Hampshire Water Transfer and Water Recycling Project

Environmental Statement – Appendix 9.4 Intertidal survey

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1 Introduction

1.1 Overview

1.1.1 This technical report supports the marine ecological assessment which is presented within Environmental Statement (ES) Chapter 9 Marine biodiversity, Volume I (Document reference 6.1, DCO Volume 6). Details of the Proposed Development are described in ES Chapter 3 Description of the Proposed Development, Volume I (Document reference 6.1, DCO Volume 6), and have informed the scope of this study.

1.1.2 This report details baseline data for marine intertidal habitats collected between 26 and 28 September 2022 and is produced to inform the marine ecological assessment presented within ES Chapter 9 Marine biodiversity, Volume I (Document reference 6.1, DCO Volume 6). The survey scoping and methodology used for establishing the ecological baseline for intertidal habitats are provided in section 2.3 and section 2.4 respectively of this report.

1.2 Objectives

1.2.1 The Environmental Impact Assessment (EIA) Scoping Report for the Proposed Development identified potential effects on intertidal habitats with additional study being recommended.

1.2.2 To inform the assessment of likely significant effects on intertidal habitats, surveys are undertaken to identify the various intertidal habitats. These surveys aim to confirm the extent of intertidal habitats, substrate type, epifaunal and infaunal community present. The surveys also intend to map areas of key importance to intertidal habitats within the survey study area for the Proposed Development.

1.3 Intertidal habitats and ecology

1.3.1 The intertidal zone is the area of seashore that is exposed at low tide and inundated at high tide. Intertidal habitats are characterised as having hard substrates which are the rocky shores, shingles, rocky pools and boulders; or soft bottom substrates which are the sand and mud flats. The intertidal area of the Proposed Development to be surveyed is characterised by mudflats that usually support a variety of macroinvertebrates and provide an overwintering feeding ground for wintering wildfowl and waders.

1.4 Legal context

1.4.1 Langstone Harbour is a designated Site of Special Scientific Interest (SSSI) under Section 28 of the Wildlife and Countryside Act 1981. Langstone Harbour is also classified as a Special Protection Area (SPA) under Article 4.2 of the EU Directive (79/409/EEC), Ramsar site under the Convention on Wetlands of International Importance (Ramsar Convention) and forms part of the Solent Maritime Special Area of Conservation (SAC) designated under the Habitats Directive (92/43/EEC). Intertidal habitats in Langstone Harbour are an integral part of these designations and are essential in supporting the designated features.

2 Methodology

2.1 Background

2.1.1 Under the Proposed Development, the entirety of Langstone Harbour including the tidal extent of Hermitage stream would potentially be affected by construction works. Habitat mapping was required in the intertidal zone in Langstone Harbour to inform potential ecological assessments associated with the works. This survey targeted areas where effects from construction are most likely and establish the intertidal ecology that could be effect in order to inform ecological assessments.

2.1.2 As part of the Proposed Development, APEM Limited was commissioned to undertake an intertidal benthic ecology survey within Langstone harbour. This comprised of Phase I habitat mapping and Phase II quantitative coring to obtain standardised information on the presence and extent of habitats within the survey area and to characterise the intertidal benthic assemblages present. The results of this survey work support ES Chapter 9 Marine biodiversity, Volume I (Document reference 6.1, DCO Volume 6) and provide information to support the Secretary of State's (SoS) consents and licensing decisions.

2.1.3 Specific aims of the Phase I survey were to:

1. Achieve 100% coverage of the intertidal zone within the survey area (Graphic 2-1).
2. Map the presence and extent of intertidal habitats within the survey area.
3. Record the presence of macroalgae, sediment characteristics, surface features and anthropogenic impacts at Phase II core stations and within the wider survey area.

2.1.4 Specific aims of the Phase II survey were to:

1. Provide quantitative data to characterise the intertidal benthic assemblages within the survey area by sampling representative habitats undertaken in Phase I survey.
2. Conduct particle size analysis (PSA) to characterise sediment within the survey area.
3. To provide additional data to inform the allocation of biotopes across the survey area.

2.2 Survey guidance

2.2.1 The following handbook and guidelines provided the framework of intertidal survey:

1. Handbook for Phase 1 habitat survey – a technique for environmental audit [1]
2. Handbook for Marine Intertidal Phase I mapping surveys [2]
3. Joint Nature Conservation Committee (JNCC) Marine Monitoring Handbook [3]
4. European Nature Information System (EUNIS) guidance [4]
5. JNCCs National Marine Habitat Classification for Britain and Ireland: Version 04.05 [5]

2.3 Zone of Influence

2.3.1 The geographical scope of the assessment has been informed by:

1. The Order Limits which includes temporary land take for construction compounds, access routes and lay down sites.
2. The likely effects of the Proposed Development on ecological features within the 'Zone of Influence' (ZoI).

2.3.2 The ZoI is the area over which ecological features may receive impacts from a development. It covers the Order Limits, and the wider landscape where pathways (ecological or hydrological links) exist for the transfer of impacts away from the works area. The ZoI for each ecological feature varies in size depending on the nature of the effects and the sensitivity of the ecological features to those effects.

2.3.3 Each ZoI has been determined by:

1. Consideration of the activities during construction and operation associated with the Proposed Development.
2. The scale, duration and timing of the works.
3. Ecological data, including aerial photography and Ordnance Survey (OS) mapping, tidal information, biological records of protected and notable species and baseline data collected from field survey, published data and migratory patterns.

2.3.4 Based on the scale and duration of the Proposed Development it is considered that construction activities within the Order Limits will typically produce temporary and localised impacts on the marine environment. Study areas have been applied for each category of ecological feature, as appropriate, to enable effective assessment of potential effects from both construction and operational effects on each ecological receptor.

2.3.5 The ZoI, study area and field survey area for intertidal habitats, are detailed below within Table 2-1.

Table 2-1 Intertidal habitats Zone of Influence, study area and field survey area

Ecological receptor	Zone of Influence	Study area	Field survey area
Intertidal habitats	Marine ecology ZoI for all designated marine sites: 2km Marine ecology ZoI for hydrologically connected statutory designated sites: 10km	Study area 1: The entirety of Langstone Harbour, including the tidal extent of Hermitage stream Study area 2: 10km from the Eastney Long Sea Outfall (LSO) within the Solent (Refer to ES Figure 9.1 Marine ecology study areas 1 and 2, Volume III (Document reference 6.3, DCO Volume 6))	The northern extremity of Langstone Harbour where the Hermitage Stream outputs into the Brockhampton Mill Lake watercourse. The survey area extends approximately 1km southwards towards the North Binness Island and Long Island whilst spans approximately 3km from Chalkdock Lake to the edge of Bridge Lake

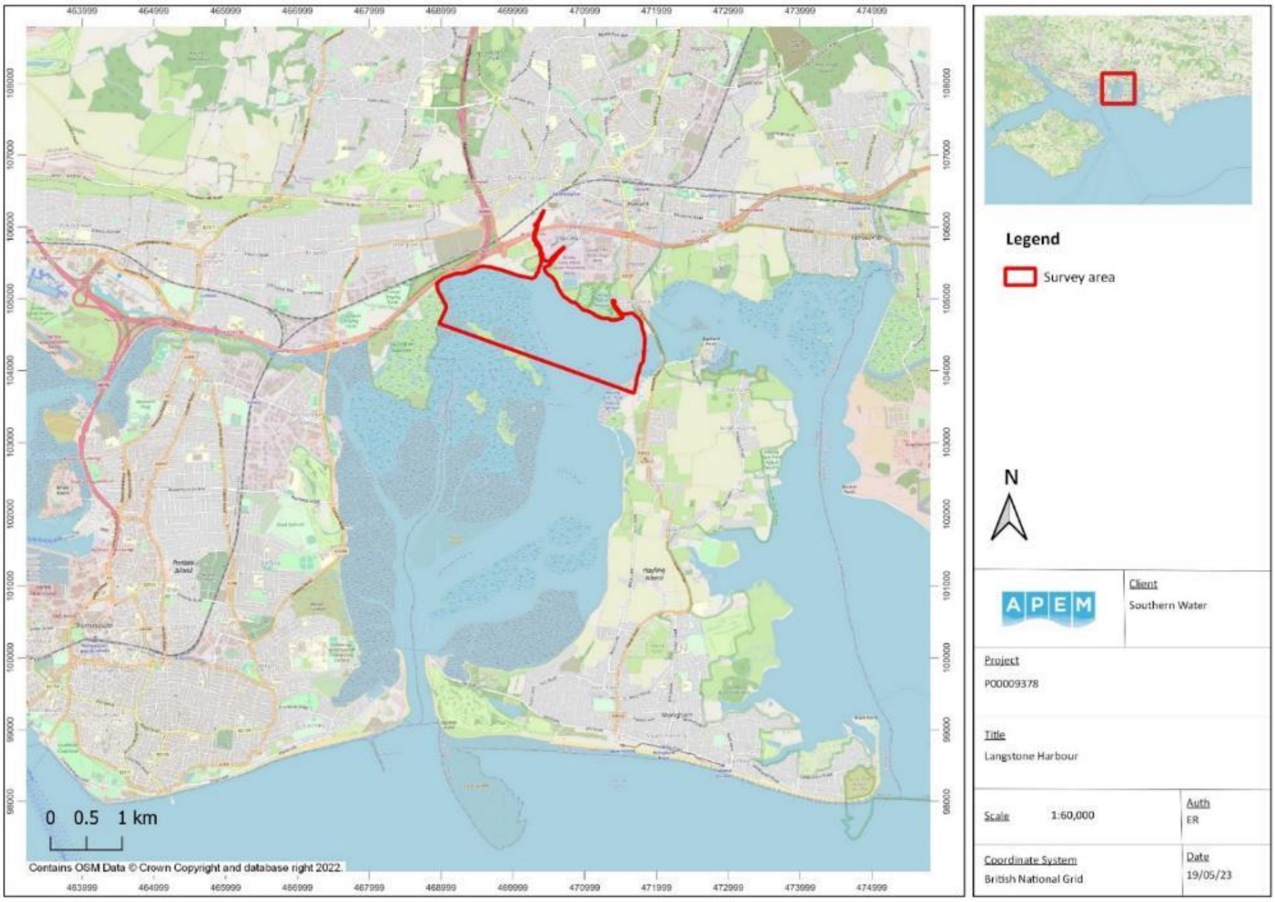
2.3.6 For marine ecology, each study area is considered to be the entirety of the hydrologically connected ZoI. This is due to hydrological connectivity within the marine environment providing the greatest potential for impacts to travel large distances. However, any hydrological effects are going to be rapidly diluted with distance from the development where the volume of water increases out towards the Solent. Justification of the marine ecology ZoI is provided in Table 9-6 in ES Chapter 9 Marine biodiversity, Volume I (Document reference 6.1, DCO Volume 6), and justification of the study area for marine ecology defined by the ZoI is provided in Table 9-7 in ES Chapter 9 Marine biodiversity, Volume I (Document reference 6.1, DCO Volume 6).

2.4 Field survey

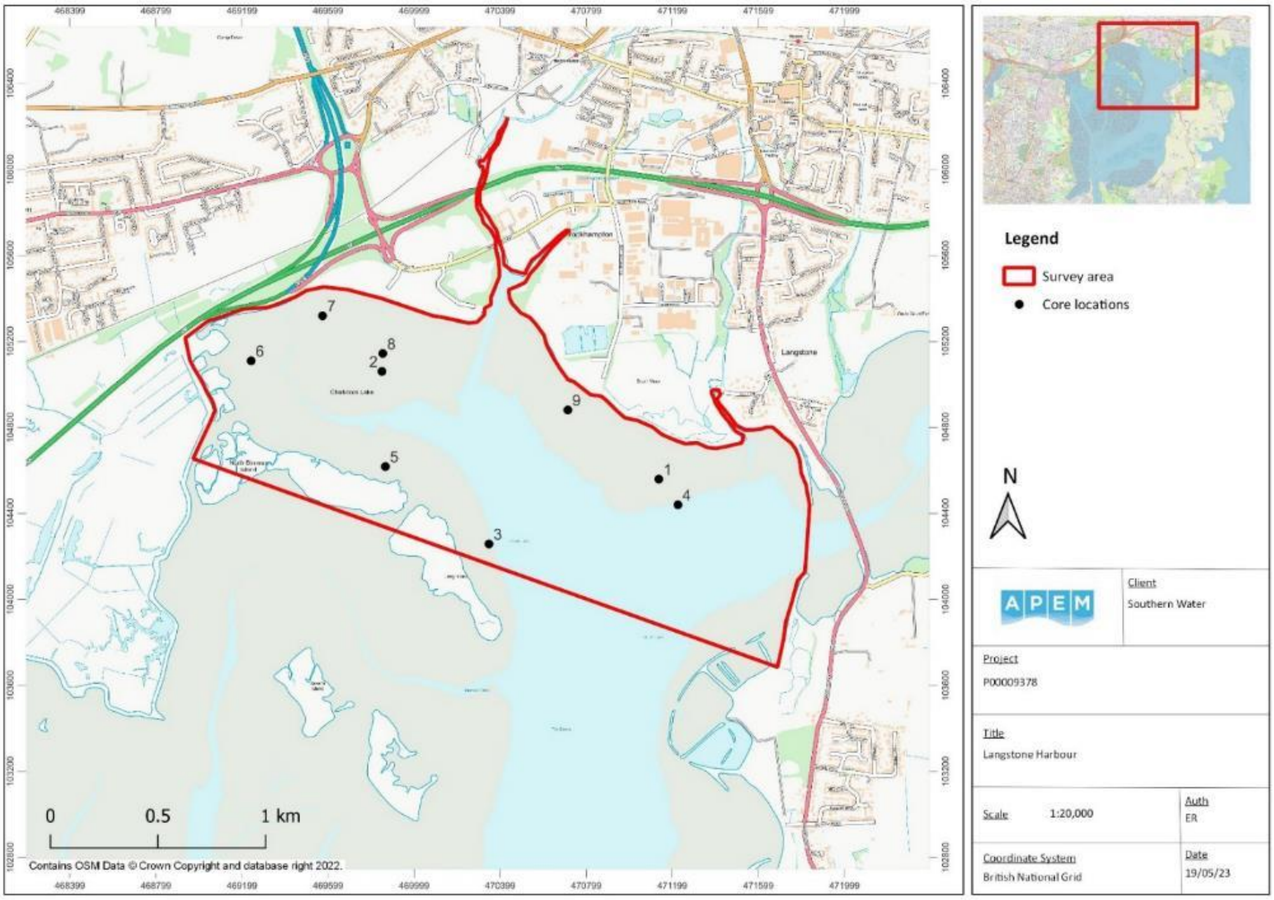
Survey area

2.4.1 Langstone Harbour is located towards the eastern part of the Solent, southern England (Graphic 2-1). It is a tidal basin where, at low water, large areas of mud flats are exposed. These mud flats are drained by three main channels which unite to make a common and narrow exit to the sea. For the purposes of the intertidal benthic ecology survey, sampling effort focussed on the north-eastern section of the harbour (Graphic 2-2).

Graphic 2-1 Langstone Harbour survey area



Graphic 2-2 Langstone Harbour survey area and sampling stations for the intertidal benthic ecology survey



Survey methods

2.4.2 Due to the soft nature of the mud and numerous steep creeks at Langstone Harbour, all survey work was completed using a hovercraft to increase efficiency and reduce the risk of potential health and safety incidents.

Phase I survey

2.4.3 The Phase I intertidal survey was designed to record the range and extent of habitats present across the intertidal survey area by assigning them in situ according to the Countryside Council for Wales (CCW) Handbook for Marine Intertidal Phase I mapping surveys [2] and the Marine Monitoring Handbook [3]. Focus was on noting any conspicuous sediment types, biota and features that were evident as it was not possible to conduct in situ sieving for logistic and health and safety reasons. Photographs of different habitat types were taken (representative examples of these are in Annex B).

2.4.4 Habitats were allocated in accordance with 2012 EUNIS guidance [4] by an experienced intertidal ecologist. Aerial imagery [6] was used in situ to provide an initial view of where different habitat types were located and visible biotope boundaries were delineated via hovercraft using the tracking function of the Global Positioning System (GPS). The Marine Habitat Classification for Britain and Ireland Version 22.04 [5] have also been provided.

Phase II survey

2.4.5 For the quantitative Phase II intertidal survey, 0.01m^2 cores were taken across each of the habitats identified during the Phase I survey. A total of eight stations were sampled in triplicate. The intention was to analyse two of the cores and retain the third replicate in storage in case subsequent analysis was considered to be beneficial. Stored replicate samples were stored in 70% Industrialised Methylated Spirits (IMS). An additional core at each station was obtained for PSA.

2.4.6 During the survey an additional ninth station was sampled. This additional station was in an area previously classified (prior to the phase 1 survey) as 'Cirratulids and *Cerastoderma edule* in littoral mixed sediment (A2.421) [7]. During the Phase I survey, field personnel were unable to identify any infauna in this area to help with its biotope classification, but instead found an abundance of Bladder wrack *Fucus vesiculosus*. It was considered that infaunal data for this area would be useful for clarifying its overall biotope classification.

2.4.7 For the Phase II survey, a handheld differential global positioning system (dGPS) (accuracy of up to 2m) was used to optimise accuracy when locating sampling points in the field. At each station, the following information was recorded:

1. Notes relating to the biotic assemblage including key taxa present when applicable
2. Substrate type (based on visual assessment)
3. Key features of interest
4. Presence of Invasive Non-Native Species (INNS)
5. Presence of macroalgal mats
6. Photograph of each sample
7. Any anthropogenic pressures (if present)

2.5 Laboratory analysis

Macrobiota

2.5.1 Sample analysis was conducted according to APEM's standard operating procedure for marine benthic sample analysis which is fully compliant with the North-East Atlantic Marine Biological Analytical Quality Control (NMBAQC) Scheme's Processing Requirement Protocol [8]. To standardise the sizes of organisms recorded, and to separate preservative from the biota, all samples were washed in a fume cupboard over a series of graduated sieves with a base mesh sieve of 0.5mm. All faunal samples were stored in formaldehyde for identification and enumeration. Taxonomic nomenclature followed the World Register of Marine Species (WoRMS) or more recent literature where appropriate.

2.5.2 Taxa were identified to the lowest practicable taxonomic level (usually species), using appropriate taxonomic literature. The NMBAQC Scheme has produced a Taxonomic Discrimination Protocol (TDP) which gives guidance on the most appropriate level to which different marine taxa should be identified, and this guidance was followed for laboratory analyses. Where required, specimens were also compared with material maintained within the laboratory reference collection. Any colonial species identified were recorded as present. Taxonomic nomenclature followed WoRMS, except where more recent revisions are known to supersede WoRMS.

2.5.3 All samples were subject to internal Quality Assurance (QA) procedures and, following analysis, 10% of samples were also subjected to formal Analytical Quality Control (AQC). APEM Ltd will maintain a full reference collection for the Proposed Development, as is standard practice for our analytical work, which contains at least one example of each taxon recorded.

Particle size analysis

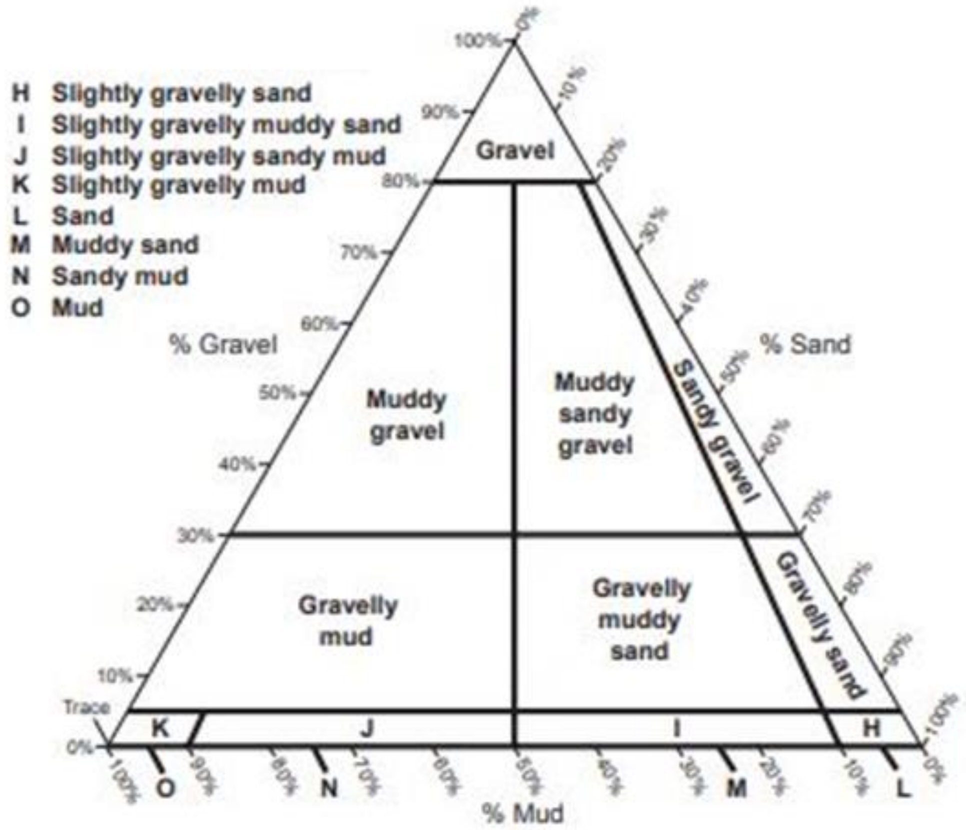
2.5.4 Sediment samples for PSA were kept chilled and suitably stored before being transported to Kenneth Pye Associates Ltd laboratory for processing. PSA samples were analysed according to NMBAQC Best Practice Guidelines for Particle Size Analysis accompanying Biological Data [9].

2.6 Data analysis

Particle size distribution

2.6.1 The PSA data from all survey samples were entered into the statistical software package GRADISTAT [10] for analysis in order to produce sediment classifications, (following Folk [11]; (Graphic 2-3)). Summary statistics were also calculated including mean (Phi), sorting, skewness, and kurtosis (following Blott and Pye [10]).

Graphic 2-3 Sediment classification pyramid (Folk, 1954)



Macrobiota

2.6.2 Before analysis, all data were checked for errors. Summary statistics were calculated, and outlying values investigated to identify possible data transcription errors. As is standard practice, truncation of the biological data was undertaken before calculation of summary statistics and other statistical analyses to avoid unnecessary weighting from colonial species, taxonomic ambiguity from small individuals and replication from juveniles (Table 2-2).

Table 2-2 Details of data truncation performed prior to statistical analysis

Taxon/records	Details of truncation performed
Tharyx killariensis	*Tharyx killariensis* combined with *Tharyx* species A
Microdeutopus anomalus	*Microdeutopus anomalus* combined with *Microdeutopus gryllotalpa*
Littorina	*Littorina* combined with *Littorina littorea*
Carcinus maenas juvenile	Combined with adult of same taxon
Cerastoderma edule juvenile	Combined with adult of same taxon

2.6.3 For analyses based on numbers of individuals, any non-countable taxa and fragments of individuals were also omitted from analysis.

2.6.4 Univariate and multivariate analyses were conducted using the PRIMER software package [12].

Univariate analysis

2.6.5 Biological diversity within a community was assessed based on taxon richness (total number of taxa present) and evenness (which considers relative abundances of different taxa). The following metrics were calculated:

1. **Shannon-Wiener Diversity Index** (H'(loge): This is a widely used measure of diversity accounting for both the number of taxa present and the evenness of distribution of the taxa [13].
2. **Margalef's species richness** (d): This is a measure of the number of species (richness) corrected to reflect the number of individuals (abundance) sampled.
3. **Pielou's Evenness Index** (J'): This represents the uniformity in distribution of individuals spread between species in a sample. High values indicate more evenness or more uniform distribution of individuals. The output range is from zero to one.
4. **Simpson's Index** (1-λ): This form is an evenness index (also known as the Gini-Simpsons Index) derived from the probability of picking two individuals from a community at random that are from the same species. Simpson's index ranges from zero to one with higher values representing a more diverse community without dominant taxa.

Multivariate analysis

2.6.6 Macrofaunal data were subjected to multivariate analysis using the PRIMER software package [13].

2.6.7 Multivariate analyses were computed from resemblance or similarity matrices. For the macrofaunal data set, the Bray-Curtis measure of similarity was used following a square root transformation of the data. For the purposes of multivariate analysis, the decision was made to remove nematoda prior to analysis. Nematoda can be patchily recorded across benthic samples which was apparent for this survey, with differences of between eight and 2,221 individuals for replicates within the same station. Because of this, the taxon is not a key consideration when defining biotopes and removing them allowed the influence of more important habitat-defining taxa such as the Laver spire shell *Peringia ulvae*, ragworm *Hediste diversicolor* and oligochaetes to be considered. Nematoda were included when calculating the univariate statistics as these summary statistics were more relevant to characterisation of the community as a whole, as opposed to providing data to inform allocation of biotopes

Cluster analysis

2.6.8 Cluster analysis was utilised to provide a visual representation of sample similarity in the form of a dendrogram. Cluster analysis was conducted in conjunction with a SIMPROF (similarity profile) test to determine whether groups of samples were statistically indistinguishable at the 5% significance level, or whether any trends in groupings were apparent. Black lines on the dendrogram indicate statistical distinctions between sampling stations, whilst red lines indicate that the samples were statistically inseparable.

Ordination analysis – non-metric multidimensional scaling

2.6.9 Non-metric multidimensional scaling (MDS) is a type of ordination method which creates a 2- or 3-dimensional ‘map’ or plot of the samples from the PRIMER resemblance matrix. The plot generated is a representation of the dissimilarity of the samples (or replicates), with distances between the replicates indicating the extent of the dissimilarity. For example, replicates that are more dissimilar are further apart on the MDS plot. No axes are present on the MDS plots as the scales and orientations of the plots are arbitrary in nature.

2.6.10 Each MDS plot provides a stress value which is a broadscale indication of the usefulness of plots, with a general guide indicated below [13]:

1. Less than 0.05 Almost perfect representation of rank similarities
2. 0.05 to less than 0.1 Good representation
3. 0.1 to less than 0.2 Still useful
4. 0.2 to less than 0.3 Should be treated with caution
5. Less than 0.3 Little better than random points

SIMPER

2.6.11 Where differences between groups of samples were found, SIMPER analysis was used to determine which taxa were principally responsible for the differences between the statistically distinct groups of stations.

2.7 Mapping outputs

2.7.1 Following the survey, the presence and extent of habitats were mapped in a Geographic Information System (GIS) to a resolution of EUNIS level 3 as a minimum (with higher resolution mapped if possible), using the most recently available aerial imagery as a basemap [6].

2.8 Programme of surveys

2.8.1 The intertidal Phase I and Phase II survey was completed between 26 and 28 September 2022, during spring low tides (Table 2-3). On 26 September 2022 efforts were concentrated on mapping and sampling the western side of the survey area and on 27 September 2022 efforts focussed on mapping and sampling the eastern side, with the final station sampled on 28 September 2022.

Table 2-3 Tide times for the survey

Date	Low tide		High tide	
	Time (BST)	Height (m)	Time (BST)	Height (m)
26/09/2022	05:36	0.86	12:45	5.03
27/09/2022	06:13	0.79	13:20	5.10
28/09/2022	06:49	0.81	13:55	5.12

3 Results

3.1 Overview

3.1.1 A habitat map was produced for the full intertidal area (Graphic 3-1), with summary information provided in Table 3-1. Records of the presence of macroalgae, sediment characteristics, surface features and anthropogenic impacts at each station are provided in Annex A . Example photos of each habitat are presented in Annex B . The Phase I survey (section 3.2) was conducted to map habitats across the survey area and was primarily informed by substrate type and epifauna present. These data were supplemented by the Phase II core results to determine infaunal assemblages and confirm sediment composition as outlined in section 3.3.

3.2 Intertidal Phase I survey

Habitat distribution and extent

3.2.1 A total of five habitats were identified across the survey area covering a total area of 193 ha (Graphic 3-1 and Table 3-1).

Littoral mud (EUNIS 2012 code: A2.3; EUNIS 2022 code: MA6; JNCC code: LS.LMu)

3.2.2 The habitat Littoral mud (EUNIS 2012 code: A2.3; EUNIS 2022 code: MA6 JNCC code: LS.Lmu) is typically formed of extensive mudflats supporting communities characterised by polychaetes, bivalves and oligochaetes (EEA 2019a). There was extensive coverage of this habitat across the central, western and eastern sections of the survey area (Graphic 3-1), with an area of 91ha (Table 3-1). Large areas of littoral mud in the survey area had no macroalgae coverage while in other areas there was 100% coverage of green mat forming algae. The presence of a small number of empty bivalve shells were also noted on the surface and the mud was often anoxic at very shallow sediment depths (0.1 cm).

Fucus vesiculosus on mid eulittoral mixed substrata (EUNIS 2012 code: A1.3132; EUNIS 2022 code: MA123D2; JNCC code: LR.LLR.F.Fves.X)

3.2.3 The habitat *Fucus vesiculosus* on mid eulittoral mixed substrata (EUNIS 2012 code: A1.3132; EUNIS 2022 code: MA123D2; JNCC code: LR.LLR.F.Fves.X), which typically occurs in sheltered or fully sheltered marine conditions is characterised by the bladder wrack and may also contain other characterising taxa such as knotted wrack *Ascophyllum nodosum*, acorn barnacle *Semibalanus balanoides*, common limpet *Patella vulgata*, dog whelk *Nucella lapillus*, common periwinkle *Littorina littorea* and flat periwinkle *Littorina obtusata* (Perry et al. 2015). This habitat had an extent of 37ha and was mainly recorded in the north-eastern section of the survey area (Graphic 3-1). During the survey, this habitat was assigned to areas with a substrate of boulders, cobbles, gravel and mud with characterising species such as the brown seaweed bladderwrack observed, with estimated coverage ranging from 30 – 60%. Gut weed *Ulva intestinalis*, which is often recorded in this biotope as occasional on the SACFOR scale, was also observed, in addition to small patches of serrated wrack *Fucus serratus*. However, patches of serrated wrack were never large enough in extent or percentage cover to be a distinguishing feature of this biotope or to qualify as a biotope in its own right. Given the high mud load and low relief of the habitat, no periwinkles or barnacles were observed during the Phase I survey. However, these were recorded during the Phase II survey (see section 3.3).

Littoral mud (EUNIS 2012 code: A2.3; EUNIS 2022 code: MA6; JNCC code: LS.Lmu)/Littoral mixed sediment (EUNIS 2012 code: A2.4; EUNIS 2022 code: MA4; JNCC code: LS.LMx)

3.2.4 The habitat Littoral mud is described above. The habitat Littoral mixed sediment (EUNIS 2012 code: A2.4; EUNIS 2022 code: MA4; JNCC code: LS.LMx) consists of mixed sediment ranging from muds with gravel and sand to pebbles, gravels, sands and mud in more even proportions [14]. This mosaic of habitats was observed to the north and north-eastern sections of the survey area covering an area of 315,579m^2 (32ha). Within the survey area this mosaic biotope comprised of boulders, cobbles and gravel, interspersed by a high coverage of anoxic mud. Green mat forming algae varied in coverage from 30 – 40% and the crumb-of-bread sponge *Hymeniacidon perlevis* was recorded frequently on hard substrata.

Coastal saltmarshes and saline reedbeds (EUNIS 2012 code: A2.5; EUNIS 2022 code: MA211; JNCC code: LS.LMp.Sm)

3.2.5 The habitat Coastal saltmarshes and saline reedbeds (EUNIS 2012 code: A2.5; EUNIS 2022 code: MA211; JNCC code: LS.LMp.Sm) occurs on the upper shores of sheltered costs and is characterised by vegetation on sandy and muddy sediments [15]. This habitat was observed in the south, west and north-western sections of the survey area (Graphic 3-1), covering a total area of 311,519m^2 (31ha). Additionally, a number of small, isolated patches (less than 25m^2) of saltmarsh were noted along the north-west of the sea wall, which extends from the public slipway in the north of the harbour to the perimeter of Farlington Marshes in the north-west of the harbour.

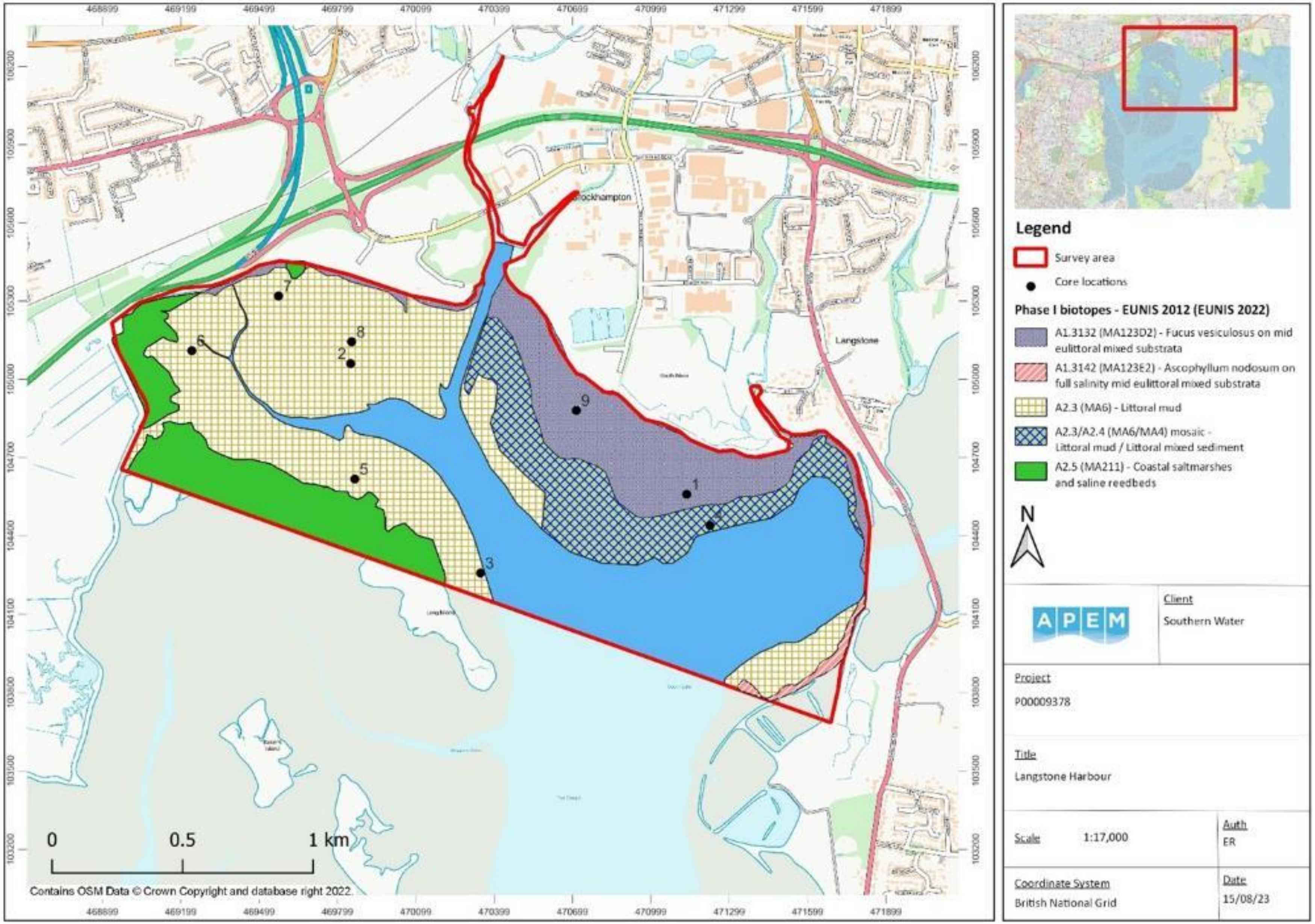
Ascophyllum nodosum on full salinity mid eulittoral mixed substrata (EUNIS 2012 code: A1.3142; EUNIS 2022 code: MA123E2; JNCC code: LR.LLR.F.Asc.X)

3.2.6 The habitat *Ascophyllum nodosum* on full salinity mid eulittoral mixed substrata (EUNIS 2012 code: A1.3142; EUNIS 2022 code: MA123E2; JNCC code: LR.LLR.F.Asc.X) is a very sheltered mixed substrata found in fully or near fully marine conditions. In addition to knotted wrack and bladder wrack, other characterising infaunal species may include lugworm *Arenicola marina*, blue mussel *Mytilus edulis*, common periwinkle and crustaceans like shore crab *Carcinus maenas* [16]. This habitat covered the least extent of those recorded (17,548m^2) (2ha) and was observed in the south-eastern section of the survey area (Graphic 3-1). It was comprised of knotted wrack and bladder wrack on boulders and cobbles. During the survey due to the soft mud and sharp rocks within this area, surveyors were unable to get a closer look at the habitat to identify any other species characteristic of this biotope.

Table 3-1 Summary of Broadscale Habitats assigned to the intertidal survey area

Broadscale Habitat with European Nature Information System and Joint Nature Conservation Committee codes	Area (m^2)	Area (ha)	Habitat description during survey
Littoral mud A2.3 (EUNIS 2012) MA6 (EUNIS 2022) LS.Lmu	912,536	91	Habitat ranged from 0% to 100% coverage of green mat forming algae. Small number of empty bivalve shells noted on the surface. Mud was often anoxic at very shallow sediment depths (0.1cm).
Fucus vesiculosus on mid eulittoral mixed substrata A1.3132 (EUNIS 2012) MA123D2 (EUNIS 2022) LR.LLR.F.Fves.X	374,252	37	Habitat occurred on substrate consisting of boulders, cobbles, gravel and mud. bladder wrack observed, ranging from 30 – 60% coverage. Gut weed also observed in addition to small patches of serrated wrack.
Littoral mud/Littoral mixed sediment A2.3/A2.4 (EUNIS 2012) MA6/MA4 (EUNIS 2022) LS.Lmu/LS.LMx	315,579	32	Mosaic habitat consisted of boulders, cobbles and gravel, interspersed by a high coverage of anoxic mud. Varying coverage of green mat forming algae. Hard substrata, where present, was frequently colonised by crumb of bread sponge.
Coastal saltmarshes and saline reedbeds A2.5 (EUNIS 2012) MA211 (EUNIS 2022) LS.LMp.Sm	311,519	31	Large areas observed in the west and south-west in addition to small isolated patches (less than 25m^2) of saltmarsh observed along the north-west of the sea wall.
Ascophyllum nodosum on full salinity mid eulittoral mixed substrata A1.3142 (ENIS 2012) MA123E2 (EUNIS 2022) LR.LLR.F.Asc.X	17,548	2	Habitat comprised of knotted wrack and bladder wrack on boulders and cobbles.

Graphic 3-1 Habitats mapped during the intertidal Phase I survey (EUNIS habitat codes indicated)



Anthropogenic pressures

Bait digging

3.2.7 It was noted that the entire bank to the north-east of the intertidal survey area was heavily disturbed by bait digging which encompassed Stations 1, 4 and 9 (locations indicated in Graphic 3-1). At least one individual was seen digging for bait within this area at all times during the survey (see records provided in Annex A).

3.3 Intertidal Phase II survey

3.3.1 Triplicate samples were successfully obtained at all nine stations across the survey area. As indicated in section 2.5, two replicates at each station were analysed and the third was stored for future analysis if required. Photographs of core samples used for analysis are presented in Annex C . Raw data for PSA is presented in Annex D.1 and microbiota data is presented in Annex D.2 respectively.

Particle size analysis

3.3.2 All samples were classified as varying degrees of poorly sorted mixed sediments. Out of the nine survey stations, five were classified as 'Very Poorly Sorted' and four were classified as 'Extremely Poorly Sorted' (Table 3-2).

3.3.3 The primary mode of the particle size distribution ranged from 13.3 micrometres (μm) at Station 5 to 38,250μm at Station 2. Using a Wentworth (1922) classification [17], the most common primary mode value was representative of Very Coarse Silt (31 – 63μm), which accounted for three of the nine stations. Coarse Gravel (16,000 – 32,000μm) was the second most frequently occurring sediment type accounting for two stations. The common mode value for the remaining stations were representative of Medium Silt (8 – 16μm), Fine Sand (125 – 250μm), Medium Gravel (8,000 – 16,000μm) and Very Coarse Gravel (32,000 – 64,000μm; Annex D).

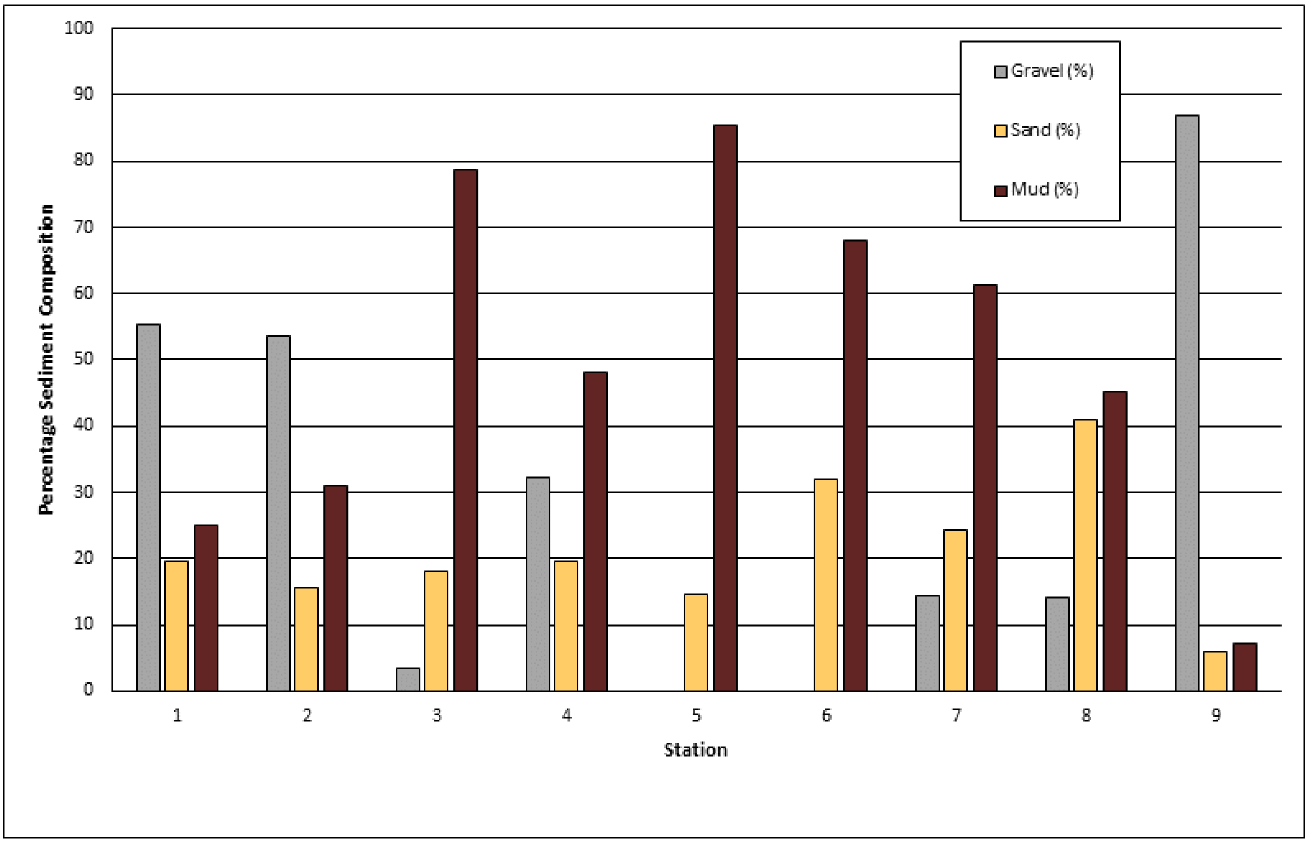
3.3.4 Mud and gravel fractions featured predominantly in sediments across stations and these fractions often provided the greatest contribution at the majority of stations. For instance, mud was seen to contribute to at least 50% of the sediment composition at four stations, whilst gravel had at least 50% contribution to sediment composition at three stations. Sand was less dominant and was only present in similar levels to mud or gravel at two stations and typically remained below 20% of the sediment composition (Table 3-2; Graphic 3-2).

3.3.5 Under the Folk Classification, Muddy Gravel was designated at the majority of stations (three stations), followed by Sandy Mud and Gravelly Mud (two stations each), then Slightly Gravelly Sandy Mud and Gravel (one station each; Table 3-2 and Graphic 3-3).

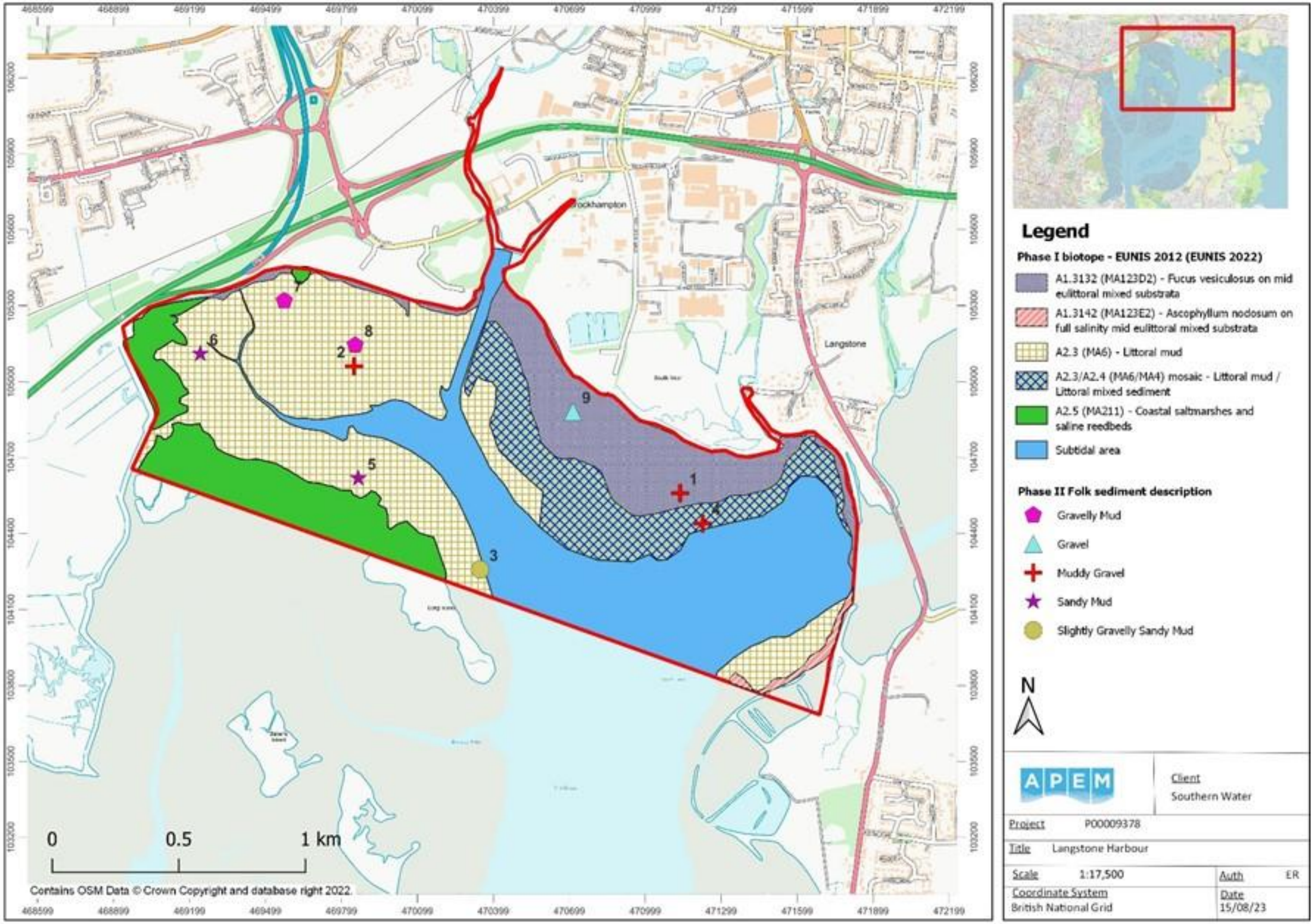
Table 3-2 Summary of particle size analysis results

Station	Mode (µm)	Gravel (%)	Sand (%)	Mud (%)	Folk	Sorting
1	26,950	55.4	19.6	25.0	Muddy Gravel	Extremely Poorly Sorted
2	38,250	53.5	15.6	30.9	Muddy Gravel	Extremely Poorly Sorted
3	37.7	3.4	18.0	78.6	Slightly Gravelly Sandy Mud	Very Poorly Sorted
4	19,200	32.3	19.5	48.2	Muddy Gravel	Extremely Poorly Sorted
5	13.3	0.0	14.7	85.3	Sandy Mud	Very Poorly Sorted
6	53.3	0.0	32.0	68.0	Sandy Mud	Very Poorly Sorted
7	37.7	14.4	24.3	61.3	Gravelly Mud	Extremely Poorly Sorted
8	150.9	14.0	40.9	45.1	Gravelly Mud	Very Poorly Sorted
9	9,600	86.8	6.0	7.2	Gravel	Very Poorly Sorted

Graphic 3-2 Relative contribution to sediment composition of gravel, sand, and mud across sample stations



Graphic 3-3 Sediment the at stations sampled during the Phase II survey in accordance with the Folk classification system



Macrobiota

Features of note

3.3.6 No species of conservation importance were recorded. The common cockle *Cerastoderma edule* which is commercially important, was recorded at five of the nine stations. However, abundances of the common cockle were low, ranging from one to four individuals across all stations.

Non-native species

3.3.7 Across the survey area, a total of four species were recorded which were confirmed to be non-native to the UK. These included the tube-building spionid polychaete *Pseudopolydora paucibranchiata*; the modest barnacle *Austrominius modestus*; slipper limpet *Crepidula fornicata* and sand gaper *Mya arenaria*.

3.3.8 The tube-building spionid polychaete was originally described from Japan and has since been reported as a non-native species in soft bottom communities across Europe [18].

3.3.9 The modest barnacle is native to Australasia and was first recorded in Britain in Chichester Harbour in the 1940s and has since spread rapidly due to a combination of pelagic larval dispersal and transport by hull fouling. The modest barnacle can dominate hard surfaces and has largely displaced native barnacles in estuaries in South West Britain, although impacts are less significant on exposed rocky shores [19].

3.3.10 The native range of the slipper limpet is from Point Escuminac, Canada along the eastern coast of America, down to the Caribbean. It is thought to have been introduced to the Solent in the 1930s and is now common along the entire southern coast of England. The slipper limpet competes with other filter-feeding species including mussels and oysters for food and space and can smother seabed species and alter seabed habitat structure dramatically [20].

3.3.11 The sand gaper is believed to have colonised European coasts between the 13th and 17th centuries, possibly introduced by the Vikings (as food or bait) [21].

3.3.12 A total of six cryptogenic species (i.e. species with uncertain origin, so it is not known if they are native or non-native) were recorded across samples. This included a potentially undescribed species belonging to the *Tharyx* genus (Tharyx species A) and the oligochaete *Tubificoides galiciensis* which is not formally recorded in the UK. Other cryptogenic species recorded were the polychaetes *Polydora cornuta* and *Cossura pygodactylata*.

3.3.13 *Streblospio* sp.; *Gammaridae* sp.; *Aoridae* sp.; *Chironomidae* sp. and *Gracilaria* sp. were also recorded within samples and each of these taxa are known to have at least one species considered as non-native in the UK. However, *Streblospio*; *Gammaridae*; *Aoridae*; *Chironomidae* and *Gracilaria* are taxonomically problematic, and individuals were not identified to species level in this study.

3.3.14 All notable taxa are presented in Annex E . It is common for large-scale surveys to include new UK records and potentially new species due to unresolved taxonomy and a lack of published data for many groups.

Summary statistics

3.3.15 Across the survey area a total of 61 taxa were recorded, of which 13 were non-countable. Post-truncation, a total of 10,402 countable individuals were recorded and of these, 36 individuals were juveniles (less than 1% of total abundance), comprising six taxa.

Abundance

3.3.16 Summary statistics for key taxonomic groups recorded within sampling stations are indicated in Table 3-3. Overall, the most abundant taxonomic group across sample stations was invertebrates classified as 'other countable taxa', with a total abundance of 8,132 individuals comprising approximately 78% of total invertebrate abundance (Table 3-3). This was due to the large abundance of Nematoda across stations. This was followed by annelids and molluscs, which had total abundances of 1,320 individuals and 674 individuals, respectively (approximately 13% and 7% of invertebrate abundance, respectively). Crustaceans had a total abundance of 256 individuals contributing to 3% of invertebrate abundance and only one echinoderm individual was recorded, contributing to less than 1% of invertebrate abundance (Table 3-3).

3.3.17 Station 9 had the greatest invertebrate abundance, with a total abundance of 4,429 individuals, 4,101 of which were nematodes (

3.3.18 Graphic 3-4). Invertebrate abundance was also relatively high at Station 7 (2,464 individuals) and Station 4 (1,673 individuals) (

3.3.19 Graphic 3-4). Abundance across the remaining station was relatively low ranging from 167 individuals at Station 6 to 1673 individuals at Station 4 (

3.3.20 Graphic 3-4). Abundance within stations was highly variable but variability in abundance was generally low across replicates for a given station. Station 8 had the lowest intrastation variability in abundance ranging from 155 to 163 individuals. Station 7 had the greatest intrastation variability in abundance, ranging from 89 to 2,378 individuals. Variability in abundance between replicates of the same station was primarily due to the number of Nematoda individuals recorded.

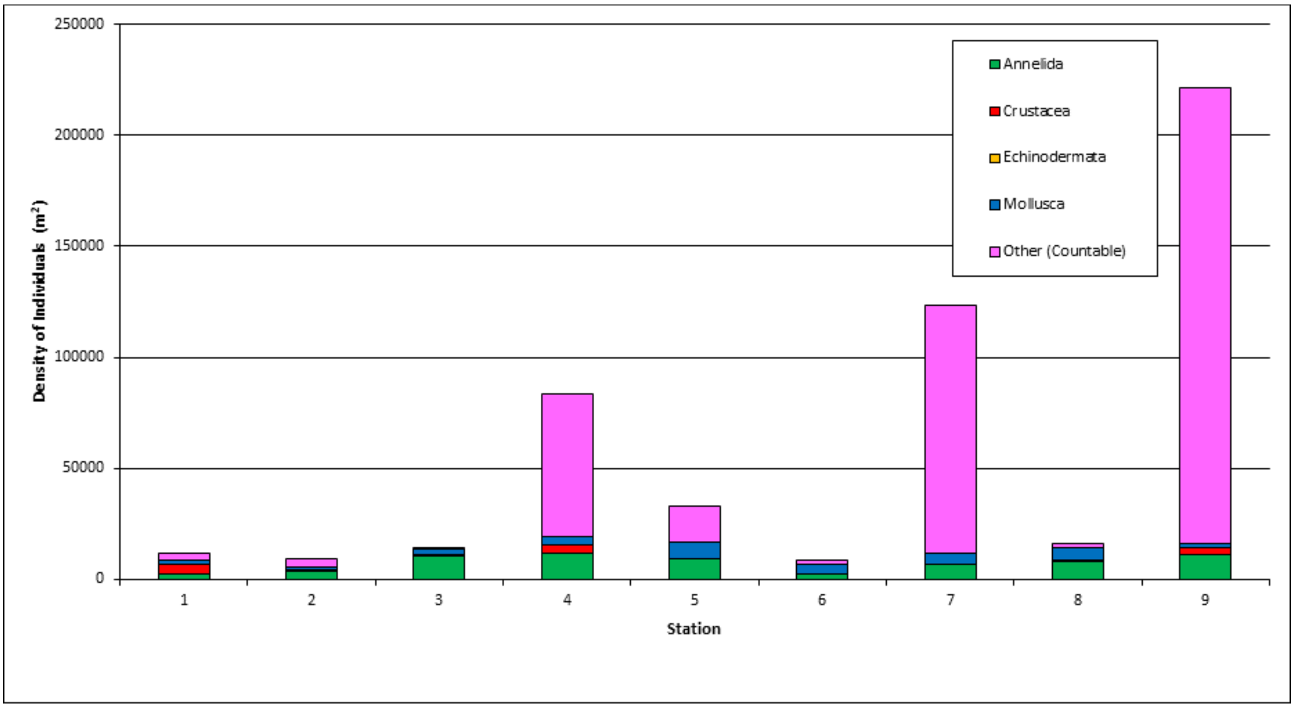
3.3.21 The most abundant taxon was Nematoda which across sample stations had a total abundance of 8,132 individuals and contributed approximately 99% of the total abundance of 'other countable taxa' and approximately 78% of total abundance. The second and third most abundant taxa across samples were the oligochaete the sludge worm *Tubificoides benedii* and the Laver spire shell, which had total abundances of 680 and 637 individuals respectively.

3.3.22 The most abundant crustacean was the amphipod *Melita palmata* which had a total abundance of 69 individuals. *Amphiuridae* sp. was the only echinoderm recorded across the survey area with one individual recorded at Station 1.

Table 3-3 Abundance and taxon richness within taxonomic groups (N/A = Not Applicable)

Key taxonomic group	Number of individuals		Taxon richness	
	Total abundance	Percent contribution	Total number of taxa	Percent contribution
Annelida	1,320	12.69	22	36.07
Crustacea	256	2.46	11	18.03
Echinodermata	1	0.01	1	1.64
Mollusca	674	6.48	9	14.75
Other (Countable)	8,151	78.36	5	8.20
Other (non-countable)	N/A	N/A	13	21.31
Total	**10,402**	**100**	**289**	**100**

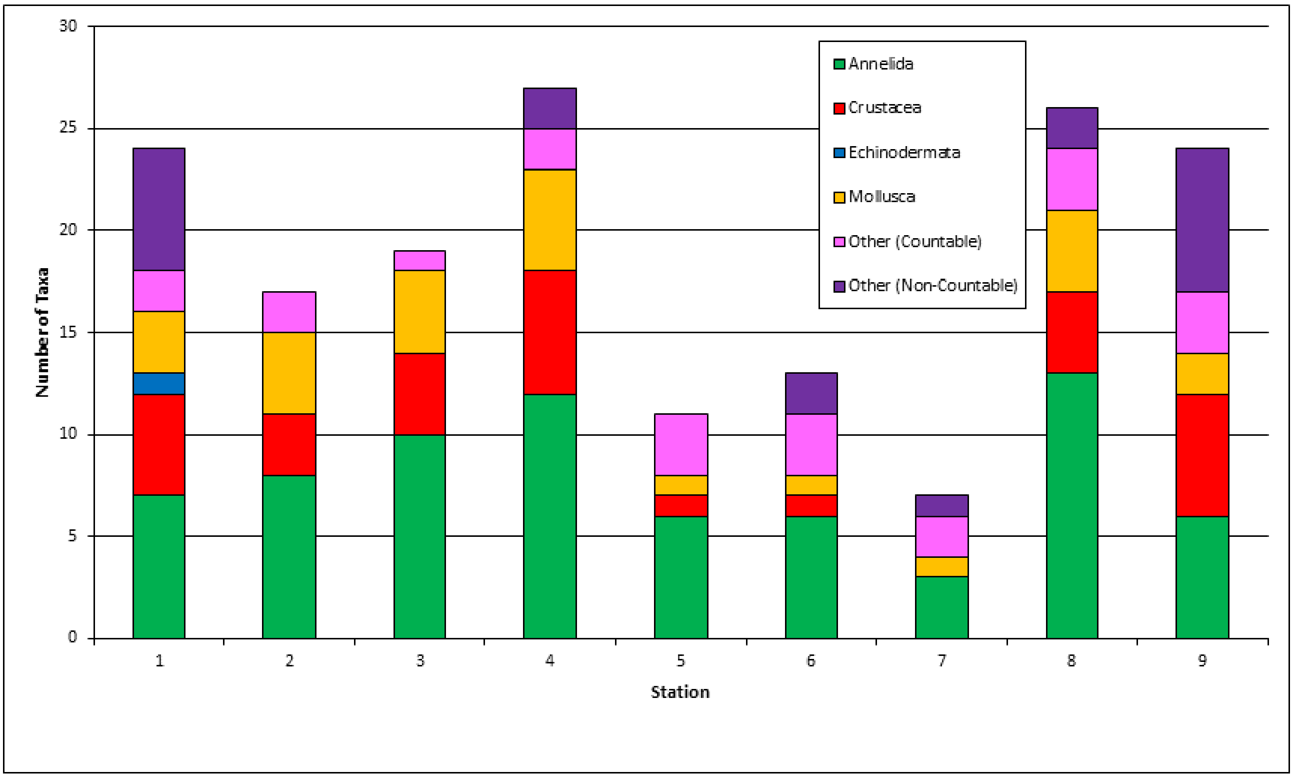
Graphic 3-4 Mean Density (individual per m^2) for taxonomic groups across sample stations



Taxon richness

3.3.23 A total of 61 taxa were recorded across sampling stations (including non-countable taxa). Annelids had the greatest taxon richness with 22 taxa recorded (36% of total taxa), (Graphic 3-5). This was followed by invertebrates classified as 'other non-countable with 13 taxa (21% of taxa), crustaceans with 11 taxa (18% of taxa), molluscs with nine taxa (15% of taxa) and other (countable) taxa with 5 taxa (8% of taxa). Echinoderms had the lowest taxon richness, with only one taxon (2% of taxa), (Graphic 3-5 and Table 3-3). Despite having the highest recorded abundances and mean densities, the category 'other (countable)' taxa was represented by the second lowest number of taxa, due to the dominance of nematodes across several stations.

Graphic 3-5 Taxon richness per 0.01m² for major taxonomic groups across stations



Diversity indices

3.3.24 Shannon-Wiener diversity index (H'(log$_e$)) values indicated that there was variable biological diversity within the marine communities sampled across the survey stations (Table 3-4). Shannon-Wiener diversity index values ranged between 0.23 at Station 9B to 2.02 at Station 1A. Similarly, Margalef's species richness index (d) was highly variable ranging from 0.39 at Station 7A to 3.34 at Station 8B. Margalef's species richness index (d) reflected the pattern observed for Shannon-Wiener index with lower values at stations with low diversity values.

3.3.25 The results for the Pielou's Evenness (J') and Simpson's index (1-λ) indicated that the evenness of benthic communities across survey stations was highly variable (Table 3-4). Pielou's Evenness ranged from 0.09 at Station 9B to 0.88 at Station 2B, whilst Simpson's index varied across stations ranging from 0.07 at Station 9B to 0.85 at Station 2B, (with a maximum potential value of 1).

3.3.26 Higher values indicate that the probability of any two individuals recorded within a station being the same species is very low and vice versa. Pielou's Evenness and Simpson's index were particularly low at Stations 3A; 4B; 7A; 9A and 9B and which is likely due to the dominance taxa such as Nematoda and *Tubificoides diazi*.

Table 3-4 Number of taxa, taxon richness and diversity indices at each station. SD = Standard Deviation

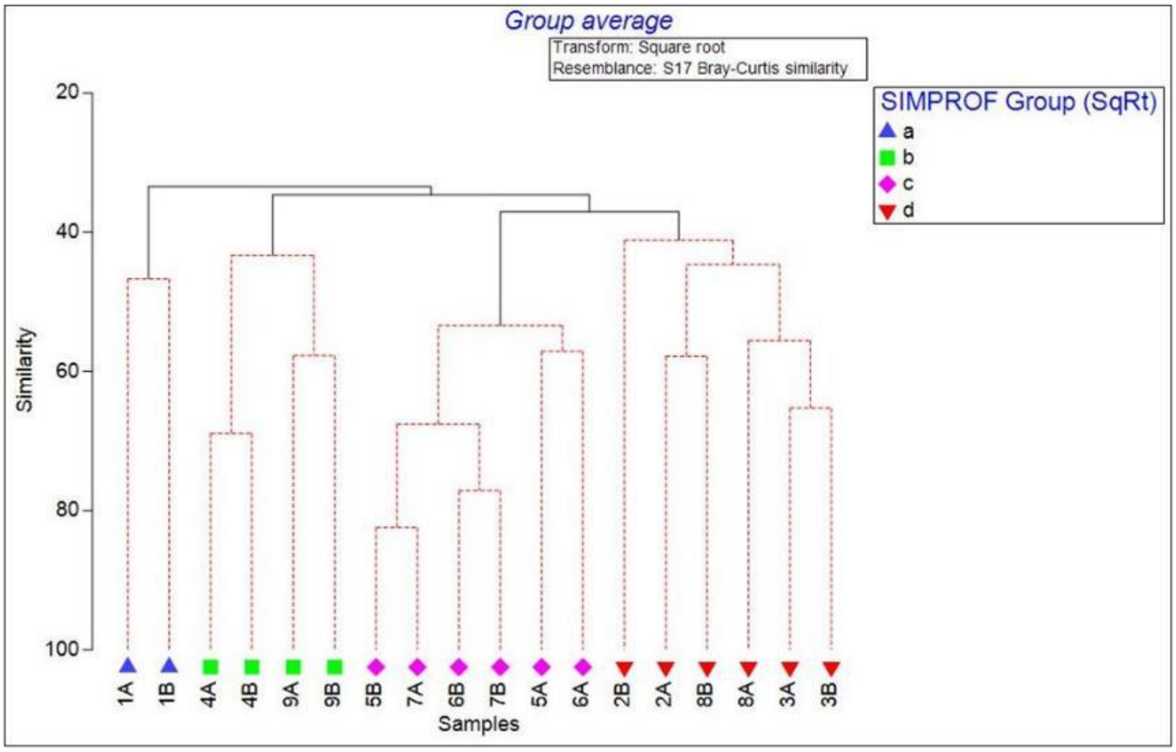
Station	Replicate	Total no. taxa	Density (individuals per m^2)	Margalef's species richness (d)	Pielou's eveness (J')	Shannon-Weiner diversity (H'(log$_e$))	Simpson's dominance (1-λ)
1	A	13	13,200	2.46	0.79	2.02	0.83
1	B	18	10,400	2.37	0.72	1.79	0.78
2	A	15	13,400	2.86	0.71	1.92	0.79
2	B	9	4,700	2.08	0.88	1.94	0.85
3	A	9	10,600	1.72	0.39	0.86	0.38
3	B	16	16,500	2.94	0.51	1.42	0.58
4	A	19	61,100	2.65	0.43	1.24	0.51
4	B	22	106,400	2.73	0.26	0.78	0.32
5	A	7	22,900	1.10	0.61	1.19	0.66
5	B	7	42600	0.99	0.43	0.84	0.42
6	A	11	10,800	1.71	0.61	1.35	0.63
6	B	6	6,100	1.22	0.61	1.10	0.61
7	A	4	237,800	0.39	0.23	0.31	0.13
7	B	6	8,900	0.89	0.69	1.10	0.62
8	A	16	15,500	2.58	0.66	1.75	0.77
8	B	18	16,300	3.34	0.58	1.69	0.67
9	A	16	102300	1.73	0.28	0.71	0.34
9	B	21	340,700	1.60	0.09	0.23	0.07
Min		**4**	**4,700**	**0.39**	**0.09**	**0.23**	**0.07**
Max		**22**	**340,700**	**3.34**	**0.88**	**2.02**	**0.85**
Mean		**13**	**57,789**	**1.96**	**0.53**	**1.24**	**0.55**
SD		**6**	**91,388**	**0.83**	**0.22**	**0.55**	**0.23**

Cluster and Multi-Dimensional Scaling analyses

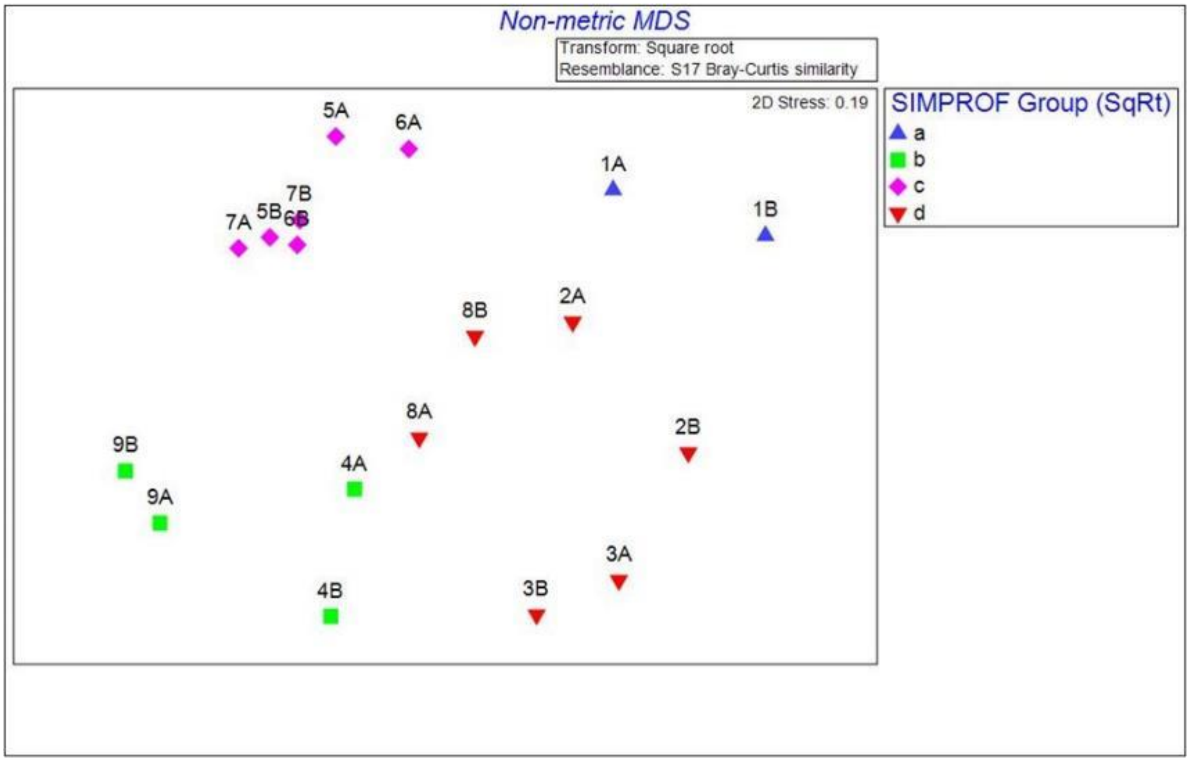
3.3.27 The results of the cluster analysis are presented in a cluster dendrogram (Graphic 3-6) and Multi-Dimensional Scaling (MDS) plot (Graphic 3-7). Black lines denote significant structure within the group to that point and red lines connect samples that cannot be significantly differentiated at the 95% confidence interval. As mentioned in section 2, due to the patchy nature of Nematoda within benthic samples, the taxon is not a key consideration when defining biotopes and removing them prior to analyses allowed the influence of more important habitat-defining taxa such as the laver spine shell, ragworm and other oligochaetes to be considered.

3.3.28 The SIMPROF test identified four groups (Group a-d) that can be considered statistically distinct from one another at the 95% confidence level. The accompanying MDS plot provides an alternative visualisation of the groupings observed in the cluster analysis (Graphic 3-7). With a stress value of 0.19, the MDS plot is considered a useful visual representation of the data [13].

Graphic 3-6 Cluster analysis dendogram with SIMPROF for benthic invertebrate abundance



Graphic 3-7 Multidimensional Scaling ordination plot for benthic grab invertebrate abundance



3.3.29 The results of SIMPER analysis indicating percentage contributions of different taxa to within-group similarity and between group dissimilarity are provided in Annex F

3.3.30 **Group a** was the smallest SIMPROF group consisting of two sample stations (1A and 1B) which separated from the other groups on the dendrogram at approximately 35% similarity and are placed towards the upper right of the MDS plot based on the representation in Annex F This group had an average within-group similarity of 46.68% and was characterised by laver spire shell with 25.18% contribution to similarity. This was followed by the modest barnacle and *M. palmata* both with 19.23%, then the sludge worm with 14.54% contribution to similarity.

3.3.31 **Group b** consisted of four sample stations (4A; 4B; 9A and 9B), separating from other groups from the dendrogram at approximately 36% similarity and placed towards the bottom left of the MDS plot based on the representation in Annex F This group had an average within-group similarity of 49.99% and was characterised by sludge worm with 29.91% contribution to similarity. This was followed by laver spire shell with 14.40%, then the amphipod *Microprotopus maculatus* with 11.98% contribution to similarity.

3.3.32 **Group c** was the joint largest group consisting of six sample stations (5A; 5B; 6A; 6B; 7A and 7B) which separated from the other groups on the dendrogram at approximately 39% similarity and are placed towards the upper left of the MDS plot based on the representation in Annex F This group had an average within-group similarity of 60.94% and was characterised by laver spire shell with 53.37% and sludge worm with 37.70% contribution to similarity.

3.3.33 **Group d** was the joint largest group consisting of six sample stations (2A; 2B; 3A; 3B; 8A and 8B) which separated from the other groups on the dendrogram at approximately 39% similarity and are placed towards the centre and bottom right of the MDS plot based on the representation in Annex F . This group had an average within-group similarity of 47.18% and was characterised by laver spire shell with 25.90% contribution to similarity. This was followed by the oligochaete *T. diazi* with 21.54%, sludge worm with 15.66% and *Streblospio* sp. with 15.21% contribution to similarity.

Station biotope assignment

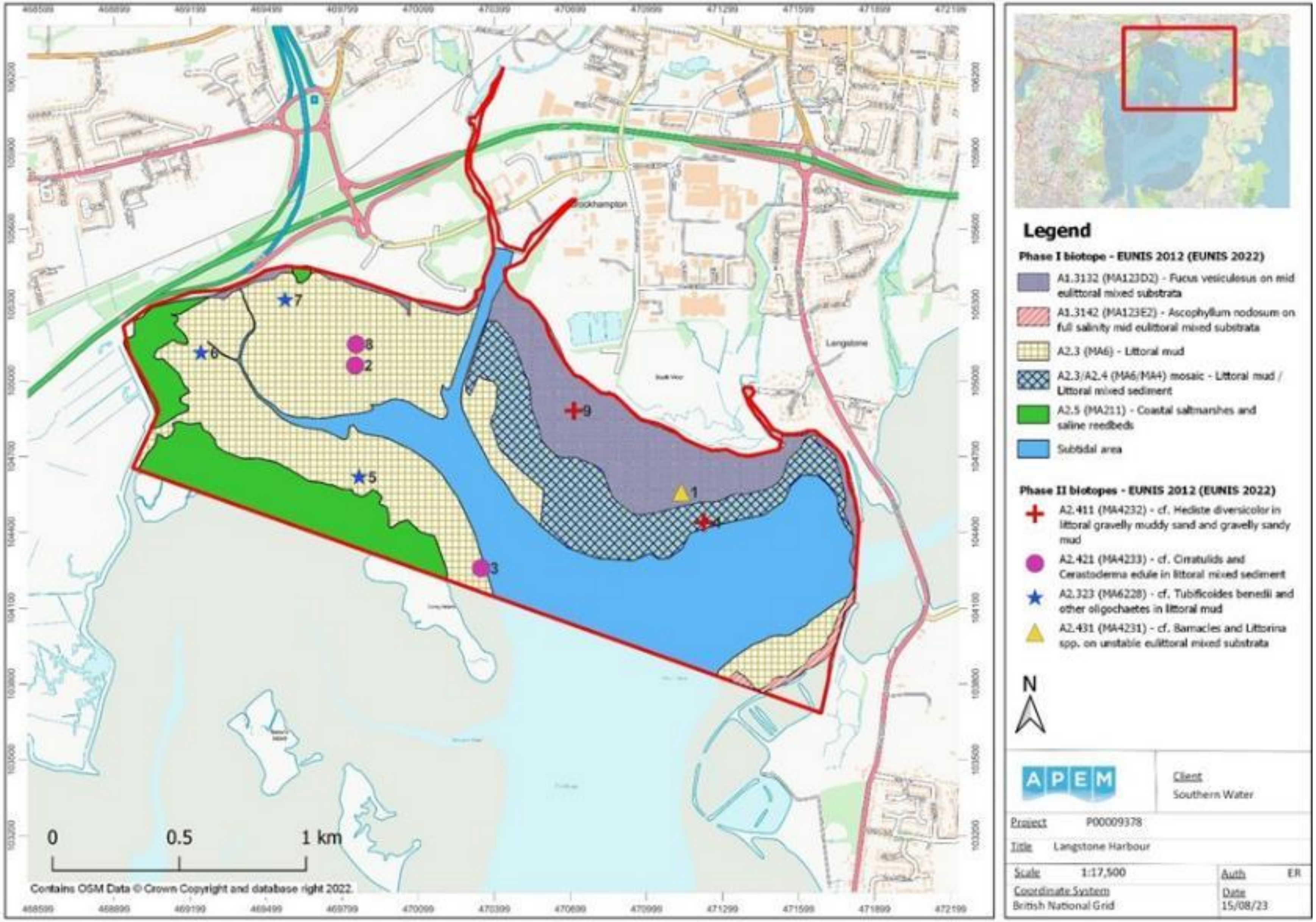
3.3.34 SIMPER analysis indicated the main species driving the differences between SIMPROF groupings (SIMPER outputs are provided in Annex F) and a combination of SIMPER outputs and the abundance of different taxa within replicates were considered when assigning biotopes to each replicate. Biotopes were assigned according to the EUNIS classification system and notes were made of any variations to the standard descriptions (Table 3-5). The prefix ‘cf.’ to the biotopes code has been used to indicate biotopes that are closest to a particular described biotope but not necessarily an exact fit. As the boundaries between the biotopes mapped during the Phase II survey could not be readily determined, a Graphic indicating the Phase I mapping outputs along with the Phase II biotopes at each station has been provided (Graphic 3-5).

3.3.35 A total of four standalone biotopes were assigned based on the SIMPROF groups and the most abundant taxa within replicates (Table 3-5).

Table 3-5 Biotope allocation for SIMPROF groups

Biotope with European Nature Information System and Joint Nature Conservation Committee codes	SIMPROF group	Station allocated	Description and information to allocate biotope type
cf. Barnacles and Littorina spp. on unstable eulittoral mixed substrata cf. LR.FLR.Eph.BLitX cf. A2.431 (EUNIS 2012) cf. MA4231 (EUNIS 2022)	a	1A; 1B	Group A (2 samples); Within-group similarity = 46.68. This biotope was assigned due to the presence of the modest barnacle which this biotope supports. However, the biotope was considered close to A2.431, rather than a good fit, due to the lack of *Littorina* spp. and is intermediate with A5.43 biotopes due to lower shore/subtidal elements.
cf. *Hediste diversicolor* in littoral gravelly muddy sand and gravelly sandy mud cf. LS.LMx.GvMu.HedMx cf. A2.411 (EUNIS 2012) cf. MA4232 (EUNIS 2022)	b	4A; 4B; 9A; 9B	Group B (4 samples); Within-group similarity = 49.99. This biotope was assigned due to abundance of ragworm in mixed sediment. *Streblospio* sp., *Nephtys* sp., *Tubificoides* sp. and laver spire shell were also abundant. However, the biotope was not fully typical, due to the high abundance of non-standard taxa. Station 9 was intermediate with LS.LMx.Mx in these samples.
cf. *Tubificoides benedii* and other oligochaetes in littoral mud cf. LS.LMu.UEst.Tben cf. A2.323 (EUNIS 2012) cf. MA6228 (EUNIS 2022)	c	5A; 5B; 6A; 6B; 7A; 7B	Group C (6 samples); Within-group similarity = 60.94. This biotope was assigned due to the dominance of sludge worm. However, at Station 5 the biotope was considered to be intermediate with SS.SMu.SmuVS.AphTubi due to the many *Tharyx* individuals in the 5A replicate sample.
Cf. Cirratulids and *Cerastoderma edule* in littoral mixed sediment cf. LS.LMx.Mx.CirCer cf. A2.421 (EUNIS 2012) cf. MA4233 (EUNIS 2022)	d	2A; 2B; 3A; 3B; 8A; 8B	Group D (6 samples); Within-group similarity = 47.18. This biotope was assigned due to the presence of several characterising species such as the polychaetes the bristle worm *Pygospio elegans*, *Capitella* sp., *M. palmata*; the sludge worm; the common cockle and modest barnacle. However, the biotope was considered similar to A2.421, rather than a good fit, due to a greater dominance of oligochaetes than the standard description of the biotope and the absence of *Cirriformia* sp.

Graphic 3-8 Habitats mapped during the intertidal Phase I and Phase II survey (EUNIS habitat codes indicated)



3.4 Sediment composition

3.4.1 Overall, sediment type varied across the survey area with particle size ranging from 13.3µm to 38,250µm. However, mud was dominant at the majority of stations. For instance, mud had the highest contribution to sediment composition at six of the nine stations ranging from 45.1% to 85.3%. According to the Folk classification (Folk 1954) these stations were characterised as Gravelly Mud (2 stations), Sandy Mud (2 stations), Slightly Gravelly Sandy Mud (1 station) and Muddy Gravel (1 station) and they were located to the south and north-west of the survey area, with the exception of Station 4 (Muddy Gravel) which was located to the north-east (Annex D). At all remaining stations, gravel dominated the sediment composition, ranging from 53.5% to 86.6%. Under the Folk classification these stations were designated as either Muddy Gravel (2 stations) and Gravel (1 station) and were located to the north-east of the survey area, with the exception of Station 2 (Muddy Gravel) which was located to the north-west.

3.5 Community composition

3.5.1 In total, 61 taxa were recorded across the nine sample stations, of which 13 taxa were non-countable.

3.5.2 The most abundant taxon was Nematoda with a mean density of 45,178 ± 89,956 individuals per m^2, accounting for 78% of the total number of countable individuals. However, it should be noted that nematodes tend to be inconsistently recorded in benthic samples. This is evident across samples from this survey where the abundance of nematodes ranged from no individuals at replicate 3A to 3,285 individuals at replicate 9B. Additionally, abundances of nematodes were also inconsistent between replicates at the same station. For instance, the abundance of nematodes at Station 7 ranged from eight to 2,221 individuals within replicates. For this reason, nematodes are not a key consideration for biotope definition. As a result, it was determined that nematodes should not be included in the multivariate analysis conducted to inform biotope assignment. The next most abundant taxa were the sludge worm (3,778 ± 4,192 individuals per m^2) and the laver spire shell (3,539 ± 2,748 individuals per m^2), which accounted for approximately 6% of the total number of countable individuals each.

3.5.3 When considering relative contributions to key taxonomic groups, the high abundance of nematodes across sampling stations resulted in ‘other countable taxa’ grouping constituting the most abundant group with a mean density of 45,283 ± 71,245 individuals per m^2. Despite this, ‘other countable taxa’ were dominant at only four of the nine stations (Stations 4, 5, 7 and 9). The remaining stations across the survey area were either dominated by annelids (Stations 2, 3 and 8), molluscs (Station 6) or crustaceans (Station 1). Additionally, despite the highest recorded abundances and mean densities, ‘other (countable)’ taxa was represented by the second lowest number of taxa with annelids having the greatest taxon richness.

3.5.4 Diversity indices calculated for sample replicates across stations indicated that biological diversity was highly variable. For instance, values of Shannon-Wiener Diversity Index, a widely used measure of diversity, which considers both the number of taxa present and the evenness of distribution of the taxa ranged from 0.23 (lower biological diversity) to 2.02 (higher biological diversity). Similarly, values for Pielou's Evenness and Simpson's index were also extremely variable ranging from 0.09 to 0.88 and 0.07 to 0.85 respectively. The primary reason for the highly variable biological diversity and evenness across replicates is due to the inconsistent abundance of nematodes.

3.5.5 No species of conservation importance were recorded. However, four non-native species within the UK were recorded. The tube-building spionid polychaete which was originally described in Japan and first recorded in Europe in 1962. The modest barnacle was first recorded in Chichester Harbour in the 1940s and can dominate hard surfaces and has largely displaced native barnacles in estuaries in South West Britain. The slipper limpet is thought to have been introduced to the Solent in the 1930s and is ubiquitous along the entire southern coast of England. The sand gaper is believed to have colonised European coasts between the 13th and 17th centuries.

3.5.6 Additionally, common cockle was also recorded which is a commercially important species and is now ubiquitous across the UK. However, abundance of common cockle was low and it not considered that commercially important populations are present within the survey area.

3.6 Habitat assignment

3.6.1 During the Phase I intertidal survey, a total of five habitats/habitat mosaics were recorded covering a total area of 1,931,433 m^2 (193 ha). In addition, the results of SIMPER analysis following the Phase II survey identified a total of four SIMPROF groups which were assigned to four different biotopes.

3.6.2 The habitat with the greatest extent during the Phase I survey was 'Littoral mud' (EUNIS 2012 code: A2.3; EUNIS 2022 code: MA6; JNCC code: LS.LMu) with coverage across the central, western and eastern sections of the survey area. The extent of this habitat overlapped with six of the nine stations sampled during the Phase II survey including Stations 3 and 5 in the south of the survey area and Stations 2, 6, 7 and 8 in the north-west of the survey area. Stations 5, 6 and 7 were assigned to a variant of the biotope '*Tubificoides benedii* and other oligochaetes in littoral mud' (EUNIS 2012 code: A2.323; EUNIS 2022 code: MA6228; JNCC code: LS.LMu.UEst.Tben) whilst Stations 2, 3 and 8 were assigned to a variant of the biotope 'Cirratulids and *Cerastoderma edule* in littoral mixed sediment' (EUNIS 2012 code: A2.421; EUNIS 2022 code: MA4233; JNCC code: LS.LMx.Mx.CirCer).

3.6.3 The habitat with next greatest extent during the Phase I survey was '*Fucus vesiculosus* on mid eulittoral mixed substrata' (EUNIS 2012 code: A1.3132; EUNIS 2022 code: MA123D2; JNCC code: LR.LLR.F.Fves.X) which was primarily recorded in the north-eastern section of the survey area. This habitat overlapped with Stations 1 and 9 which were assigned to variants of the biotopes 'Barnacles and *Littorina spp*. on unstable eulittoral mixed substrata' (EUNIS 2012 code: A2.431; EUNIS 2022 code: MA4231; JNCC code: LR.FLR.Eph.BLitX) and '*Hediste diversicolor in* littoral gravelly muddy sand and gravelly sandy mud' (EUNIS 2012 code: A2.311; EUNIS code 2022: MA4232; JNCC code: LS.LMu.MEst.NhomMacStr), respectively.

3.6.4 A mosaic of 'Littoral mud'/'Littoral mixed sediment' (EUNIS 2012 code: A2.3/A2.4; EUNIS 2022 code: MA6/MA4; JNCC code: LS.LMu/LS.LMx) observed to the north and north-eastern sections of the survey area overlapped Station 4. This station was assigned to a variant of the biotope '*Hediste diversicolor* in littoral gravelly muddy sand and gravelly sandy mud' (EUNIS 2012 code: A2.311; EUNIS 2022 code: MA4232; JNCC code LS.LMu.MEst.NhomMacStr).

3.6.5 During the Phase I survey, two other habitats were assigned to the rest of the intertidal area including 'Coastal saltmarshes and saline reedbeds' (EUNIS 2012 code: A2.5; EUNIS 2022 code: MA211; JNCC: LS.LMp.Sm) and '*Ascophyllum nodosum* on full salinity mid eulittoral mixed substrata' (EUNIS 2012 code: A1.3142; EUNIS 2022 code: MA123E2; JNCC code: LR.LLR.F.Asc.X).

3.6.6 During the Phase I and Phase II intertidal survey it was noted that there was considerable bait digging activity across the north-east section of the intertidal survey area (Annex A).

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Annex A Station feature records

Table A-1 Station feature record notes from the Phase I survey

Station	Arenicola casts (m-2)	Large holes >5mm (m-2)	Small holes <5mm (m-2)	Scrobicularia holes (m-2)	Lanice tubes (m-2)	Firmness (1-5) (firm-soft)	Sorting (1-5) (highly sorted-poorly sorted)	Stability (1-5) (stabile-mobile)	Relief (1-5) (even-uneven)	Anoxic layer depth (cm)	Macroalgae present (%)	Sediment underwater (%)	Surface features (e.g. fauna, algal film)	Anthropogenic pressures
1a	0	0	0	0	0	1	5	2	4	0.1	20	0	*Fucus vesiculosus*	Bait digging
1b	0	0	0	0	0	1	5	2	4	0.1	60	0	*Fucus vesiculosus*	Bait digging
1c	0	0	0	0	0	1	5	2	4	0.1	50	0	*Fucus vesiculosus*	Bait digging
2a	0	0	1	0	0	4	3	4	2	0.1	5	0	Unidentified eggs	None identified
2b	0	1	1	0	0	4	3	4	2	0.1	5	20	Unidentified eggs	None identified
2c	0	0	3	0	0	4	3	4	2	0.1	5	80	Unidentified eggs	None identified
3a	0	0	0	0	0	4	1	2	1	0.5	90	100	*Ulva*	None identified
3b	0	0	0	0	0	4	1	2	1	0.5	80	100	*Ulva*	None identified
3c	0	0	0	0	0	4	1	2	1	0.5	90	100	*Ulva*	None identified
4a	0	0	0	0	0	5	2	4	3	1	40	0	N/A	Bait digging
4b	0	0	0	0	0	2	5	4	3	0.1	40	0	N/A	Bait digging
4c	0	0	0	0	0	0	2	4	3	1	40	0	N/A	Bait digging
5a	0	0	0	0	0	3	2	2	1	0.1	40	80	*Ulva*	None identified
5b	0	0	0	0	0	3	2	2	1	0.1	100	100	*Ulva*	None identified
5c	0	0	0	0	0	3	2	2	1	0.1	90	10	*Ulva*	None identified
6a	0	0	0	0	0	4	4	3	1	0.1	40	100	*Ulva*; Shell fragments	None identified
6b	0	0	0	0	0	4	4	3	1	0.1	90	100	*Ulva*; Shell fragments	None identified
6c	0	0	0	0	0	4	4	3	1	0.1	80	100	*Ulva*; Shell fragments	None identified
7a	0	0	0	0	0	2	4	2	1	0.1	90	100	*Ulva*; Shell fragments	None identified
7b	0	0	0	0	0	2	4	2	1	0.1	95	100	*Ulva*; Shell fragments	None identified
7c	0	0	0	0	0	2	4	2	1	0.1	80	100	*Ulva*; Shell fragments	None identified
8a	0	0	0	0	0	3	4	3	1	0.1	90	100	*Ulva*; Shell fragments	None identified
8b	0	0	0	0	0	3	4	3	1	0.1	95	100	*Ulva*; Shell fragments	None identified
8c	0	0	0	0	0	3	4	3	1	0.1	90	100	*Ulva*; Shell fragments	None identified
9a	0	0	0	0	0	1	5	2	4	0.1	20	0	Small patch of *Fucus serratus*	Bait digging
9b	0	0	0	0	0	1	5	2	4	0.1	30	0	Small patch *of Fucus serratus*	Bait digging
9c	0	0	0	0	0	1	5	2	4	0.1	90	0	Small patch of *Fucus serratus*	Bait digging

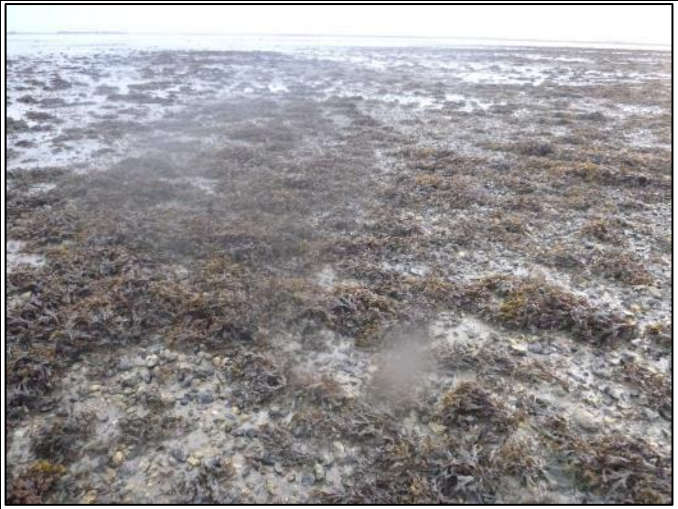
Annex B Example habitats observed

Table B-1 Example habitats observed during the survey

Habitat	Image
Littoral mud A2.3 LS.LMu	 

<table>
<tr><th>Habitat</th><th colspan="2">Image</th></tr>
<tr><td>Fucus vesiculosus on mid eulittoral mixed substrata

A1.3132

LR.LLR.F.Fves.X</td><td></td><td></td></tr>
<tr><td>Littoral mud/Littoral mixed sediment

A2.3/A2.4

LS.LMu/LS.LMx</td><td></td><td></td></tr>
</table>

Habitat	Image	
Coastal saltmarshes and saline reedbeds A2.5 LS.LMp.Sm		

Habitat	Image
Ascophyllum nodosum on full salinity mid eulittoral mixed substrata A1.3142 LR.LLR.F.Asc.X	

Annex C Core sample survey

Table C-1 Core sample photographs

Station	Core A	Core B
1		
2		
3		
4		

Station	Core A	Core B
5		
6		
7		
8		

Station	Core A	Core B
9		

Annex D Raw data

D.1 Raw and GRADISTAT PSA data

Table D-1 GRADISTAT descriptive sediment classification

Sample ID	Date Sampled	Visual Description pre-analysis	Blott and Pye (2012) classification	Folk (1954) classification	BGS (1982) classification (modified from Folk, 1954)	Statistics calculated using Folk and Ward (1957) formulae							
						Mean		Sorting		Skewness		Kurtosis	
						(µm)	(description)	(phi)	(description)	(phi)	(description)	(phi)	(description)
St.1 PSA	27/09/2022	Gravelly sandy mud with a few shells	Slightly sandy muddy gravel	Muddy Gravel	Muddy Gravel	1049.9	Very Coarse Sand	4.769	Extremely Poorly Sorted	0.444	Very Fine Skewed	0.674	Platykurtic
St.2 PSA	26/09/2022	Gravelly sandy mud with a few shells	Slightly sandy muddy gravel	Muddy Gravel	Muddy Gravel	1403.3	Very Coarse Sand	5.161	Extremely Poorly Sorted	0.606	Very Fine Skewed	0.594	Very Platykurtic
St.3 PSA	26/09/2022	Sandy mud with one shell	Very slightly gravelly slightly sandy mud	Slightly Gravelly Sandy Mud	Slightly Gravelly Sandy Mud	15.1	Medium Silt	2.784	Very Poorly Sorted	0.120	Fine Skewed	1.122	Leptokurtic
St.4 PSA	27/09/2022	Sandy mud with a few shells	Slightly sandy gravelly mud	Muddy Gravel	Muddy Gravel	181.3	Fine Sand	4.978	Extremely Poorly Sorted	-0.237	Coarse Skewed	0.641	Very Platykurtic
St.5 PSA	26/09/2022	Sandy mud	Slightly sandy mud	Sandy Mud	Sandy Mud	11.9	Medium Silt	2.526	Very Poorly Sorted	0.133	Fine Skewed	1.220	Leptokurtic
St.6 PSA	26/09/2022	Sandy mud	Sandy mud	Sandy Mud	Sandy Mud	23.9	Coarse Silt	2.725	Very Poorly Sorted	0.311	Very Fine Skewed	1.242	Leptokurtic
St.7 PSA	26/09/2022	Sandy mud with a few shells and few gravel particles	Slightly gravelly sandy mud	Gravelly Mud	Gravelly Mud	47.2	Very Coarse Silt	4.412	Extremely Poorly Sorted	-0.184	Coarse Skewed	1.266	Leptokurtic
St.8 PSA	26/09/2022	Gravelly sandy mud with a few shells	Slightly gravelly sandy mud	Gravelly Mud	Gravelly Mud	86.1	Very Fine Sand	3.818	Very Poorly Sorted	-0.058	Symmetrical	1.225	Leptokurtic
St.9 PSA	28/09/2022	Sandy muddy gravel with shells	Slightly sandy slightly muddy gravel	Gravel	Gravel	9856.9	Medium Gravel	2.369	Very Poorly Sorted	0.373	Very Fine Skewed	2.476	Very Leptokurtic

Table D-2 GRADISTAT descriptive sediment classification continued

Sample ID	Primary Mode (µm)	d10 (µm)	d50 (µm)	d90 (µm)	Gravel (>2mm) (%)	Sand (63-2000µm) (%)	Mud (<63µm) (%)	V Coarse Gravel (32-64mm) (%)	Coarse Gravel (16-32mm) (%)	Medium Gravel (8-16mm) (%)	Fine Gravel (4-8mm) (%)	V Fine Gravel (2-4mm) (%)	V Coarse Sand (1-2mm) (%)	Coarse Sand (500-1000µm) (%)
St.1 PSA	26950.0	6.9	3043.0	32098.5	55.44	19.56	25.00	10.09	18.94	8.99	8.04	9.39	6.14	3.02
St.2 PSA	38250.0	4.8	6734.7	40481.8	53.53	15.60	30.87	32.22	10.81	6.00	2.67	1.83	1.26	1.40
St.3 PSA	37.7	1.1	17.2	139.7	3.40	18.04	78.56	0.00	0.00	3.40	0.00	0.00	0.00	0.34
St.4 PSA	19200.0	3.0	76.8	18158.7	32.28	19.53	48.19	0.00	14.12	8.00	5.20	4.96	2.91	2.35
St.5 PSA	13.3	0.9	13.1	98.0	0.00	14.66	85.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00
St.6 PSA	53.3	1.5	35.3	158.8	0.00	32.01	67.99	0.00	0.00	0.00	0.00	0.00	0.04	3.76
St.7 PSA	37.7	1.3	34.5	7193.8	14.39	24.28	61.33	0.00	4.76	4.61	3.25	1.78	2.14	1.90
St.8 PSA	150.9	4.0	89.1	10194.3	13.99	40.88	45.13	0.00	5.98	4.81	1.76	1.43	2.10	3.04
St.9 PSA	9600.0	174.3	10577.9	34570.5	86.80	5.96	7.23	12.93	21.99	29.70	17.92	4.27	1.17	0.65

Table D-3 GRADISTAT descriptive sediment classification continued and particle fraction percentage dry weights

Sample ID	Medium Sand (250-500µm) (%)	Fine Sand (125-250µm) (%)	V Fine Sand (63-125µm) (%)	V Coarse Silt (31-63µm) (%)	Coarse Silt (16-31µm) (%)	Medium Silt (8-16µm) (%)	Fine Silt (4-8µm) (%)	V Fine Silt (2-4µm) (%)	Clay (<2µm) (%)	Percentages of the distribution in each 'half-phi' size interval, expressed in µm (sieving for >2mm fraction, laser diffraction for <2mm fraction)									
										>63000	45000 to 63000	31500 to 45000	22400 to 31500	16000 to 22400	11200 to 16000	8000 to 11200	5600 to 8000	4000 to 5600	2800 to 4000
St.1 PSA	2.84	4.13	3.43	3.79	4.52	5.68	4.94	2.73	3.34	0.00	0.00	10.56	10.74	7.74	4.99	4.00	3.95	4.08	5.15
St.2 PSA	2.61	5.21	5.12	6.01	5.86	5.51	4.85	3.21	5.44	0.00	0.00	33.71	0.00	9.32	4.36	1.64	2.02	0.65	1.07
St.3 PSA	2.15	5.16	10.39	15.61	14.83	13.28	12.14	8.36	14.33	0.00	0.00	0.00	0.00	0.00	3.40	0.00	0.00	0.00	0.00
St.4 PSA	3.41	4.82	6.05	8.57	8.95	9.94	8.55	5.08	7.10	0.00	0.00	0.00	3.16	10.96	5.62	2.37	2.84	2.36	2.91
St.5 PSA	1.62	5.37	7.67	12.65	17.95	17.61	13.94	8.59	14.59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
St.6 PSA	2.89	6.51	18.81	21.78	13.61	8.60	7.06	5.24	11.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
St.7 PSA	2.55	6.92	10.77	13.49	11.48	8.59	7.75	6.45	13.58	0.00	0.00	0.00	0.00	4.76	2.89	1.72	2.13	1.12	0.63
St.8 PSA	7.84	16.10	11.81	8.75	8.78	10.18	7.77	4.09	5.56	0.00	0.00	0.00	0.00	5.98	3.71	1.10	0.64	1.12	0.59
St.9 PSA	0.76	1.50	1.89	1.61	1.67	1.72	1.14	0.50	0.59	0.00	0.00	13.53	5.39	16.00	12.09	17.60	11.44	6.47	3.01

Table D-4 Particle fraction percentage sample dry weights continued

Sample ID	Percentages of the distribution in each 'half-phi' size interval, expressed in µm (sieving for >2mm fraction, laser diffraction for <2mm fraction)																			
	2000 to 2800	1400 to 2000	1000 to 1400	710 to 1000	500 to 710	355 to 500	250 to 355	180 to 250	125 to 180	90 to 125	63 to 90	44.19 to 63	31.25 to 44.19	22.097 to 31.25	15.625 to 22.097	11.049 to 15.625	7.813 to 11.049	5.524 to 7.813	3.906 to 5.524	2.762 to 3.906	1.953 to 2.762
St.1 PSA	4.24	3.46	2.68	1.90	1.12	1.31	1.53	2.06	2.07	1.86	1.57	1.63	2.16	2.21	2.31	2.81	2.86	2.68	2.26	1.64	1.09
St.2 PSA	0.76	0.65	0.61	0.64	0.76	0.90	1.70	2.36	2.85	2.78	2.34	2.71	3.30	3.08	2.78	2.83	2.67	2.55	2.30	1.83	1.38
St.3 PSA	0.00	0.00	0.00	0.00	0.34	0.83	1.32	1.89	3.27	4.80	5.59	6.89	8.72	7.95	6.89	6.79	6.48	6.31	5.83	4.76	3.60
St.4 PSA	2.04	1.65	1.26	0.87	1.48	1.51	1.89	2.15	2.67	3.01	3.04	3.74	4.83	4.56	4.39	4.98	4.96	4.61	3.94	2.97	2.11
St.5 PSA	0.00	0.00	0.00	0.00	0.00	0.02	1.61	3.11	2.26	4.28	3.39	5.06	7.59	8.75	9.21	9.26	8.35	7.50	6.45	5.00	3.60
St.6 PSA	0.00	0.00	0.04	1.52	2.24	1.74	1.15	1.88	4.63	8.49	10.32	11.00	10.78	8.03	5.58	4.64	3.96	3.67	3.39	2.87	2.37
St.7 PSA	1.15	1.09	1.04	1.00	0.90	1.14	1.41	2.72	4.20	5.54	5.23	5.98	7.51	6.47	5.01	4.60	3.99	3.92	3.83	3.35	3.10

Sample ID	Percentages of the distribution in each 'half-phi' size interval, expressed in µm (sieving for >2mm fraction, laser diffraction for <2mm fraction)																			
	2000 to 2800	1400 to 2000	1000 to 1400	710 to 1000	500 to 710	355 to 500	250 to 355	180 to 250	125 to 180	90 to 125	63 to 90	44.19 to 63	31.25 to 44.19	22.097 to 31.25	15.625 to 22.097	11.049 to 15.625	7.813 to 11.049	5.524 to 7.813	3.906 to 5.524	2.762 to 3.906	1.953 to 2.762
St.8 PSA	0.84	0.98	1.12	1.43	1.61	3.03	4.81	7.55	8.55	7.10	4.71	4.07	4.68	4.37	4.41	5.19	4.99	4.33	3.44	2.44	1.65
St.9 PSA	1.26	0.81	0.36	0.33	0.32	0.35	0.41	0.59	0.91	1.06	0.83	0.77	0.85	0.82	0.84	0.91	0.82	0.66	0.48	0.31	0.19

Table D-5 Particle fraction percentage sample dry weights continued

Sample ID	Percentages of the distribution in each 'half-phi' size interval, expressed in µm (sieving for >2mm fraction, laser diffraction for <2mm fraction)											
	1.381 to 1.953	0.977 to 1.381	0.691 to 0.977	0.488 to 0.691	0.345 to 0.488	0.244 to 0.345	0.173 to 0.244	0.122 to 0.173	0.086 to 0.122	0.061 to 0.086	0.043 to 0.061	0.01 to 0.043
St.1 PSA	0.74	0.53	0.42	0.37	0.35	0.31	0.25	0.19	0.12	0.05	0.01	0.00
St.2 PSA	1.05	0.81	0.66	0.62	0.61	0.56	0.46	0.35	0.22	0.09	0.01	0.00
St.3 PSA	2.72	2.09	1.74	1.63	1.58	1.48	1.23	0.96	0.62	0.25	0.03	0.00
St.4 PSA	1.54	1.17	0.93	0.81	0.72	0.64	0.51	0.39	0.25	0.10	0.01	0.00
St.5 PSA	2.54	1.84	1.59	1.70	1.84	1.77	1.41	1.02	0.61	0.24	0.03	0.00
St.6 PSA	2.00	1.68	1.44	1.35	1.31	1.23	1.04	0.83	0.54	0.23	0.03	0.00
St.7 PSA	3.12	2.90	2.36	1.78	1.27	0.88	0.57	0.38	0.22	0.09	0.01	0.00
St.8 PSA	1.18	0.88	0.70	0.62	0.57	0.52	0.43	0.34	0.22	0.09	0.01	0.00
St.9 PSA	0.12	0.09	0.07	0.07	0.06	0.06	0.05	0.04	0.02	0.01	0.00	0.00

D.2 Raw macrobiota data

The table below shows the species abundance data for each core and station from the intertidal survey.

Table D-6 Macrobiota abundances per stations

Code	Station		1A	1B	2A	2B	3A	3B	4A	4B	5A	5B	6A	6B	7A	7B	8A	8B	9A	9B
	Taxa ID	Qualifiers																		
A5050	*Folliculinidae*		-	-	-	-	-	-	-	-	-	-	P	-	-	-	-	-	-	P
C0000	*Animalia*	eggs	-	-	-	-	-	-	-	-	-	-	P	-	-	-	P	-	-	-
C0001	*Porifera*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	P
D0662	*Actiniaria*		-	-	-	-	-	-	2	-	-	-	2	-	-	3	1	-	1	-
G0047	*Lineidae*		1	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
HD0001	*Nematoda*		38	28	53	12	-	3	420	870	3	317	25	4	2221	8	27	2	816	3285
P0118	*Eteone longa*	aggregate	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
P0265	*Glycera tridactyla*		1	-	-	-	-	-	-	-	-	-	1	1	-	1	-	1	-	-
P0430	*Sphaerosyllis cf. taylori*		-	-	-	-	-	-	4	1	-	-	-	-	-	-	-	-	1	-
P0462	*Hediste diversicolor*		-	-	1	1	1	-	2	3	-	-	-	-	-	-	-	1	13	33
P0494	*Nephtys*	juvenile	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-

Code	Station		1A	1B	2A	2B	3A	3B	4A	4B	5A	5B	6A	6B	7A	7B	8A	8B	9A	9B
	Taxa ID	Qualifiers																		
P0499	*Nephtys hombergii*		-	-	-	-	1	2	1	1	-	-	-	-	-	-	1	-	-	-
P0738	*Malacoceros tetracerus*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
P0752	*Polydora ciliata*	aggregate	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
P0753	*Polydora cornuta*		-	-	-	11	-	-	1	-	-	-	-	-	-	-	4	1	1	1
P0773	*Pseudopolydora paucibranchiata*		-	-	-	-	-	2	-	1	-	-	-	-	-	-	-	-	-	-
P0776	*Pygospio elegans*		-	-	-	-	1	-	-	-	1	-	4	-	-	-	-	1	-	-
P0798	*Streblospio*		5	1	8	5	3	4	13	9	2	-	5	-	-	-	4	7	-	-
P0839	*Cirriformia tentaculata*		2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P0847	*Tharyx species A*		-	-	15	-	-	-	-	-	88	-	3	-	-	-	-	12	-	-
P0871	*Cossura pygodactylata*		-	-	-	-	2	5	-	-	-	-	-	-	-	-	2	8	-	-
P0906	*Capitella*		-	4	-	6	-	-	1	-	-	13	-	1	29	-	1	-	2	6
P1124	*Melinna palmata*		-	-	-	-	-	1	-	1	-	-	-	-	-	-	1	1	-	-
P1324	*Serpulidae*		-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P1487	*Tubificoides galiciensis*		-	-	-	-	-	-	7	-	-	-	-	-	-	-	-	-	-	-
P1490	*Tubificoides benedii*		16	4	17	3	2	4	69	112	41	33	6	24	62	41	61	15	157	13
P1494	*Tubificoides diazi*	aggregate	6	4	1	3	83	103	7	2	-	-	-	-	-	-	25	18	-	-
P1496	*Tubificoides insularis*		-	-	-	-	-	-	1	2	-	-	-	-	-	-	-	-	-	-
R0068	*Austrominius modestus*		7	36	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
R0142	*Copepoda*		-	-	1	-	-	2	11	5	-	-	-	-	-	-	-	1	-	-
S0416	*Dexamine thea*		-	-	-	-	-	-	2	3	-	-	-	-	-	-	-	-	-	-
S0464	*Gammaridae*	juvenile	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	6	2
S0478	*Gammarus locusta*		-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S0525	*Melita palmata*		32	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	17	13
S0550	*Microprotopus maculatus*		-	-	-	-	1	-	26	22	-	-	-	-	-	-	-	-	3	8
S0577	*Aoridae*	female	1	-	-	-	-	1	-	4	-	1	-	1	-	-	-	2	1	7
S0596	*Microdeutopus gryllotalpa*		-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	4
S0885	*Jaera albifrons*	aggregate	9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S1594	*Carcinus maenas*		-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S1594	*Carcinus maenas*	juvenile	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	1	-
T0003	*Chironomidae*	larva	-	-	-	-	-	-	-	-	-	1	1	-	-	-	1	-	-	4
W0296	*Littorina littorea*		-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
W0385	*Peringia ulvae*		12	16	18	5	12	29	40	13	93	60	61	30	66	36	24	89	4	29
W0439	*Crepidula fornicata*	juvenile	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
W1127	*Alderia modesta*		-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-
W1961	*Cerastoderma edule*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-
W1961	*Cerastoderma edule*	juvenile	-	-	-	-	-	4	-	4	-	-	-	-	-	-	-	-	-	1

Code	Station		1A	1B	2A	2B	3A	3B	4A	4B	5A	5B	6A	6B	7A	7B	8A	8B	9A	9B
	Taxa ID	Qualifiers																		
W2063	*Abra tenuis*		-	-	2	1	-	2	3	7	-	-	-	-	-	-	1	-	-	-
W2104	*Timoclea ovata*		-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
W2115	*Ruditapes decussatus*		-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
W2149	*Mya arenaria*	juvenile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
ZB0148	*Amphiuridae*	juvenile	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZG0478	*Pomatoschistus microps*		-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZM0194	*Corallinaceae*		-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZM0256	*Gelidium*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	P
ZM0345	*Chondrus crispus*		-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZM0431	*Gracilaria*		-	P	-	-	-	-	-	P	-	-	-	-	-	-	-	-	-	-
ZR0191	*Ralfsia verrucosa*		-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZR0376	*Fucus*	juvenile	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZS0174	*Ulva*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	-	-	P
ZS0179	*Ulva lactuca*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P
ZS0189	*Chaetomorpha*		-	P	-	-	-	-	P	P	-	-	-	-	-	P	-	-	P	P
ZS0195	*Cladophora*		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P

Annex E Notable taxa recorded in samples

Taxa which are notable in some way e.g. non-native or commercially important, are listed below.

Table E-1 Notable taxa

Code	Taxa ID	Qualifiers	Notes
A5050	*Folliculinidae*		(Previously recorded as Lagotia viridis);
P0430	*Sphaerosyllis cf. taylori*		Possible undescribed species;
P0752	*Polydora ciliata*	aggregate	May include undescribed species;
P0753	*Polydora cornuta*		Cryptogenic;
P0773	*Pseudopolydora paucibranchiata*		Non-native in the UK;
P0798	*Streblospio*		May include non-native species;
P0847	*Tharyx species A*		May be T. robustus Blake and Goransson, 2015; Cryptogenic; Possible undescribed species;
P0871	*Cossura pygodactylata*		Cryptogenic; Representative of organic enrichment;
P0906	*Capitella*		Representative of organic enrichment;
P1487	*Tubificoides galiciensis*		Cryptogenic; Not formally recorded from UK;
P1494	*Tubificoides diazi*	aggregate	(Previously included as T. pseudogaster agg.);
R0068	*Austrominius modestus*		Non-native in the UK;
R2432	*Eusarsiella zostericola*		Non-native in the UK;
S0464	*Gammaridae*	juvenile	May include non-native species;
S0577	*Aoridae*	female	May include non-native species;
T0003	*Chironomidae*	larva	May include non-native species;
W0439	*Crepidula fornicata*	juvenile	Non-native in the UK;
W1961	*Cerastoderma edule*		Commercially important;
W1961	*Cerastoderma edule*	juvenile	Commercially important;
W2149	*Mya arenaria*	juvenile	Non-native in the UK;
ZM0431	*Gracilaria*		May include non-native species;

Annex F SIMPER analysis results

Outputs from the PRIMER-E statistical analysis software for the SIMPER analysis conducted on the species abundance data.

SIMPER
Similarity Percentages - species contributions

One-Way Analysis

Data worksheet
Name: SqRt_Abundnace
Data type: Abundance
Sample selection: All
Variable selection: All

Parameters
Resemblance: S17 Bray-Curtis similarity
Cut off for low contributions: 70.00%

SIMPROF Group	Sample	Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
a (Average similarity: 46.68)	1A, 1B	*Peringia ulvae*	3.73	11.76	0.38	25.18	25.18
		Austrominius modestus	4.32	8.98	2.37	19.23	44.42
		Melita palmata	4.15	8.98	2.13	19.23	63.65
		Tubificoides benedii	3	6.79	1.41	14.54	78.19
b (Average similarity: 49.99)	4A, 4B, 9A, 9B	*Tubificoides benedii*	8.76	14.95	2.01	29.91	29.91
		Peringia ulvae	4.33	7.2	2.48	14.4	44.32
		Microprotopus maculatus	3.59	5.99	2.61	11.98	56.3
		Hediste diversicolor	3.12	4.53	1.91	9.06	65.36
		Chaetomorpha	1	2.36	15.74	4.73	70.09
c (Average similarity: 60.94)	5A, 5B, 6A, 6B, 7A, 7B	*Peringia ulvae*	7.47	32.52	9.49	53.37	53.37
		Tubificoides benedii	5.63	22.98	2.65	37.7	91.08
d (Average similarity: 47.18)	2A, 2B, 3A, 3B, 8A, 8B	*Peringia ulvae*	4.94	12.22	5.75	25.9	25.9
		Tubificoides diazi (aggregate)	5.21	10.16	1.28	21.54	47.44
		Tubificoides benedii	3.49	7.39	2.83	15.66	63.11
		Streblospio	2.24	7.18	5.08	15.21	78.31

Benthic samples: Average dissimilarity (%) between SIMPROF groups. (Given the hierarchical split between some groups, these simple results only partially represent the structure of the separation.)

Group	a	b	c
b	68.78		
c	67.18	65.01	
d	64.42	65.69	62.93

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