Tests between fishing activity categories

One-way ANOVA: **All taxa** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	921.7	460.86	19.83	0.000
Error	951	22103.8	23.24		
Total	953	23025.5			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	68	11.868	5.717	(10.720, 13.015)	A
Static and mobile gear - low activity	483	11.723	4.945	(11.292, 12.153)	A
Static gear - high activity	403	9.752	4.496	(9.281, 10.223)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	980.4	490.22	22.59	0.000
Error	951	20638.1	21.70		
Total	953	21618.5			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	68	11.500	5.552	(10.391, 12.609)	A
Static and mobile gear - low activity	483	11.476	4.823	(11.060, 11.892)	A
Static gear - high activity	403	9.427	4.280	(8.971, 9.882)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	958.8	479.41	25.09	0.000
Error	951	18172.7	19.11		
Total	953	19131.5			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Static and mobile gear - low activity	483	10.843	4.595	(10.452, 11.233	A
Mobile gear - high activity	68	10.000	4.856	(8.960, 11.040)	AB
Static gear - high activity	403	8.754	3.995	(8.327, 9.182)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges & anthozoa** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	39.18	19.589	7.95	0.000
Error	741	1826.44	2.465		
Total	743	1865.61			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	55	3.436	2.217	(3.021, 3.852)	A
Static gear - high activity	296	2.5946	1.4606	(2.4154, 2.7737)	B
Static and mobile gear - low activity	393	2.5420	1.5416	(2.3865, 2.6975)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	22.54	11.272	7.76	0.000
Error	435	631.56	1.452		
Total	437	654.11			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	46	2.761	1.791	(2.412, 3.110)	A
Static gear - high activity	180	2.2333	1.0888	(2.0568, 2.4099)	B
Static and mobile gear - low activity	212	2.0047	1.1416	(1.8421, 2.1674)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	32.28	16.138	9.70	0.000
Error	741	1232.66	1.664		
Total	743	1264.93			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	55	2.982	1.881	(2.640, 3.323)	A
Static and mobile gear - low activity	393	2.2392	1.2793	(2.1115, 2.3669)	B
Static gear - high activity	296	2.1520	1.1647	(2.0049, 2.2992)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus fishing activity – from **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	23.25	11.6268	12.12	0.000
Error	435	417.14	0.9589		
Total	437	440.39			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	46	2.217	1.534	(1.934, 2.501)	A
Static gear - high activity	180	1.5056	0.9245	(1.3621, 1.6490)	B
Static and mobile gear - low activity	212	1.4434	0.8662	(1.3112, 1.5756)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges and anthozoa** versus fishing activity – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	45.27	22.637	4.38	0.014
Error	184	950.74	5.167		
Total	186	996.01			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	19	5.053	2.697	(4.024, 6.081)	A
Static and mobile gear - low activity	109	3.826	2.372	(3.396, 4.255)	AB
Static gear - high activity	59	3.288	1.912	(2.704, 3.872)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges** versus fishing activity – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	48.80	24.400	6.23	0.002
Error	192	751.58	3.914		
Total	194	800.38			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	19	3.579	2.317	(2.684, 4.474)	A
Static and mobile gear - low activity	112	1.893	1.965	(1.524, 2.262)	B
Static gear - high activity	64	1.891	1.895	(1.403, 2.378)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus fishing activity – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	43.10	21.549	5.99	0.003
Error	192	690.70	3.597		
Total	194	733.79			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	19	4.158	2.218	(3.300, 5.016)	A
Static and mobile gear - low activity	112	3.277	1.969	(2.923, 3.630)	A
Static gear - high activity	64	2.563	1.651	(2.095, 3.030)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus fishing activity – from **video**

Source	DF	Adj SS	Adj MS	F value	P value
Activity	2	26.68	13.339	5.99	0.003
Error	192	427.39	2.226		
Total	194	454.07			

Fishing activity	N	Mean	StDev	95% CI	Grouping[a]
Mobile gear - high activity	19	2.684	1.765	(2.009, 3.359)	A
Static and mobile gear - low activity	112	1.446	1.463	(1.168, 1.724)	B
Static gear - high activity	64	1.422	1.456	(1.054, 1.790)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOSIM: **All taxa** versus target fishing activity – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.157	0.1
Mobile gear - high activity, Static and mobile gear - low activity	0.274	0.1
Static gear - high activity, Static and mobile gear - low activity	0.078	0.1

One-way ANOSIM: **All taxa, sponge morphs** versus target fishing activity – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.160	0.1
Mobile gear - high activity, Static and mobile gear - low activity	0.276	0.1
Static gear - high activity, Static and mobile gear - low activity	0.079	0.1

One-way ANOSIM: **All taxa, no sponges** versus target fishing activity – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.157	0.1
Mobile gear - high activity, Static and mobile gear - low activity	0.276	0.1
Static gear - high activity, Static and mobile gear - low activity	0.081	0.1

One-way ANOSIM: **Sponges & anthozoa** versus target fishing activity – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.050	1.8
Mobile gear - high activity, Static and mobile gear - low activity	0.140	0.1
Static gear - high activity, Static and mobile gear - low activity	0.038	0.1

One-way ANOSIM: **Sponge morphs & anthozoa** versus target fishing activity – from **stills**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.052	1.5
Mobile gear - high activity, Static and mobile gear - low activity	0.145	0.1
Static gear - high activity, Static and mobile gear - low activity	0.038	0.1

One-way ANOSIM: **All taxa** versus target fishing activity – from **video**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.147	2.7
Mobile gear - high activity, Static and mobile gear - low activity	0.177	1
Static gear - high activity, Static and mobile gear - low activity	0.158	0.1

One-way ANOSIM: **All taxa, sponge morphs** versus target fishing activity – from **video**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.149	2.3
Mobile gear - high activity, Static and mobile gear - low activity	0.182	1.5
Static gear - high activity, Static and mobile gear - low activity	0.165	0.1

One-way ANOSIM: **All taxa, no sponges** versus target fishing activity – from **video**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	0.158	2
Mobile gear - high activity, Static and mobile gear - low activity	0.211	0.1
Static gear - high activity, Static and mobile gear - low activity	0.171	0.1

One-way ANOSIM: **Sponges & anthozoa** versus target fishing activity – from **video**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	-0.037	74.1
Mobile gear - high activity, Static and mobile gear - low activity	0.181	0.6
Static gear - high activity, Static and mobile gear - low activity	0.186	0.1

One-way ANOSIM: **Sponge morphs & anthozoa** versus target fishing activity – from **video**

Pairwise tests	R statistic	Sig. level (%)
Mobile gear - high activity, Static gear - high activity	-0.034	73.9
Mobile gear - high activity, Static and mobile gear - low activity	0.207	0.1
Static gear - high activity, Static and mobile gear - low activity	0.203	0.1

A2.3 Tests between observed Annex I reef categories

One-way ANOVA: **All taxa** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	9301	1860.15	94.72	0.000
Error	1565	30736	19.64		
Total	1570	40036			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Stony-High	6	15.17	4.71	(11.62, 18.72)	ABC
Stony-Medium	67	14.060	5.305	(12.998, 15.122)	A
Bedrock-confirmed	200	13.950	4.248	(13.335, 14.565)	A
Stony-Low	464	11.539	4.241	(11.135, 11.942)	C
Bedrock-potential	326	11.334	4.026	(10.853, 11.816)	BC
None	508	7.295	4.779	(6.910, 7.681)	D

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	8543	1708.55	93.44	0.000
Error	1565	28617	18.29		
Total	1570	37159			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Stony-High	6	14.83	4.36	(11.41, 18.26)	ABC
Stony-Medium	67	13.851	5.209	(12.826, 14.875)	A
Bedrock-confirmed	200	13.355	4.086	(12.762, 13.948)	A
Stony-Low	464	11.265	4.154	(10.876, 11.654)	C
Bedrock-potential	326	10.862	3.811	(10.397, 11.327)	BC
None	508	7.106	4.594	(6.734, 7.478)	D

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	7921	1584.21	100.33	0.000
Error	1565	24711	15.79		
Total	1570	32632			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Stony-High	6	13.67	3.98	(10.48, 16.85)	ABC
Stony-Medium	67	13.000	4.982	(12.048, 13.952)	A
Bedrock-confirmed	200	12.180	3.771	(11.629, 12.731)	A
Stony-Low	464	10.634	4.028	(10.272, 10.995)	C
Bedrock-potential	326	9.865	3.514	(9.433, 10.297)	BC
None	508	6.384	4.128	(6.038, 6.730)	D

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges & anthozoa** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	204.5	40.892	16.33	0.000
Error	1164	2915.0	2.504		
Total	1169	3119.5			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	192	3.401	1.682	(3.177, 3.625)	A
Stony-High	6	3.000	1.897	(1.732, 4.268)	ABCD
Bedrock-potential	302	2.9636	1.5515	(2.7849, 3.1422)	B
Stony-Medium	55	2.745	1.965	(2.327, 3.164)	ABCD
None	310	2.3226	1.5598	(2.1462, 2.4989)	D
Stony-Low	305	2.3180	1.4870	(2.1402, 2.4958)	CD

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly

different.

One-way ANOVA: **Sponges** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	20.87	4.175	2.48	0.030
Error	768	1291.66	1.682		
Total	773	1312.54			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	139	2.547	1.229	(2.331, 2.763)	A
Stony-Medium	28	2.536	1.598	(2.055, 3.017)	AB
Bedrock-potential	198	2.4192	1.3257	(2.2383, 2.6001)	AB
None	205	2.2585	1.3885	(2.0807, 2.4363)	AB
Stony-High	4	2.250	1.258	(0.977, 3.523)	AB
Stony-Low	200	2.1000	1.1648	(1.9200, 2.2800)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	125.4	25.077		0.000
Error	1164	1987.7	1.708		
Total	1169	2113.1	14.68		

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	192	2.7813	1.3820	(2.5962, 2.9663)	A
Stony-High	6	2.667	1.633	(1.620, 3.713)	ABCD
Stony-Medium	55	2.491	1.665	(2.145, 2.837)	AB
Bedrock-potential	302	2.4536	1.2534	(2.3061, 2.6012)	AB
None	310	2.0129	1.3194	(1.8673, 2.1585)	BD
Stony-Low	305	1.9016	1.2154	(1.7548, 2.0484)	CD

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus Annex I reef – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	5	15.27	3.053	2.71	0.019
Error	768	864.69	1.126		
Total	773	879.95			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Stony-Medium	28	2.036	1.261	(1.642, 2.429)	AB
None	205	1.7902	1.1504	(1.6448, 1.9357)	A
Stony-High	4	1.750	0.957	(0.709, 2.791)	AB
Bedrock-confirmed	139	1.6906	1.1154	(1.5140, 1.8673)	AB
Bedrock-potential	198	1.6414	1.0460	(1.4934, 1.7894)	AB
Stony-Low	200	1.4650	0.9016	(1.3177, 1.6123)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	3508	876.90	11.97	0.000
Error	272	19922	73.24		
Total	276	23430			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	46	22.54	10.51	(20.06, 25.03)	A
Stony-Low	97	18.165	8.289	(16.454, 19.876)	B
Bedrock-potential	58	15.948	5.498	(13.736, 18.161)	B
Stony-Medium	7	15.57	7.98	(9.20, 21.94)	ABC
None	69	11.75	9.59	(9.73, 13.78)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	3099	774.68	11.37	0.000
Error	272	18530	68.13		
Total	276	21629			

Annex I reef	N	Mean	StDev	95% CI	Grouping
Bedrock-confirmed	46	21.59	9.99	(19.19, 23.98)	A
Stony-Low	97	17.340	8.094	(15.690, 18.990)	B
Bedrock-potential	58	15.379	5.291	(13.246, 17.513)	BC
Stony-Medium	7	15.29	7.72	(9.14, 21.43)	ABC
None	69	11.39	9.23	(9.44, 13.35)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	2580	644.95	11.40	0.000
Error	272	15393	56.59		
Total	276	17972			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	46	19.43	9.17	(17.25, 21.62)	A
Stony-Low	97	15.052	7.589	(13.548, 16.555)	B
Stony-Medium	7	13.71	7.13	(8.12, 19.31)	ABC
Bedrock-potential	58	13.586	4.694	(11.642, 15.531)	BC
None	69	9.986	8.154	(8.203, 11.768)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges & anthozoa** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	78.27	19.568	3.51	0.008
Error	260	1450.39	5.578		
Total	264	1528.66			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	46	5.065	2.498	(4.379, 5.751)	A
Stony-Low	95	4.389	2.394	(3.912, 4.867)	AB
Bedrock-potential	55	3.964	2.252	(3.337, 4.591)	AB
Stony-Medium	7	3.571	1.902	(1.814, 5.329)	AB
None	62	3.452	2.345	(2.861, 4.042)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	92.33	23.083	4.71	0.001
Error	260	1332.75	4.900		
Total	264	1425.08			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Stony-Low	97	3.113	2.445	(2.671, 3.556)	A
Bedrock-confirmed	46	3.109	2.213	(2.466, 3.751)	A
Bedrock-potential	58	2.362	1.989	(1.790, 2.934)	AB
Stony-Medium	7	1.857	1.676	(0.210, 3.504)	AB
None	69	1.768	2.087	(1.243, 2.293)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	55.16	13.789	3.58	0.007
Error	272	1048.29	3.854		
Total	276	1103.44			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Bedrock-confirmed	46	4.109	1.888	(3.539, 4.679)	A
Stony-Low	97	3.474	1.882	(3.082, 3.867)	AB
Stony-Medium	7	3.286	1.496	(1.825, 4.747)	AB
Bedrock-potential	58	3.190	2.047	(2.682, 3.697)	AB
None	69	2.739	2.084	(2.274, 3.204)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus Annex I reef – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Annex I reef	4	35.69	8.922	3.26	0.012
Error	272	743.72	2.734		
Total	276	779.41			

Annex I reef	N	Mean	StDev	95% CI	Grouping[a]
Stony-Low	97	2.289	1.779	(1.958, 2.619)	A
Bedrock-confirmed	46	2.152	1.549	(1.672, 2.632)	AB
Bedrock-potential	58	1.793	1.576	(1.366, 2.221)	AB
Stony-Medium	7	1.571	1.272	(0.341, 2.802)	AB
None	69	1.406	1.630	(1.014, 1.798)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOSIM: **All taxa** versus Annex I reef – from **stills**

Pairwise tests	R statistic	Sig. level (%)
None, Stony-Low	0.053	0.1
None, Bedrock-confirmed	0.057	0.6
None, Stony-Medium	-0.064	94
None, Bedrock-potential	0.116	0.1
None, Stony-High	0.061	32
Stony-Low, Bedrock-confirmed	0.150	0.1
Stony-Low, Stony-Medium	0.029	14.4
Stony-Low, Bedrock-potential	0.210	0.1
Stony-Low, Stony-High	0.210	1.9
Bedrock-confirmed, Stony-Medium	0.254	0.1
Bedrock-confirmed, Bedrock-potential	0.125	0.1
Bedrock-confirmed, Stony-High	0.079	25.2
Stony-Medium, Bedrock-potential	0.288	0.1
Stony-Medium, Stony-High	0.044	33.6
Bedrock-potential, Stony-High	0.162	8.1

One-way ANOSIM: **All taxa, sponge morphs** versus Annex I reef – from **stills**

Pairwise tests	R statistic	Sig. level (%)
None, Stony-Low	0.053	0.1
None, Bedrock-confirmed	0.06	0.1
None, Stony-Medium	-0.061	94.5
None, Bedrock-potential	0.118	0.1
None, Stony-High	0.067	30.3
Stony-Low, Bedrock-confirmed	0.161	0.1
Stony-Low, Stony-Medium	0.031	14.1
Stony-Low, Bedrock-potential	0.217	0.1
Stony-Low, Stony-High	0.222	1.9
Bedrock-confirmed, Stony-Medium	0.232	0.1
Bedrock-confirmed, Bedrock-potential	0.134	0.1
Bedrock-confirmed, Stony-High	0.056	30.4
Stony-Medium, Bedrock-potential	0.283	0.1
Stony-Medium, Stony-High	0.046	29.1
Bedrock-potential, Stony-High	0.164	8.3

One-way ANOSIM: **All taxa, no sponges** versus Annex I reef – from **stills**

Pairwise tests	R statistic	Sig. level (%)
None, Stony-Low	0.057	0.1
None, Bedrock-confirmed	0.086	0.1
None, Stony-Medium	-0.046	86.9
None, Bedrock-potential	0.133	0.1
None, Stony-High	0.087	24.2
Stony-Low, Bedrock-confirmed	0.177	0.1
Stony-Low, Stony-Medium	0.026	17.4
Stony-Low, Bedrock-potential	0.222	0.1
Stony-Low, Stony-High	0.221	2.6
Bedrock-confirmed, Stony-Medium	0.208	0.1
Bedrock-confirmed, Bedrock-potential	0.146	0.1
Bedrock-confirmed, Stony-High	0.013	42.1
Stony-Medium, Bedrock-potential	0.268	0.1
Stony-Medium, Stony-High	0.055	28.5
Bedrock-potential, Stony-High	0.141	12.4

One-way ANOSIM: **All taxa** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	0.035	13.5
Stony-Low, None	0.173	0.1
Stony-Low, Stony-Medium	0.014	40.3
Stony-Low, Bedrock-potential	0.075	0.2
Bedrock-confirmed, None	0.08	0.8
Bedrock-confirmed, Stony-Medium	0.247	2.9
Bedrock-confirmed, Bedrock-potential	0.338	0.1
None, Stony-Medium	-0.176	95.4
None, Bedrock-potential	0.151	0.1
Stony-Medium, Bedrock-potential	0.239	1.4

One-way ANOSIM: **All taxa, sponge morphs** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	0.037	14
Stony-Low, None	0.172	0.1
Stony-Low, Stony-Medium	-0.009	50.9
Stony-Low, Bedrock-potential	0.081	0.2
Bedrock-confirmed, None	0.083	0.5
Bedrock-confirmed, Stony-Medium	0.222	4.3
Bedrock-confirmed, Bedrock-potential	0.338	0.1
None, Stony-Medium	-0.178	94.6
None, Bedrock-potential	0.155	0.1
Stony-Medium, Bedrock-potential	0.225	1.7

One-way ANOSIM: **All taxa, no sponges** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	0.044	9.9
Stony-Low, None	0.148	0.1
Stony-Low, Stony-Medium	-0.046	60.9
Stony-Low, Bedrock-potential	0.073	0.6
Bedrock-confirmed, None	0.096	0.2
Bedrock-confirmed, Stony-Medium	0.206	5.2
Bedrock-confirmed, Bedrock-potential	0.360	0.1
None, Stony-Medium	-0.167	91
None, Bedrock-potential	0.164	0.1
Stony-Medium, Bedrock-potential	0.218	1.9

One-way ANOSIM: **Sponges & anthozoa** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	-0.038	93.7
Stony-Low, None	0.091	0.1
Stony-Low, Stony-Medium	0.029	35.2
Stony-Low, Bedrock-potential	0.019	15.7
Bedrock-confirmed, None	-0.032	96.9
Bedrock-confirmed, Stony-Medium	0.151	6.4
Bedrock-confirmed, Bedrock-potential	0.071	0.2
None, Stony-Medium	-0.097	88.5
None, Bedrock-potential	0.044	0.4
Stony-Medium, Bedrock-potential	-0.011	51.3

One-way ANOSIM: **Sponges** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	-0.012	62.5
Stony-Low, None	0.099	0.1
Stony-Low, Stony-Medium	0.116	15.7
Stony-Low, Bedrock-potential	0.015	22.3
Bedrock-confirmed, None	0.010	24
Bedrock-confirmed, Stony-Medium	0.154	10.2
Bedrock-confirmed, Bedrock-potential	0.017	11.1
None, Stony-Medium	-0.018	58.7
None, Bedrock-potential	0.024	4.1
Stony-Medium, Bedrock-potential	0.076	22.9

One-way ANOSIM: **Sponge morphs & anthozoa** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	-0.042	96.7
Stony-Low, None	0.090	0.1
Stony-Low, Stony-Medium	-0.009	50.8
Stony-Low, Bedrock-potential	0.029	8.4
Bedrock-confirmed, None	-0.041	99.8
Bedrock-confirmed, Stony-Medium	0.081	16.7
Bedrock-confirmed, Bedrock-potential	0.063	0.6
None, Stony-Medium	-0.114	91
None, Bedrock-potential	0.045	0.5
Stony-Medium, Bedrock-potential	-0.048	69.3

One-way ANOSIM: **Sponge morphs** versus Annex I reef – from **video**

Pairwise tests	R statistic	Sig. level (%)
Stony-Low, Bedrock-confirmed	-0.020	68.9
Stony-Low, None	0.100	0.1
Stony-Low, Stony-Medium	0.077	23.7
Stony-Low, Bedrock-potential	0.023	14.7
Bedrock-confirmed, None	0.002	36
Bedrock-confirmed, Stony-Medium	0.082	23.3
Bedrock-confirmed, Bedrock-potential	0.000	40.4
None, Stony-Medium	-0.040	70
None, Bedrock-potential	0.024	4.5
Stony-Medium, Bedrock-potential	0.050	26.4

A2.4 Tests between observed reef elevation categories

One-way ANOVA: **All taxa** versus reef elevation – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	5	10157	2031.33	106.39	0.000
Error	1565	29880	19.09		
Total	1570	40036			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
1.1m - 5m	115	13.670	4.065	(12.870, 14.469)	A
64mm - 1m	496	13.254	4.200	(12.869, 13.639)	A
5.1m - 10m	18	10.78	4.75	(8.76, 12.80)	AB
Unknown	274	10.620	3.731	(10.103, 11.138)	B
<64mm	160	10.137	4.692	(9.460, 10.815)	B
N/A	508	7.295	4.779	(6.915, 7.676)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus reef elevation – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	5	9531	1906.21	107.98	0.000
Error	1565	27628	17.65		
Total	1570	37159			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
1.1m - 5m	115	13.261	3.972	(12.492, 14.029)	A
64mm - 1m	496	12.877	4.059	(12.507, 13.247)	A
5.1m - 10m	18	10.67	4.56	(8.72, 12.61)	AB
Unknown	274	10.197	3.500	(9.699, 10.695)	B
<64mm	160	9.738	4.543	(9.086, 10.389)	B
N/A	508	7.106	4.594	(6.741, 7.472)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus reef elevation – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	5	8950	1790.02	118.29	0.000
Error	1565	23682	15.13		
Total	1570	32632			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
1.1m - 5m	115	12.235	3.784	(11.523, 12.946)	A
64mm - 1m	496	12.004	3.832	(11.661, 12.347)	A
5.1m - 10m	18	10.056	4.193	(8.257, 11.854)	AB
Unknown	274	9.365	3.191	(8.904, 9.826)	B
<64mm	160	8.944	4.387	(8.341, 9.547)	B
N/A	508	6.384	4.128	(6.045, 6.722)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge & anthozoa** versus reef elevation – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	5	67.19	13.438	5.12	0.000
Error	1164	3052.32	2.622		
Total	1169	3119.51			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
1.1m - 5m	112	3.071	1.456	(2.771, 3.372)	A
64mm - 1m	384	2.8411	1.8017	(2.6790, 3.0033)	A
5.1m - 10m	16	2.750	1.612	(1.956, 3.544)	AB
<64mm	110	2.718	1.575	(2.415, 3.021)	AB
Unknown	238	2.7143	1.4706	(2.5083, 2.9202)	AB
N/A	310	2.3226	1.5598	(2.1421, 2.5030)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus reef elevation – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	5	43.47	8.694	4.89	0.000
Error	1164	2069.65	1.778		
Total	1169	2113.12			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
1.1m - 5m	112	2.652	1.299	(2.405, 2.899)	A
5.1m - 10m	16	2.625	1.500	(1.971, 3.279)	ABC
64mm - 1m	384	2.3542	1.4684	(2.2207, 2.4877)	AB
Unknown	238	2.2269	1.1579	(2.0573, 2.3965)	ABC
<64mm	110	2.136	1.238	(1.887, 2.386)	BC
N/A	310	2.0129	1.3194	(1.8643, 2.1615)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly

different.

One-way ANOVA: **All taxa** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	4564	760.62	10.78	0.000
Error	271	19114	70.53		
Total	277	23677			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
>10m	2	33.5	17.7	(21.8, 45.2)	AB
5.1m - 10m	8	26.88	13.26	(21.03, 32.72)	A
1.1m - 5m	54	21.76	8.82	(19.51, 24.01)	A
<64mm	18	17.56	6.27	(13.66, 21.45)	ABCD
64mm - 1m	94	16.596	7.776	(14.890, 18.301)	BC
Unknown	32	15.281	5.396	(12.358, 18.204)	CD
N/A	70	11.76	9.52	(9.78, 13.73)	D

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	4047	674.51	10.26	0.000
Error	271	17809	65.72		
Total	277	21856			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
>10m	2	32.0	15.6	(20.7, 43.3)	ABC
5.1m - 10m	8	25.50	12.77	(19.86, 31.14)	A
1.1m - 5m	54	20.87	8.40	(18.70, 23.04)	A
<64mm	18	16.78	6.15	(13.02, 20.54)	ABCD
64mm - 1m	94	15.840	7.640	(14.194, 17.487)	C
Unknown	32	14.906	5.133	(12.085, 17.728)	BCD
N/A	70	11.40	9.17	(9.49, 13.31)	D

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	3213	535.58	9.72	0.000
Error	271	14932	55.10		
Total	277	18145			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
>10m	2	30.00	12.73	(19.67, 40.33)	A
5.1m - 10m	8	22.38	12.12	(17.21, 27.54)	A
1.1m - 5m	54	18.30	7.63	(16.31, 20.28)	AB
<64mm	18	15.17	6.19	(11.72, 18.61)	ABCD
64mm - 1m	94	13.755	7.249	(12.248, 15.263)	C
Unknown	32	13.563	4.384	(10.979, 16.146)	BCD
N/A	70	10.014	8.098	(8.268, 11.761)	D

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges & anthozoa** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	180.4	30.062	5.75	0.000
Error	258	1348.3	5.226		
Total	264	1528.7			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
5.1m - 10m	8	6.750	2.659	(5.158, 8.342)	A
>10m	2	6.00	4.24	(2.82, 9.18)	ABCD
1.1m - 5m	54	5.130	2.434	(4.517, 5.742)	AB
64mm - 1m	92	4.283	2.245	(3.813, 4.752)	ABCD
<64mm	18	3.667	1.847	(2.606, 4.728)	BCD
N/A	62	3.452	2.345	(2.880, 4.023)	D
Unknown	29	3.103	2.024	(2.268, 3.939)	CD

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	153.1	25.518	5.41	0.000
Error	271	1278.7	4.718		
Total	277	1431.8			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
5.1m - 10m	8	4.500	2.138	(2.988, 6.012)	A
>10m	2	3.50	4.95	(0.48, 6.52)	ABC
1.1m - 5m	54	3.463	2.271	(2.881, 4.045)	A
64mm - 1m	92	2.840	2.201	(2.399, 3.282)	AB
<64mm	18	2.389	2.279	(1.381, 3.397)	ABC
N/A	62	1.743	2.083	(1.232, 2.254)	C
Unknown	29	1.719	1.888	(0.963, 2.475)	BC

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	138.8	23.132	6.42	0.000
Error	271	975.7	3.600		
Total	277	1114.5			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
5.1m - 10m	8	5.375	2.066	(4.054, 6.696)	A
>10m	2	4.50	2.12	(1.86, 7.14)	ABCD
1.1m - 5m	54	4.241	1.990	(3.732, 4.749)	AB
64mm - 1m	94	3.436	1.799	(3.051, 3.821)	ABCD
<64mm	18	2.889	1.278	(2.008, 3.769)	BCD
N/A	70	2.700	2.095	(2.254, 3.146)	D
Unknown	32	2.438	1.795	(1.777, 3.098)	CD

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus reef elevation – **video**

Source	DF	Adj SS	Adj MS	F value	P value
Reef elevation	6	69.62	11.603	4.41	0.000
Error	271	713.48	2.633		
Total	277	783.10			

Elevation	N	Mean	StDev	95% CI	Grouping[a]
5.1m - 10m	8	3.125	1.458	(1.996, 4.254)	ABC
1.1m - 5m	54	2.574	1.711	(2.139, 3.009)	A
64mm - 1m	94	2.085	1.611	(1.756, 2.415)	ABC
>10m	2	2.00	2.83	(-0.26, 4.26)	ABC
<64mm	18	1.611	1.539	(0.858, 2.364)	ABC
N/A	70	1.386	1.627	(1.004, 1.768)	C
Unknown	32	1.344	1.516	(0.779, 1.908)	BC

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOSIM: **All taxa** versus reef elevation – from **stills**

Pairwise tests	R statistic	Sig. level (%)
N/A, 64mm - 1m	0.141	0.1
N/A, Unknown	0.071	0.1
N/A, 1.1m - 5m	0.007	38.2
N/A, <64mm	-0.120	100
N/A, 5.1m - 10m	0.164	2.1
64mm - 1m, Unknown	0.217	0.1
64mm - 1m, 1.1m - 5m	0.035	7.4
64mm - 1m, <64mm	0.132	0.1
64mm - 1m, 5.1m - 10m	0.311	0.1
Unknown, 1.1m - 5m	0.179	0.1
Unknown, <64mm	0.354	0.1
Unknown, 5.1m - 10m	0.351	0.1
1.1m - 5m, <64mm	0.300	0.1
1.1m - 5m, 5.1m - 10m	0.232	0.2
<64mm, 5.1m - 10m	0.524	0.1

One-way ANOSIM: **All taxa, sponge morphs** versus reef elevation – from **stills**

Pairwise tests	R statistic	Sig. level (%)
N/A, 64mm - 1m	0.141	0.1
N/A, Unknown	0.075	0.1
N/A, 1.1m - 5m	0.012	33.3
N/A, <64mm	-0.123	100
N/A, 5.1m - 10m	0.169	1.9
64mm - 1m, Unknown	0.228	0.1
64mm - 1m, 1.1m - 5m	0.041	5
64mm - 1m, <64mm	0.131	0.1
64mm - 1m, 5.1m - 10m	0.310	0.1
Unknown, 1.1m - 5m	0.185	0.1
Unknown, <64mm	0.366	0.1
Unknown, 5.1m - 10m	0.343	0.1
1.1m - 5m, <64mm	0.320	0.1
1.1m - 5m, 5.1m - 10m	0.222	0.4
<64mm, 5.1m - 10m	0.537	0.1

One-way ANOSIM: **All taxa, no sponges** versus reef elevation – from **stills**

Pairwise tests	R statistic	Sig. level (%)
N/A, 64mm - 1m	0.149	0.1
N/A, Unknown	0.092	0.1
N/A, 1.1m - 5m	0.041	6.9
N/A, <64mm	-0.118	100
N/A, 5.1m - 10m	0.196	0.6
64mm - 1m, Unknown	0.236	0.1
64mm - 1m, 1.1m - 5m	0.058	0.8
64mm - 1m, <64mm	0.130	0.1
64mm - 1m, 5.1m - 10m	0.322	0.1
Unknown, 1.1m - 5m	0.206	0.1
Unknown, <64mm	0.379	0.1
Unknown, 5.1m - 10m	0.358	0.1
1.1m - 5m, <64mm	0.352	0.1
1.1m - 5m, 5.1m - 10m	0.207	1
<64mm, 5.1m - 10m	0.578	0.1

One-way ANOSIM: **Sponge morphs & anthozoa** versus reef elevation – from **stills**

Pairwise tests	R statistic	Sig. level (%)
N/A, 64mm - 1m	0.040	0.1
N/A, Unknown	0.020	1.3
N/A, 1.1m - 5m	-0.075	100
N/A, <64mm	-0.033	100
N/A, 5.1m - 10m	-0.041	92.2
64mm - 1m, Unknown	0.034	0.1
64mm - 1m, 1.1m - 5m	-0.120	100
64mm - 1m, <64mm	0.038	1.3
64mm - 1m, 5.1m - 10m	-0.023	64.9
Unknown, 1.1m - 5m	0.043	1.7
Unknown, <64mm	0.134	0.1
Unknown, 5.1m - 10m	0.067	13.6
1.1m - 5m, <64mm	0.032	0.7
1.1m - 5m, 5.1m - 10m	0.140	2.8
<64mm, 5.1m - 10m	-0.040	80.8

One-way ANOSIM: **All taxa** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.035	63.9
64mm - 1m, N/A	0.313	0.1
64mm - 1m, 1.1m - 5m	-0.012	73.8
64mm - 1m, Unknown	0.120	0.8
64mm - 1m, <64mm	-0.048	81.2
64mm - 1m, >10m	0.185	13.9
5.1m - 10m, N/A	-0.069	70.2
5.1m - 10m, 1.1m - 5m	-0.021	54.6
5.1m - 10m, Unknown	0.633	0.1
5.1m - 10m, <64mm	0.124	9.1
5.1m - 10m, >10m	0.050	44.4
N/A, 1.1m - 5m	0.310	0.1
N/A, Unknown	0.099	0.6
N/A, <64mm	-0.108	95.7
N/A, >10m	-0.004	37.2
1.1m - 5m, Unknown	0.389	0.1
1.1m - 5m, <64mm	0.130	2.1
1.1m - 5m, >10m	0.136	22.2
Unknown, <64mm	0.441	0.1
Unknown, >10m	0.727	1.6
<64mm, >10m	0.212	11.6

One-way ANOSIM: **All taxa, sponge morphs** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.046	67.9
64mm - 1m, N/A	0.306	0.1
64mm - 1m, 1.1m - 5m	-0.015	71.5
64mm - 1m, Unknown	0.121	0.8
64mm - 1m, <64mm	-0.040	75.8
64mm - 1m, >10m	0.181	13.4
5.1m - 10m, N/A	-0.075	73.3
5.1m - 10m, 1.1m - 5m	-0.010	51.3
5.1m - 10m, Unknown	0.637	0.1
5.1m - 10m, <64mm	0.109	11.2
5.1m - 10m, >10m	0.039	46.7
N/A, 1.1m - 5m	0.310	0.1
N/A, Unknown	0.104	0.3
N/A, <64mm	-0.107	97.1
N/A, >10m	0.001	44.6
1.1m - 5m, Unknown	0.403	0.1
1.1m - 5m, <64mm	0.144	0.9
1.1m - 5m, >10m	0.134	22.9
Unknown, <64mm	0.449	0.1
Unknown, >10m	0.725	1.8
<64mm, >10m	0.209	11.1

One-way ANOSIM: **All taxa, no sponges** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.007	48.5
64mm - 1m, N/A	0.278	0.1
64mm - 1m, 1.1m - 5m	-0.015	73.3
64mm - 1m, Unknown	0.073	7.4
64mm - 1m, <64mm	-0.049	77.2
64mm - 1m, >10m	0.170	19.5
5.1m - 10m, N/A	-0.031	59.1
5.1m - 10m, 1.1m - 5m	0.031	38.1
5.1m - 10m, Unknown	0.654	0.1
5.1m - 10m, <64mm	0.137	6.4
5.1m - 10m, >10m	0.015	44.4
N/A, 1.1m - 5m	0.313	0.1
N/A, Unknown	0.119	0.1
N/A, <64mm	-0.090	93.9
N/A, >10m	0.036	37.4
1.1m - 5m, Unknown	0.366	0.1
1.1m - 5m, <64mm	0.129	2.6
1.1m - 5m, >10m	0.098	29.5
Unknown, <64mm	0.467	0.1
Unknown, >10m	0.740	1.8
<64mm, >10m	0.222	11.6

One-way ANOSIM: **Sponges & anthozoa** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.105	91.9
64mm - 1m, N/A	0.215	0.1
64mm - 1m, 1.1m - 5m	-0.026	90.4
64mm - 1m, Unknown	0.194	0.1
64mm - 1m, <64mm	0.001	47.7
64mm - 1m, >10m	0.013	41.5
5.1m - 10m, N/A	-0.198	99.6
5.1m - 10m, 1.1m - 5m	-0.078	80.6
5.1m - 10m, Unknown	0.136	7.9
5.1m - 10m, <64mm	0.001	40
5.1m - 10m, >10m	0.157	31.1
N/A, 1.1m - 5m	0.171	0.1
N/A, Unknown	0.025	11.3
N/A, <64mm	-0.089	99.7
N/A, >10m	-0.192	93.3
1.1m - 5m, Unknown	0.235	0.1
1.1m - 5m, <64mm	0.093	3.1
1.1m - 5m, >10m	0.081	29.3
Unknown, <64mm	0.052	11.9
Unknown, >10m	-0.004	42.4
<64mm, >10m	0.006	42.6

One-way ANOSIM: **Sponges** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.149	94.6
64mm - 1m, N/A	0.145	0.1
64mm - 1m, 1.1m - 5m	-0.026	85.9
64mm - 1m, Unknown	0.110	1.2
64mm - 1m, <64mm	0.000	46.7
64mm - 1m, >10m	0.084	35.8
5.1m - 10m, N/A	-0.175	100
5.1m - 10m, 1.1m - 5m	-0.138	91.9
5.1m - 10m, Unknown	-0.112	92.1
5.1m - 10m, <64mm	-0.011	46.7
5.1m - 10m, >10m	0.218	20
N/A, 1.1m - 5m	0.147	0.1
N/A, Unknown	-0.017	83.6
N/A, <64mm	-0.061	96.8
N/A, >10m	-0.100	74.9
1.1m - 5m, Unknown	0.162	0.1
1.1m - 5m, <64mm	0.094	9.6
1.1m - 5m, >10m	0.187	23.4
Unknown, <64mm	-0.037	81.7
Unknown, >10m	-0.032	57
<64mm, >10m	0.079	33.7

One-way ANOSIM: **Sponge morphs & anthozoa** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.125	95.9
64mm - 1m, N/A	0.203	0.1
64mm - 1m, 1.1m - 5m	-0.033	95.1
64mm - 1m, Unknown	0.215	0.1
64mm - 1m, <64mm	0.024	29.3
64mm - 1m, >10m	0.005	41
5.1m - 10m, N/A	-0.222	100
5.1m - 10m, 1.1m - 5m	-0.058	72.1
5.1m - 10m, Unknown	0.172	3.9
5.1m - 10m, <64mm	-0.036	60.8
5.1m - 10m, >10m	0.185	31.1
N/A, 1.1m - 5m	0.156	0.1
N/A, Unknown	0.034	8.2
N/A, <64mm	-0.081	99.3
N/A, >10m	-0.185	92.7
1.1m - 5m, Unknown	0.258	0.1
1.1m - 5m, <64mm	0.115	1.9
1.1m - 5m, >10m	0.082	29.9
Unknown, <64mm	0.061	7.3
Unknown, >10m	-0.013	47.4
<64mm, >10m	-0.025	48.9

One-way ANOSIM: **Sponge morphs** versus reef elevation – from **video**

Pairwise tests	R statistic	Sig. level (%)
64mm - 1m, 5.1m - 10m	-0.173	97.9
64mm - 1m, N/A	0.137	0.1
64mm - 1m, 1.1m - 5m	-0.033	92.8
64mm - 1m, Unknown	0.130	0.9
64mm - 1m, <64mm	0.017	36.4
64mm - 1m, >10m	0.063	45.3
5.1m - 10m, N/A	-0.200	100
5.1m - 10m, 1.1m - 5m	-0.130	91.3
5.1m - 10m, Unknown	-0.107	90.6
5.1m - 10m, <64mm	-0.058	64.2
5.1m - 10m, >10m	0.166	37.8
N/A, 1.1m - 5m	0.135	0.1
N/A, Unknown	-0.008	58.5
N/A, <64mm	-0.054	94
N/A, >10m	-0.099	79.1
1.1m - 5m, Unknown	0.189	0.1
1.1m - 5m, <64mm	0.110	5.7
1.1m - 5m, >10m	0.172	26.5
Unknown, <64mm	-0.040	84.8
Unknown, >10m	-0.063	72.2
<64mm, >10m	0.021	47.9

A2.5 Tests between observed MNCR biotope categories

One-way ANOVA: **All taxa** versus MNCR biotope – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	3	9623	3207.68	165.27	0.000
Error	1567	30413	19.41		
Total	1570	40036			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	1055	12.113	4.446	(11.847, 12.379)	A
CR.MCR.EcCr/SS.SCS.CCS	58	11.534	4.780	(10.400, 12.669)	AB
SS.SMx.CMx	74	9.581	4.823	(8.577, 10.586)	B
SS.SCS.CCS	384	6.305	4.145	(5.864, 6.746)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus MNCR biotope – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	3	8838	2945.90	162.99	0.000
Error	1567	28322	18.07		
Total	1570	37159			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	1055	11.711	4.281	(11.454, 11.968)	A
CR.MCR.EcCr/SS.SCS.CCS	58	11.414	4.776	(10.319, 12.509)	A
SS.SMx.CMx	74	9.257	4.578	(8.287, 10.226)	B
SS.SCS.CCS	384	6.156	4.016	(5.731, 6.582)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus MNCR biotope – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	3	8172	2724.13	174.52	0.000
Error	1567	24459	15.61		
Total	1570	32632			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	1055	10.828	4.003	(10.590, 11.067)	A
CR.MCR.EcCr/SS.SCS.CCS	58	10.776	4.546	(9.758, 11.793)	A
SS.SMx.CMx	74	8.378	4.183	(7.478, 9.279)	B
SS.SCS.CCS	384	5.503	3.653	(5.107, 5.898)	C

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges & anthozoa** versus MNCR biotope – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	3	77.88	25.962	9.95	0.000
Error	1166	3041.62	2.609		
Total	1169	3119.51			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	844	2.8436	1.6644	(2.7345, 2.9527)	A
CR.MCR.EcCr/SS.SCS.CCS	48	2.500	1.384	(2.043, 2.957)	AB
SS.SMx.CMx	57	2.368	1.633	(1.949, 2.788)	AB
SS.SCS.CCS	221	2.2127	1.4570	(1.9995, 2.4258)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs & anthozoa** versus MNCR biotope – **stills**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	3	32.03	10.677	5.98	0.000
Error	1166	2081.09	1.785		
Total	1169	2113.12			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr/SS.SCS.CCS	48	2.354	1.280	(1.976, 2.733)	AB
CR.MCR.EcCr	844	2.3412	1.3594	(2.2510, 2.4315)	A
SS.SCS.CCS	221	1.9548	1.2820	(1.7784, 2.1311)	B
SS.SMx.CMx	57	1.947	1.231	(1.600, 2.295)	AB

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa** versus MNCR biotope – **video**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	2	1956	978.00	12.38	0.000
Error	275	21721	78.99		
Total	277	23677			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	179	18.559	8.448	(17.251, 19.866)	A
SS.SMx.CMx	11	17.73	10.61	(12.45, 23.00)	AB
SS.SCS.CCS	88	12.82	9.52	(10.95, 14.68)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, sponge morphs** versus MNCR biotope – **video**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	2	1759	879.47	12.03	0.000
Error	275	20097	73.08		
Total	277	21856			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	179	17.816	8.110	(16.558, 19.074)	A
SS.SMx.CMx	11	16.73	10.35	(11.65, 21.80)	AB
SS.SCS.CCS	88	12.364	9.172	(10.570, 14.158)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **All taxa, no sponges** versus MNCR biotope – **video**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	2	1563	781.34	12.96	0.000
Error	275	16583	60.30		
Total	277	18145			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
CR.MCR.EcCr	179	15.838	7.494	(14.695, 16.981)	A
SS.SMx.CMx	11	13.82	9.25	(9.21, 18.43)	AB
SS.SCS.CCS	88	10.693	8.116	(9.064, 12.323)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponges** versus MNCR biotope – **video**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	2	41.19	20.596	4.07	0.018
Error	275	1390.57	5.057		
Total	277	1431.76			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
SS.SMx.CMx	11	3.909	2.071	(2.574, 5.244)	A
CR.MCR.EcCr	179	2.721	2.206	(2.390, 3.052)	AB
SS.SCS.CCS	88	2.125	2.353	(1.653, 2.597)	B

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOVA: **Sponge morphs** versus MNCR biotope – **video**

Source	DF	Adj SS	Adj MS	F value	P value
MNCR biotope	2	16.83	8.417	3.02	0.050
Error	275	766.26	2.786		
Total	277	783.10			

Biotope	N	Mean	StDev	95% CI	Grouping[a]
SS.SMx.CMx	11	2.909	1.640	(1.918, 3.900)	A
CR.MCR.EcCr	179	1.978	1.611	(1.732, 2.223)	A
SS.SCS.CCS	88	1.670	1.786	(1.320, 2.021)	A

[a] Grouping information using the Tukey method and 95% CI. Groups that do not share a letter are significantly different.

One-way ANOSIM: **All taxa** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.294	0.1
SS.SMx.CMx, SS.SCS.CCS	-0.081	99.8
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.394	0.1
CR.MCR.EcCr, SS.SCS.CCS	0.366	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	-0.012	65.5
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.066	94.2

One-way ANOSIM: **All taxa, sponge morphs** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.295	0.1
SS.SMx.CMx, SS.SCS.CCS	-0.081	99.5
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.398	0.1
CR.MCR.EcCr, SS.SCS.CCS	0.360	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	-0.026	80.5
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.063	94.8

One-way ANOSIM: **All taxa, no sponges** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.299	0.1
SS.SMx.CMx, SS.SCS.CCS	-0.071	97.9
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.413	0.1
CR.MCR.EcCr, SS.SCS.CCS	0.349	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	-0.042	91.3
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.045	85.2

One-way ANOSIM: **Sponges & anthozoa** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.128	0.1
SS.SMx.CMx, SS.SCS.CCS	-0.035	99.7
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.198	0.1
CR.MCR.EcCr, SS.SCS.CCS	0.172	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	-0.011	63.5
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.043	100

One-way ANOSIM: **Sponges** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.031	12.6
SS.SMx.CMx, SS.SCS.CCS	-0.040	100
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.012	12.6
CR.MCR.EcCr, SS.SCS.CCS	0.120	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	0.087	0.1
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.022	94.2

One-way ANOSIM: **Sponge morphs & anthozoa** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.129	0.1
SS.SMx.CMx, SS.SCS.CCS	-0.035	99.6
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.198	0.1
CR.MCR.EcCr, SS.SCS.CCS	0.169	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	-0.028	80.4
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.043	100

One-way ANOSIM: **Sponge morphs** versus MNCR biotope – from **stills**

Pairwise tests	R statistic	Sig. level (%)
SS.SMx.CMx, CR.MCR.EcCr	0.026	16.9
SS.SMx.CMx, SS.SCS.CCS	-0.041	100
SS.SMx.CMx, CR.MCR.EcCr/SS.SCS.CCS	0.010	14.5
CR.MCR.EcCr, SS.SCS.CCS	0.115	0.1
CR.MCR.EcCr, CR.MCR.EcCr/SS.SCS.CCS	0.076	1.2
SS.SCS.CCS, CR.MCR.EcCr/SS.SCS.CCS	-0.024	95.8

One-way ANOSIM: **All taxa** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	0.316	0.1
SS.SMX.CMx, SS.SCS.CCS	-0.024	57.4
CR.MCR.EcCr, SS.SCS.CCS	0.285	0.1

One-way ANOSIM: **All taxa, sponge morphs** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	0.321	0.1
SS.SMX.CMx, SS.SCS.CCS	-0.028	57.4
CR.MCR.EcCr, SS.SCS.CCS	0.286	0.1

One-way ANOSIM: **All taxa, no sponges** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	0.375	0.1
SS.SMX.CMx, SS.SCS.CCS	0.002	44.2
CR.MCR.EcCr, SS.SCS.CCS	0.275	0.1

One-way ANOSIM: **Sponges & anthozoa** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	0.085	14.2
SS.SMX.CMx, SS.SCS.CCS	0.001	47
CR.MCR.EcCr, SS.SCS.CCS	0.112	0.1

One-way ANOSIM: **Sponges** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	-0.067	76.7
SS.SMX.CMx, SS.SCS.CCS	-0.104	93.7
CR.MCR.EcCr, SS.SCS.CCS	0.103	0.1

One-way ANOSIM: **Sponge morphs & anthozoa** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	0.077	14.3
SS.SMX.CMx, SS.SCS.CCS	-0.004	52.1
CR.MCR.EcCr, SS.SCS.CCS	0.105	0.1

One-way ANOSIM: **Sponge morphs** versus MNCR biotope – from **video**

Pairwise tests	R statistic	Sig. level (%)
SS.SMX.CMx, CR.MCR.EcCr	-0.085	84.2
SS.SMX.CMx, SS.SCS.CCS	-0.109	96
CR.MCR.EcCr, SS.SCS.CCS	0.100	0.1

Appendix 3   Characteristic taxa of various sample groups

The tables below present the output from SIMPER routines that deliver the average similarity of taxa to each group within which they occur. Similarity contribution values have been colour coded on a scale from red (high) to yellow (medium) to green (low) for ease of interpretation.

A3.1 Tests between observed Annex I reef categories

Results from SIMPER routine on **all taxa** from **stills**

Taxa	None	Stony - Low	Stony - Medium	Stony – High	Bedrock - potential	Bedrock - confirmed
Bryozoa_EN	0.62	0.95	0.97	1	0.87	0.8
Spirobranchus	0.71	0.94	0.97	0.67	0.9	0.87
Ophiocomina nigra	0.07	0.36	0.53	0.83	0.58	0.81
Corallinaceae	0.03	0.23	0.31	0.83	0.75	0.77
Hydrozoa_AR	0.37	0.6	0.66	0.5	0.18	0.48
Celleporidae_GEN.INDET	0.05	0.31	0.62	0.83	0.32	0.54
Parasmittina	0.16	0.48	0.62	0.5	0.33	0.45
Porifera_EN	0.23	0.33	0.31	0.33	0.54	0.63
Caryophyllia	0.07	0.16	0.49	0.67	0.37	0.57
Ophiothrix fragilis	0.02	0.16	0.43	0.67	0.32	0.55
Calliostoma	0.03	0.14	0.38	0.83	0.21	0.41
Hymedesmia (Hymedesmia) paupertas	0.13	0.24	0.19	0.33	0.42	0.56
Serpulidae_GEN.INDET	0.22	0.52	0.38		0.27	0.43
Alcyonium digitatum	0.03	0.09	0.12	0.5	0.44	0.41
Ophiuroidea	0.07	0.22	0.12	0.33	0.57	0.23
Securiflustra securifrons	0.1	0.24	0.34	0.33	0.19	0.22
Bryozoa_AR	0.18	0.42	0.26	0.17	0.18	0.14
Flustra foliacea	0.14	0.23	0.28	0.33	0.13	0.11
Gastropoda	0.08	0.23	0.49		0.2	0.14
Sessilia	0.15	0.22	0.37	0.17	0.11	0.12
Abietinaria abietina	0.02	0.15	0.4	0.33	0.11	0.06
Animalia_EN	0.06	0.15	0.06	0.17	0.14	0.43
Urticina_SP.INDET	0.02	0.06	0.24	0.33	0.1	0.26
Porifera_MA	0.07	0.08	0.06	0.33	0.16	0.14
Caridea	0.08	0.12	0.21	0.33	0.03	0.07
Crossaster papposus	0.04	0.09	0.12		0.29	0.27
Hydrozoa_UN	0.01	0.03	0.1	0.5	0.06	0.11
Smittinoidea	0.15	0.25			0.01	0.37
Porifera_FL	0.06	0.06	0.16	0.17	0.13	0.14
Antedon_SP.INDET	0.01	0.05	0.04	0.5	0.02	0.08
Munida rugosa	0.02	0.09	0.26	0.17	0.04	0.09
Porania (Porania) pulvillus	0.1	0.17	0.15		0.09	0.09
Cellepora pumicosa	0.01	0.06	0.03	0.33	0.04	0.09
Ophiura albida	0.15	0.18	0.09		0.04	0.08
Animalia_AR	0.07	0.16			0.29	
Nemertesia_SP.INDET	0.02	0.07	0.22	0.17	0.02	0.02
Axinellidae_GEN.INDET	0.04	0.03	0.13	0.17	0.01	0.12
Asteriidae_GEN.INDET		0.02	0.03	0.33	0.03	0.03
Rhizocaulus	0.1	0.18	0.13		0.01	0.02
Haleciidae	0.02	0.05	0.09	0.17		0.07
Ebalia	0.04	0.09	0.04	0.17	0.02	0.01
Gibbula	0.01	0.04	0.12		0.08	0.12
Porifera_UN	0.04	0.04	0.04	0.17	0.05	0.03

Taxa	None	Stony - Low	Stony - Medium	Stony – High	Bedrock - potential	Bedrock - confirmed
Serpula	0.11	0.13				0.13
Thuiaria thuja	0.01	0.06	0.13		0.07	0.1
Trisopterus_SP.INDET		0.01		0.33	0.01	0.01
Polyplacophora	0.02	0.06	0.04	0.17	0.02	0.04
Galatheidae_GEN.INDET	0.06	0.16	0.04		0.01	0.07
Spirorbis	0.01	0.06	0.15		0.07	0.03
Antedon bifida		0.01	0.22		0.03	0.05
Luidia	0.01	0.04	0.01	0.17	0.02	0.06
Paguridae_GEN.INDET	0.03	0.04	0.13		0.04	0.06
Actiniidae	0.01	0.04			0.25	
Parazoanthus	0.05	0.08	0.13			
Sertulariidae_GEN.INDET	0.03	0.09	0.09			0.05
Actiniaria_FAM.INDET	0.08	0.04	0.04		0.01	0.06
Tubularia			0.01	0.17	0.02	0.02
Scleractinia	0.04	0.03	0.13			0.02
Porifera_GL	0.06	0.02	0.04		0.04	0.05
Reteporella	0.04	0.06	0.09		0.01	0.01
Rhodophyta_FAM.INDET		0.02			0.14	0.04
Echinoidea		0.05	0.03		0.07	0.04
Pagurus	0.02	0.02	0.01		0.13	0.01
Asteroidea	0.01	0.04			0.08	0.05
Necora puber				0.17		0.01
Polymastia boletiformis	0.06	0.02	0.01		0.04	0.05
Stichastrella rosea		0.03	0.04		0.02	0.07
Alcyonidium diaphanum	0.01	0.03	0.03		0.02	0.06
Asterias rubens		0.02	0.07		0.02	0.02
Sabellidae_GEN.INDET	0.01	0.02	0.09			0.01
Smittina	0.02	0.05				0.06
Crisiidae		0.01	0.1			0.01
Actinopterygii	0.02	0.03	0.01		0.03	0.03
Omalosecosa ramulosa	0.01	0.03	0.03		0.01	0.04
Chaetopterus	0.02	0.03	0.04		0.01	0.01
Echinus		0.01			0.04	0.06
Flustrina	0.02	0.03				0.06
Porella compressa	0.03	0.05				0.03
Axinella infundibuliformis	0.01	0.03	0.01		0.04	0.02
Anomiidae	0.01	0.02	0.06			0.01
Antedonidae_GEN.INDET		0.03			0.02	0.05
Lanice conchilega	0.03	0.03	0.03			0.01
Pecten maximus	0.03	0.02	0.04			0.01
Porifera_AR	0.01	0.01	0.04		0.01	0.03
Anthozoa	0.02	0.04				0.03
Caryophylliidae_GEN.INDET	0.03	0.02	0.01			0.03
Corynactis viridis		0.01			0.04	0.04
Palaemonidae	0.01	0.07				
Sagartiidae_GEN.INDET		0.01			0.03	0.04
Ascidia virginea		0.01	0.01		0.04	0.02
Ascidiacea		0.02				0.05
Decapoda		0.03	0.01		0.03	
Cellaria		0.03			0.01	0.02
Crangonidae		0.03			0.03	
Gracilechinus acutus			0.03		0.02	0.01
Inachidae_GEN.INDET		0.01	0.03		0.01	0.01
Nemertesia ramosa		0.02	0.03			0.01
Polychaeta	0.02	0.02			0.01	0.01
Henricia					0.01	0.04
Nudibranchia		0.01	0.03			0.01
Tunicata	0.01	0.01	0.01		0.01	0.01
Urticina felina		0.01			0.02	0.02

Taxa	None	Stony - Low	Stony - Medium	Stony – High	Bedrock - potential	Bedrock - confirmed
Adamsia	0.01		0.01		0.01	0.01
Ascidia mentula			0.03			0.01
Brachyura	0.01	0.01				0.02
Gadidae_GEN.INDET			0.03			0.01
Suberites		0.01	0.01		0.01	0.01
Ascidiidae_GEN.INDET		0.01				0.02
Bryozoa_UN	0.01	0.01				0.01
Leptothecata	0.01	0.01				0.01
Littorinimorpha_FAM.INDET	0.01	0.01				0.01
Ophiactis			0.01		0.01	0.01
Palmiskenea skenei	0.01	0.01				0.01
Porifera_PA	0.01	0.01			0.01	
Sertularella	0.01	0.01				0.01
Stomphia coccinea	0.01	0.01				0.01
Buccinidae_GEN.INDET		0.01				0.01
Bugulidae						0.02
Cancer pagurus		0.01			0.01	
Chelidonichthys	0.01	0.01				
Colus	0.01		0.01			
Eudendriidae						0.02
Halcampoides purpureus	0.01	0.01				
Hydrallmania falcata		0.02				
Patellogastropoda		0.01				0.01
Pectinidae_GEN.INDET	0.01					0.01
Pisces	0.02					
Sabella	0.01					0.01
Solaster endeca					0.01	0.01
Trisopterus luscus	0.01					0.01
Trisopterus minutus						0.02
Tubulariidae_GEN.INDET						0.02
Acanthocardia aculeata						0.01
Aequipecten opercularis						0.01
Amphiura filiformis						0.01
Brachiopoda					0.01	
Buccinum undatum						0.01
Cereus pedunculatus						0.01
Chlamys			0.01			
Ciona intestinalis						0.01
Cliona celata						0.01
Decapodiformes						0.01
Flabellinidae						0.01
Gadus			0.01			
Galathea nexa						0.01
Gobiidae			0.01			
Haliclona (Haliclona) oculata						0.01
Leptometra celtica					0.01	
Macropodia					0.01	
Melanogrammus aeglefinus					0.01	
Phakellia ventilabrum			0.01			
Pleuronectiformes_FAM.INDET	0.01					
Polyclinum						0.01
Pyura						0.01
Sagartia						0.01
Salmacina						0.01
Sertularia						0.01
Stolonifera	0.01					
Urticina eques						0.01

Results from SIMPER routine on **sponge morphs & anthozoa** from **stills**

Taxon	None	Stony - Low	Stony - Medium	Stony - High	Bedrock - potential	Bedrock - confirmed
Caryophyllia	0.37	1.69	13.86	13.28	5.01	11.26
Porifera_EN	3.81	6.61	2.93	1.9	11.48	13.28
Alcyonium digitatum	0.08	0.37	0.47	6.24	7.78	6.25
Urticina_SP.INDET	0.04	0.2	2.32	2.22	0.32	2.33
Porifera_MA	0.18	0.3	0.05	2.22	0.79	0.43
Porifera_UN	0.24	0.16	0.63	1.48	0.09	0.44
Actiniidae	0.02	0.12			2.83	
Porifera_FL	0.13	0.14	0.66		0.54	0.4
Parazoanthus	0.16	0.27	0.36			
Actiniaria_FAM.INDET	0.42	0.11	0.05			0.09
Scleractinia	0.07	0.02	0.36			0.01
Porifera_GL	0.15	0.03	0.05		0.04	0.06
Porifera_PA	0.19	0.02			0.04	0.04
Corynactis viridis		0.01			0.06	0.04
Anthozoa	0.03	0.05				0.01
Porifera_AR	0.01		0.05			0.02
Caryophylliidae_GEN.INDET	0.03	0.01				0.03
Sagartiidae_GEN.INDET		0.01			0.02	0.04
Urticina felina					0.02	
Stomphia coccinea	0.01					

Results from SIMPER routine on **all taxa** from **video**

Taxa	None	Stony - Low	Stony - Medium	Bedrock - potential	Bedrock - confirmed
Bryozoa_EN	4.07	3.97	7.04	5.72	3.86
Spirobranchus	4.84	4.81	4.93	5.63	2.76
Crossaster papposus	0.53	2.62	2.77	4.68	2.87
Ophiurida_FAM.INDET	0.54	0.64	2.86	5.81	1.06
Rhodophyta	0.24	0.73	2.86	3.53	3.01
Urticina	0.52	0.78	4.79	1.2	2.79
Porania (Porania) pulvillus	1.64	2.5	0.68	3	2.24
Porifera_EN	0.73	2.14		1.68	1.82
Flustra foliacea	0.81	1.61	1.83	1.19	0.53
Hydrozoa	0.57	1.55	1.6		1.38
Luidia ciliaris		1.03	2.32	0.52	1.1
Hymedesmia (Hymedesmia) paupertas	0.43	1.54		1.1	1.82
Serpulidae_FAM.INDET	0.76	0.7	0.8		2.18
Alcyonium digitatum	0.31		0.94	2.28	0.55
Pisces	1.44	1.39		1.25	
Asteroidea	0.27	0.56		1.14	0.97
Asteriidae_GEN.INDET		0.41	1.54	0.62	
Parasmittina trispinosa		0.37	0.84		1.33
Securiflustra securifrons	0.44	1.21			0.83
Echinoidea		0.43		1.82	
Echinus		0.31			1.8
Ophiocomina nigra		0.36			1.68
Smittinidae_GEN.INDET	0.24				1.61
Porifera_MA		0.89		0.85	
Porifera_FL		0.85			0.79
Bryozoa_AR	0.27	1.04			
Celleporidae_GEN.INDET					0.83
Caryophyllia (Caryophyllia) smithii					0.76
Stichastrella rosea					0.72
Axinellidae					0.61

Taxa	None	Stony - Low	Stony - Medium	Bedrock - potential	Bedrock - confirmed
Porifera_UN		0.6			
Animalia_EN					0.52
Asterias rubens				0.45	
Polymastia boletiformis	0.38				
Porifera_GL	0.38				
Chelidonichthys cuculus		0.33			
Animalia_UN	0.29				
Pecten maximus	0.27				

Results from SIMPER routine on **sponge morphs & anthozoa** from **video**

Row Labels	None	Stony - Low	Stony - Medium	Bedrock - potential	Bedrock - confirmed
Urticina	4.04	4.26	14.27	4.28	13.16
Porifera_EN	3.21	10.51	3.33	8.62	10.36
Alcyonium digitatum	1.5	1.93	13.02	9.76	2.44
Porifera_UN	1.08	3.57	3.61	0.8	4.13
Porifera_FL	0.99	3.51	1.19	1.65	3.85
Porifera_MA	0.35	3.41		3.58	1.37
Caryophyllia (Caryophyllia) smithii	1.84	0.51		1.08	1.84
Actiniaria_FAM.INDET	1.83	0.51		0.03	2.5
Porifera_PA	1.32	0.91		0.66	0.28
Porifera_GL	1.32	0.98		0.36	0.28
Stomphia coccinea	0.27	0.02			0.34
Parazoanthus	0.03	0.08			0.02
Zoantharia_FAM.INDET	0.01	0.09			
Actiniidae_GEN.INDET		0.05		0.04	
Corynactis viridis	0.01	0.01		0.06	
Caryophylliidae_GEN.INDET		0.01			0.03
Sagartiidae				0.03	
Metridium dianthus	0.01				
Scleractinia	0.01				

A3.2 Tests between observed reef elevation categories

Results from SIMPER routine on **all taxa** from **stills**

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	Unknown
Spirobranchus	8.73	9.78	6.69	6.29	1.57	7.99
Bryozoa_EN	5.64	9.22	6.58	5.63	3.35	7.72
Corallinaceae	0.01	0.2	1.2	4.46	6.96	5.58
Ophiocomina nigra	0.05	0.6	2.51	4.22	2.51	2.16
Ophiuroidea	0.07	0.21	0.2	2.55	4.03	4.14
Hydrozoa_AR	1.55	4.43	2.45	1.1	0.29	0.07
Porifera_EN	0.59	1.27	1.3	2.76	1.05	1.74
Parasmittina	0.24	0.62	2.23	1.47	2.25	0.57
Alcyonium digitatum	0.02	0.15	0.22	1.16	3.45	1.66
Ophiothrix fragilis	0.01	0.08	0.9	2.88	1.64	0.21
Serpulidae_GEN.INDET	0.58	1.61	2	0.26	0.05	0.77
Caryophyllia	0.07	0.4	0.73	2.21	1	0.66
Hymedesmia (Hymedesmia) paupertas	0.15	0.84	0.72	1.09	0.04	1.39
Celleporidae_GEN.INDET	0.02	0.44	1.68	1.26	0.27	0.54
Bryozoa_AR	0.33	1.53	0.8	0.16	0.04	0.29
Calliostoma	0.01	0.11	0.42	1.01	1.03	0.27
Animalia_AR	0.07	0.29	0.02			1.67

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	Unknown
Crossaster papposus	0.02	0.04	0.16	0.48	0.43	0.7
Securiflustra securifrons	0.09	0.49	0.51	0.39	0.04	0.21
Echinus				0.06	1.36	
Smittinoidea	0.18		0.78	0.12	0.31	
Flustra foliacea	0.23	0.62	0.33	0.06		0.11
Gastropoda	0.06	0.36	0.52	0.06	0.09	0.25
Animalia_EN	0.04	0.04	0.48	0.18	0.31	0.24
Actiniidae		0.01				1.15
Urticina_SP.INDET	0.01	0.01	0.19	0.64	0.31	
Sessilia	0.22	0.26	0.36	0.12		0.08
Corynactis viridis		0.01		0.02	0.89	
Hydrozoa_UN			0.01	0.67	0.14	
Ophiura albida	0.21	0.26	0.15	0.01		0.02
Porania (Porania) pulvillus	0.1	0.22	0.16	0.05		0.1
Porifera_MA	0.05	0.15	0.07	0.08		0.2
Asteriidae_GEN.INDET			0.01	0.02	0.5	
Abietinaria abietina		0.13	0.16	0.05		0.11
Rhizocaulus	0.08	0.2	0.14			
Porifera_FL	0.03	0.13	0.06	0.03		0.09
Cellepora pumicosa			0.03	0.29		
Munida rugosa		0.03	0.1	0.03	0.13	0.01
Spirorbis		0.26	0.01			0.03
Thuiaria thuja		0.01	0.04	0.19	0.06	
Serpula	0.1		0.16	0.02		
Antedon_SP.INDET			0.02	0.12	0.12	
Asteroidea			0.01		0.14	0.1
Caridea	0.05	0.05	0.1	0.05		
Pagurus	0.01					0.24
Galatheidae_GEN.INDET	0.03	0.08	0.13			
Rhodophyta_FAM.INDET				0.01		0.22
Paguridae_GEN.INDET	0.01		0.02	0.14		
Actinopterygii	0.01		0.01	0.01	0.13	
Echinoidea		0.01	0.01	0.02		0.09
Parazoanthus	0.02	0.09	0.02			
Gibbula			0.04	0.03		0.04
Actiniaria_FAM.INDET	0.08	0.01	0.02			
Porifera_UN	0.02	0.07	0.01	0.01		
Sertulariidae_GEN.INDET	0.01	0.05	0.05			
Nemertesia_SP.INDET		0.06	0.04	0.01		
Axinellidae_GEN.INDET	0.01	0.01	0.03	0.03		
Axinella infundibuliformis		0.06	0.01			
Ebalia	0.01	0.02	0.02			0.01
Polymastia boletiformis	0.03		0.01	0.01		0.01
Porifera_GL	0.03		0.01	0.01		0.01
Stichastrella rosea			0.01	0.05		
Reteporella	0.02	0.02	0.02			
Urticina felina					0.06	
Chaetopterus		0.05				
Haleciidae			0.04	0.01		
Antedon bifida		0.02	0.01	0.01		
Crangonidae						0.04
Luidia		0.02	0.01	0.01		
Polyplacophora		0.02	0.02			
Sagartiidae_GEN.INDET				0.04		
Caryophylliidae_GEN.INDET	0.01			0.02		
Decapoda		0.01				0.02
Palaemonidae		0.02	0.01			
Porella compressa	0.01		0.01	0.01		
Scleractinia	0.01	0.01	0.01			

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	Unknown
Smittina			0.03			
Alcyonidium diaphanum			0.01			0.01
Anthozoa	0.01		0.01			
Asterias rubens			0.01	0.01		
Pecten maximus	0.01	0.01				
Antedonidae_GEN.INDET			0.01			
Ascidia virginea						0.01
Ascidiacea			0.01			
Cellaria		0.01				
Crisiidae		0.01				
Flustrina			0.01			
Gracilechinus acutus				0.01		
Henricia				0.01		
Hydrallmania falcata		0.01				
Lanice conchilega	0.01					
Nemertesia ramosa		0.01				
Omalosecosa ramulosa			0.01			
Tubularia				0.01		

Results from SIMPER routine on **sponge morphs & anthozoa** from **stills**

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	Unknown
Porifera_EN	3.81	7.01	7.98	14.4	4.4	9.02
Alcyonium digitatum	0.08	0.76	1.17	5.3	14.2	7.47
Caryophyllia	0.37	2.94	4.73	11.86	4.07	3.08
Actiniidae	0.02	0.06				5.27
Urticina_SP.INDET	0.04	0.07	1.13	2.91	1.08	0.01
Corynactis viridis		0.03		0.08	3.66	0.01
Porifera_MA	0.18	0.59	0.27	0.33		0.8
Porifera_FL	0.13	0.64	0.26	0.14		0.37
Porifera_UN	0.24	0.46	0.29	0.31	0.15	0.01
Parazoanthus	0.16	0.4	0.11			
Actiniaria_FAM.INDET	0.42	0.03	0.13	0.02		
Porifera_PA	0.19		0.05	0.04		0.02
Porifera_GL	0.15		0.07	0.05		0.02
Urticina felina		0.02		0.01	0.19	
Sagartiidae_GEN.INDET			0.02	0.18		
Caryophylliidae_GEN.INDET	0.03		0.01	0.09		
Scleractinia	0.07	0.03	0.03			
Anthozoa	0.03		0.04			
Porifera_AR	0.01		0.01			
Stomphia coccinea	0.01					

Results from SIMPER routine on **all taxa** from **video**

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	>10m	Unknown
Spirobranchus	4.81	5.34	4.48	4.3	1.67	2.99	5.23
Bryozoa_EN	4.39	4.5	4.71	3.98	2.85	2.99	4.85
Crossaster papposus	0.51	4.48	2.43	3.02	2.63	2.99	5.85
Porania (Porania) pulvillus	1.24	1.95	2.11	2.89	3.19		3.43
Pisces	1.46	2.74	0.62	0.68		2.99	2.97
Hydrozoa	0.22	4.16	0.96	1.85	1.03	2.99	
Porifera_EN	0.61	2.01	2.14	2.25	2.63		0.7
Ophiurida_FAM.INDET	0.78	0.48	1.54	1.3	0.74		5.31
Rhodophyta		1	1.46	1.65	0.73		4.94
Asteroidea	0.2			0.44	2.63		4.82
Serpulidae_FAM.INDET	0.99	0.99	0.63	1.04	1.03	2.99	

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	>10m	Unknown
Hymedesmia (Hymedesmia) paupertas	0.23	1.61	1.65	1.46	2.63		
Parasmittina trispinosa			0.37	1.26	2.85	2.99	
Luidia ciliaris	0.28	1.18	1.23	1.24	3.19		
Urticina		0.61	1.82	2.55	1.67		
Flustra foliacea	0.87	1.04	1.38	1.06	0.63		1.23
Ophiocomina nigra		0.65		0.82	1.03	2.99	
Echinoidea		0.76					4.17
Smittinidae_GEN.INDET				0.74	1.03	2.99	
Alcyonium digitatum	0.38		0.47	0.58			3.3
Securiflustra securifrons	0.3	1.18	1.08	0.79	1.1		
Bryozoa_AR	0.2	0.88	0.72	0.48	2.08		
Porifera_FL	0.24		0.76	0.83	1.94		
Animalia_EN					0.62	2.99	
Caryophyllia (Caryophyllia) smithii				0.47		2.99	
Ascidiacea						2.99	
Galatheoidea						2.99	
Gastropoda						2.99	
Thuiaria thuja						2.99	
Animalia_UN	0.4				0.64		1.82
Echinus				1.61	1.23		
Porifera_MA	0.2	1.05	0.85	0.39			
Axinellidae				0.41	1.94		
Asteriidae_GEN.INDET		0.65	0.9				
Porifera_UN		0.41	0.63				
Asterias rubens				0.77			
Stichastrella rosea					0.66		
Celleporidae_GEN.INDET			0.58				
Pecten maximus	0.3						

Results from SIMPER routine on **sponge morphs & anthozoa** from **video**

Taxa	N/A	<64mm	64mm - 1m	1.1m - 5m	5.1m - 10m	Unknown
Porifera_EN	2.12	12.6	9.79	12.61	13.17	3.87
Urticina	0.9	4.4	8.84	8.88	6.86	0.07
Alcyonium digitatum	2.33	3.31	2.27	3.36		17.08
Porifera_UN	1.26	1.83	3.52	3.78	13.17	
Porifera_FL	1.11	1.5	2.96	3.68	9.49	1.36
Porifera_MA	0.84	5.25	2.9	1.67	1.79	3.48
Caryophyllia (Caryophyllia) smithii	0.77	1.09	0.33	1	1.65	2
Actiniaria_FAM.INDET	2.52	0.19	0.82	0.61	1.79	
Porifera_PA	0.59		0.55	1.93		0.43
Porifera_GL	0.59		0.56	1.46		0.43
Stomphia coccinea	0.04			0.12	1.64	
Caryophylliidae_GEN.INDET			0.01		1.02	
Actiniidae_GEN.INDET		0.15	0.05			0.05
Zoantharia_FAM.INDET	0.03	0.19	0.03			
Parazoanthus	0.03		0.08			
Corynactis viridis			0.01	0.01		0.05
Sagartiidae				0.04		
Scleractinia	0.01					

A3.3 Tests between observed MNCR biotope categories

Results from SIMPER routine on **all taxa** from **stills**

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMx.CMx	CR.MCR.EcCr/ SS.SCS.CCS
Spirobranchus	7.17	9.17	8.91	8.06
Bryozoa_EN	7.03	5.58	5.29	8.01
Hydrozoa_AR	1.63	1.16	3.87	1.18
Ophiocomina nigra	1.97	0.04		5.66
Porifera_EN	1.56	0.45	1.51	0.73
Celleporidae_GEN.INDET	0.94	0.01	0.01	3.07
Serpulidae_GEN.INDET	1.31	0.49	1.28	0.71
Parasmittina	1.35	0.15	0.59	1.58
Caryophyllia	0.7	0.06		2.72
Corallinaceae	2.04	0.01		0.83
Securiflustra securifrons	0.35	0.07	0.08	2.09
Bryozoa_AR	0.72	0.21	0.81	0.02
Hymedesmia (Hymedesmia) paupertas	0.95	0.09	0.55	0.08
Ophiothrix fragilis	0.61			1.06
Ophiuroidea	1.01	0.05	0.5	0.02
Flustra foliacea	0.25	0.18	0.41	0.73
Alcyonium digitatum	0.51	0.02		0.89
Ophiura albida	0.12	0.1	1.13	0.01
Sessilia	0.24	0.16	0.58	0.07
Gastropoda	0.34	0.04	0.07	0.59
Porania (Porania) pulvillus	0.15	0.04	0.82	0.03
Smittinoidea	0.24	0.13	0.5	0.02
Urticina_SP.INDET	0.08	0.01	0.01	0.62
Calliostoma	0.37			0.3
Serpula	0.05	0.06	0.48	
Caridea	0.05	0.02	0.33	0.05
Crossaster papposus	0.27	0.02	0.01	0.08
Animalia_EN	0.3	0.04	0.02	0.01
Animalia_AR	0.24	0.1		0.01
Rhizocaulus	0.08	0.05	0.22	
Parazoanthus	0.01	0.01	0.32	
Spirorbis	0.02		0.01	0.3
Lanice conchilega			0.28	
Abietinaria abietina	0.12			0.15
Galatheidae_GEN.INDET	0.06	0.01	0.18	
Actiniaria_FAM.INDET	0.01	0.07	0.15	0.01
Reteporella	0.01		0.21	
Porifera_MA	0.11	0.06	0.04	
Nemertesia_SP.INDET	0.02			0.17
Ebalia	0.02		0.16	
Porifera_FL	0.08	0.01	0.08	0.01
Haleciidae	0.01			0.14
Bryozoa_UN			0.15	
Polymastia boletiformis	0.01	0.04	0.02	0.03
Sabellidae_GEN.INDET				0.1
Actiniidae	0.09	0.01		
Porifera_GL	0.01	0.03	0.02	0.03
Antedon bifida	0.01			0.07
Paguridae_GEN.INDET	0.02	0.01	0.05	
Axinellidae_GEN.INDET	0.02		0.04	0.01
Munida rugosa	0.05			0.02
Palaemonidae	0.01		0.05	
Sertulariidae_GEN.INDET	0.02		0.01	0.03
Thuiaria thuja	0.03			0.03

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMx.CMx	CR.MCR.EcCr/ SS.SCS.CCS
Gibbula	0.03			0.02
Pisces			0.05	
Porifera_UN	0.01	0.03	0.01	
Stichastrella rosea	0.01			0.04
Actinopterygii	0.01	0.01		0.02
Porella compressa	0.01		0.03	
Scleractinia	0.01		0.03	
Anthozoa			0.03	
Hydrozoa_UN	0.02			0.01
Pagurus	0.02	0.01		
Rhodophyta_FAM.INDET	0.03			
Antedon_SP.INDET	0.02			
Asteroidea	0.02			
Cellepora pumicosa	0.02			
Crisiidae				0.02
Echinoidea	0.02			
Flustrina	0.01		0.01	
Pecten maximus			0.02	
Polyplacophora	0.01		0.01	
Smittina	0.01		0.01	
Alcyonidium diaphanum	0.01			
Antedonidae_GEN.INDET	0.01			
Asterias rubens				0.01
Asteriidae_GEN.INDET	0.01			
Axinella infundibuliformis	0.01			
Caryophylliidae_GEN.INDET		0.01		
Corynactis viridis	0.01			
Echinus	0.01			
Hydrallmania falcata				0.01
Inachidae_GEN.INDET				0.01
Luidia	0.01			
Porifera_AR				0.01
Trisopterus luscus			0.01	

Results from SIMPER routine on **sponge morphs & anthozoa** from **stills**

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMx.CMx	CR.MCR.EcCr/ SS.SCS.CCS
Porifera_EN	8.95	2.71	9.43	3.71
Caryophyllia	4.04	0.32		16.81
Alcyonium digitatum	2.49	0.11		4.1
Urticina_SP.INDET	0.47	0.04	0.04	2.87
Parazoanthus	0.06	0.09	2.27	
Actiniaria_FAM.INDET	0.06	0.34	0.78	0.04
Porifera_MA	0.43	0.24	0.17	
Porifera_UN	0.23	0.2	0.32	0.03
Porifera_FL	0.36	0.07	0.3	0.03
Porifera_PA	0.03	0.2	0.11	0.17
Actiniidae	0.42	0.04		
Porifera_GL	0.04	0.13	0.16	0.09
Scleractinia	0.03	0.02	0.2	
Anthozoa	0.02	0.02	0.1	
Caryophylliidae_GEN.INDET	0.01	0.04	0.01	
Porifera_AR			0.01	0.05
Halcampoides abyssorum			0.03	
Stomphia coccinea		0.01	0.02	
Corynactis viridis	0.02			
Sagartiidae_GEN.INDET	0.02			

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMx.CMx	CR.MCR.EcCr/ SS.SCS.CCS
Adamsia		0.01		
Urticina felina	0.01			

Results from SIMPER routine on **all taxa** from **video**

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMX.CMx
Spirobranchus	4.43	4.91	3.64
Bryozoa_EN	4.72	3.98	1.76
Porania (Porania) pulvillus	2.55	1.5	4.88
Crossaster papposus	3.63	0.61	1.32
Porifera_EN	1.83	0.99	1.85
Porifera_FL	0.61	0.27	3.04
Luidia ciliaris	0.9	0.27	2.63
Flustra foliacea	1.06	1.19	1.25
Pisces	0.96	1.5	0.86
Hymedesmia (Hymedesmia) paupertas	1.37	0.66	1.28
Ophiurida_FAM.INDET	2	0.59	0.54
Bryozoa_AR	0.5	0.36	1.87
Rhodophyta	2.4	0.22	
Hydrozoa	1.11	0.7	0.72
Urticina	1.37	0.81	0.06
Asteroidea	0.84	0.23	0.72
Serpulidae_FAM.INDET	0.62	0.7	0.29
Securiflustra securifrons	0.79	0.8	
Porifera_MA	0.68	0.16	0.68
Alcyonium digitatum	0.89	0.34	
Parasmittina trispinosa	0.51	0.2	0.45
Pecten maximus	0.01	0.24	0.86
Porifera_UN	0.3	0.1	0.68
Axinellidae	0.1	0.1	0.7
Echinoidea	0.79	0.03	
Porifera_GL	0.09	0.5	0.21
Polymastia boletiformis	0.07	0.5	0.21
Echinus	0.55	0.13	
Smittinidae_GEN.INDET	0.21	0.23	0.19
Ophiocomina nigra	0.4	0.11	
Asterias rubens	0.29	0.11	0.1
Asteriidae_GEN.INDET	0.47	0.02	
Lanice conchilega			0.45
Ophiura albida	0.01	0.01	0.43
Chelidonichthys cuculus	0.09	0.16	0.19
Animalia_UN	0.17	0.23	
Actiniaria_FAM.INDET	0.1	0.25	0.05
Celleporidae_GEN.INDET	0.35	0.05	
Caryophyllia (Caryophyllia) smithii	0.29	0.09	
Axinella infundibuliformis	0.07	0.01	0.28
Animalia_EN	0.21	0.1	
Luidia sarsii			0.26
Calliostoma zizyphinum	0.23		
Stichastrella rosea	0.15	0.07	
Flustridae_GEN.INDET	0.04	0.12	
Gastropoda	0.12	0.03	
Paguridae_GEN.INDET	0.04	0.02	0.09
Sessilia	0.02	0.12	
Luidia_SP.INDET	0.06	0.06	
Galatheoidea	0.04		0.07
Serpula	0.01	0.05	0.05

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMX.CMx
Stomphia coccinea	0.01	0.03	0.07
Melanogrammus aeglefinus	0.03	0.02	0.06
Abietinaria abietina	0.03	0.01	0.06
Parazoanthus	0.01	0.01	0.08
Buccinidae_GEN.INDET		0.01	0.08
Munida rugosa	0.08	0.01	
Caryophylliidae_GEN.INDET			0.08
Sertulariidae	0.02	0.01	0.05
Antedonidae_GEN.INDET	0.05		
Cancer pagurus	0.04	0.01	
Ophiothrix fragilis	0.04		
Raja montagui		0.04	
Marthasterias glacialis	0.03		
Scyliorhinus	0.02	0.01	
Ascidiacea	0.02		
Decapoda_FAM.INDET	0.01	0.01	
Henricia	0.02		
Nemertesia antennina	0.01	0.01	
Salmacina dysteri	0.01	0.01	
Smittina	0.01	0.01	
Trisopterus	0.01	0.01	
Actiniidae_GEN.INDET	0.01		
Alcyonidium diaphanum	0.01		
Ascidia virginea	0.01		
Cellepora pumicosa	0.01		
Cephalopoda		0.01	
Corynactis viridis	0.01		
Pleuronectiformes		0.01	
Plumulariidae_GEN.INDET		0.01	
Solaster endeca	0.01		
Thuiaria thuja	0.01		
Zoantharia_FAM.INDET	0.01		

Results from SIMPER routine on **sponge morphs & anthozoa** from **video**

Taxa	CR.MCR.EcCr	SS.SCS.CCS	SS.SMX.CMx
Porifera_EN	10.05	3.9	8.18
Porifera_FL	2.71	1.12	12.66
Porifera_UN	2.48	1.38	8.39
Urticina	6.18	5.37	0.36
Alcyonium digitatum	4.48	1.95	
Porifera_MA	2.88	0.58	2.82
Porifera_PA	0.45	1.84	0.88
Porifera_GL	0.39	1.84	0.88
Caryophyllia (Caryophyllia) smithii	0.97	1.63	
Actiniaria_FAM.INDET	0.48	1.71	0.33
Stomphia coccinea	0.03	0.19	0.33
Scleractinia			0.24
Parazoanthus	0.04	0.02	
Actiniidae_GEN.INDET	0.04		
Corynactis viridis	0.03	0.01	
Zoantharia_FAM.INDET	0.01	0.01	
Caryophylliidae_GEN.INDET	0.01		