APPENDIX UES10-5

MARINE SURVEYS AT NORTH KILLINGHOLME AND CHERRY COBB SANDS (SPRING 2013)

ABLE MARINE ENERGY PARK

(Material Change 2 – TR030006)

Report to: Able UK Ltd

Marine Surveys at North Killingholme and Cherry Cobb Sands (Spring 2013).

Date: April 2014

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1. Introduction

The proposed development of the Able Marine Energy Park (AMEP) east of North Killingholme on the Lincolnshire Coast will partly affect the Humber Estuary Special Area of Conservation (SAC) and the Special Protection Area (SPA) / Ramsar site. Consequently a series of measures have been derived to both compensate and mitigate for the effects of the AMEP on the habitats and species within this area of the Humber estuary and these will be implemented as part of any future development. As part of this process a Marine Environmental Management and Monitoring Plan (MEMMP) was produced in April 2013 following close consultation with stakeholders and in addition to other components included requirements for the monitoring of intertidal and subtidal benthic invertebrate and fish communities in the vicinity of the proposed development at North Killingholme (NKM) and the compensation site at Cherry Cobb Sands (CCS). The current report summarises the results of the Spring 2013 intertidal and subtidal benthic invertebrate and fish surveys at North Killingholme and Cherry Cobb Sands undertaken in May and June 2013.

2. Methods

2.1 Intertidal Benthic Survey

The methods employed for the survey follow those outlined in the MEMMP and utilised a survey design which aimed to allow detection of possible impacts on intertidal benthic infauna by comparison of impact monitoring with baseline data and wider comparison with data collected during the previous characterisation survey (May 2010) to highlight natural temporal variability in benthic assemblages in the area (comparisons to the May 2010 data are provided in an additional technical note). The survey design and methods outlined in the MEMMP are based on existing guidelines and methodologies followed Procedural Guideline No. 3-6: Quantitative sampling of intertidal sediment species using cores (from the Marine Monitoring Handbook - Davies et al, 2001).

The survey design utilised a beyond BACI (Before-After Control-Impact) gradient design to take into account the existence of different zones of impact (primary impact, under the direct footprint of the quay development, and secondary impact) and also control areas subject to no impact. The survey design also takes into account shore level (upper, middle and lower shore strata) to account for the variability of communities that occur at different shore levels. The proposed survey design outlined in the MEMMP including sampling along a series of 12 transects running from the seawall or lower extent of the saltmarsh to approximately mean low water (tides permitting) which cover the impact zones and a control area to the north. At representative sites on the upper, mid and low shore three replicate 0.01m^2 cores were taken from the sediment using a hand held corer (0.01 m^2) and placed into sealable plastic bags, each carrying a unique code for the station. For the NKM survey sites were positioned (where possible) in close proximity to sample sites utilised for the 2010 characterisation survey. Cores were taken to a depth no less than 15cm to ensure adequate recovery of burrowing invertebrates and an additional sample at each sampling station was collected for Particle Size Analysis.

A summary of the survey design for the NKM and CCS surveys is provided below and the positions of the samples provided is in Figure 1 in Section 3. The CCS site differs in terms of general topography from the NKM site as this area has a much wider intertidal area with increasingly sandy sediments on the low shore. There is also extensive encroachment of saltmarsh (*Spartina*) with dense creek systems on the upper shore in the region of the northern control sites which made much of the upper shore area inaccessible – for transects CN1 and CN2 the upper shore site was taken from the fringe of Stone Creek which runs parallel to the shore in this area.

North Killingholme (NKM)				**Number of replicate benthic cores by shore level stations**		
Survey areas		**Area code**	**Transect**	**Upper**	**Mid**	**Lower**
Impact	Under direct footprint of quay development	**DI**	DI1	3	3	3
			DI2	3	3	3
			DI3	3	3	3
	Under the area of indirect impact north of the quay development	**IN**	IN1	3	3	3
			IN2	3	3	3
			IN3	3	3	3
	Under the area of indirect impact south of the quay development	**IS**	IS1	3	3	3
			IS2	3	3	3
			IS3	3	3	3
Control	Control area north of NKM	**CN**	CN1	3	3	3
			CN2	3	3	3
			CN3	3	3	3

12 transects
3 sites x transect = 36 sites
3 replicates per site = 108 samples

Cherry Cobb Sands (CCS)				**Number of replicate benthic cores by shore level stations**		
Survey areas	**Area location**	**Area code**	**Transect**	**Upper**	**Mid**	**Lower**
Impact	Under direct footprint	**I**	I1	3	3	3
			I2	3	3	3
			I3	3	3	3
Control	North	**CN**	CN1	3	3	3
			CN2	3	3	3
			CN3	3	3	3
	South	**CS**	CS1	3	3	3
			CS2	3	3	3
			CS3	3	3	3

9 transects
3 sites per transect = 27 sites
3 replicates per site = 81 samples

The samples collected were kept cool until laboratory processing which took place the following day in which samples were sieved through a 0.5mm mesh sieve and stored in 4% buffered saline formalin solution. Due to the nature of the sediments in the area (soft mud) sampling was undertaken using a hovercraft platform and sample positions were logged using a Magellan Promark 3 GPS logger. The intertidal survey was undertaken on the 26th and 27th May 2013 for the NKM survey and hovercraft survey for the CCS site was undertaken on the 29th May and 10th June 2013.

2.2 Subtidal Benthic Survey

As outlined in the MEMMP a subtidal benthic was required to assess the benthic invertebrate communities in the vicinity of the proposed development and adjacent habitats. A total of 30 sample sites were surveyed eight sites in the area of direct impact, eight sites in adjacent seabed habitats (secondary or indirect impact) and seven sites to the upstream to the north and downstream to the south respectively as controls. The positioning of the sites follows those outlined in the MEMMP and three replicate samples were taken at each site. Methodologies for grab sampling followed Marine Monitoring Handbook procedural guideline 3-9 and other best practice guidelines (Ware & Kenny, 2011; Worsfold & Hall, 2010).

Survey was undertaken using the survey vessel ‘Precision 1’ which was deployed from Hull Marina and utilised a 0.1m^2 day grab as this is the standard technique employed by the Environment Agency in the Humber. At each pre-determined station position, the 0.1m^2 Day grab was lowered to the seabed and the resulting sample recovered. To ensure adequate material is retained for analysis, sample volumes were checked prior to the grab sample being accepted with the sediment sample measured by depth of sample. Small samples (<7cm depth) or those with material such as stones caught in the jaws of the grab were discarded. When samples were within the prescribed limits, each sample was photographed and sub-sampled for subsequent Particle Size Analysis (PSA) and Loss On Ignition determination (LOI). Sites located in areas of harder ground (e.g. coarser sediments or firm clay) or those with repeated failures were repositioned slightly as required to obtain an adequate and representative sample but within 20m of the original location.

A full survey log was maintained throughout the survey detailing time of sampling, DGPS position, number of attempts required, station number, water depth, physical characteristics of the sample and presence of any other relevant features. Sample processing was undertaken utilising a 0.5mm sieve with a nested sieving technique (0.5mm and 1mm) employed if required to reduce the potential for small and delicate invertebrates being damaged by cobble and gravel. Each acceptable sample was removed from the day grab and gently washed through the sieve in order to separate the sediment from the infauna. The sieved residue was then back-washed into sealable containers and borax buffered 4% formo-saline solution is added as a fixative. The survey was undertaken on the 7th and 14th of June 2013 and the results from the survey and locations of sampling sites are provide in Section 4.

2.3 Intertidal Fish Surveys

2.3.1 Beam Trawl Surveys

As outlined in the MEMMP a total of 8 beam trawl stations, with replicates at each station (16 trawls), were designed to provide coverage throughout the middle stretch of the Humber estuary and which would give coverage of the development/impact area (4 stations – BT1 – BT4). In addition 4 beam trawl stations were located upstream (BT5 – BT8) of the impact area to act as control stations. Special dispensation to trawl was requested from the Marine Management Organisation (MMO) and the North Eastern Inshore Fisheries and Conservation Authority (NEIFCA). Following further discussion with the MMO it was determined that dispensation was not required as the vessel was a survey boat and not a fishing vessel, dispensation was required by the NEIFCA, which was issued prior to the commencement of the survey.

The beam trawl survey was undertaken aboard the 12m survey catamaran Precision 1, owned and operated by Precision Marine Survey Limited, this survey was designed to investigate the fish assemblage along the intertidal zone and in close proximity to the development zone and control stations upstream of the impact area. The methodology followed that prescribed by the Environment Agency for the Water Framework Directive's transitional fish surveillance (EA, 2013). Recommendations within the guidelines dictate that a standard beam trawl of 1.5m should be used to ensure compatibility of sampling gears. The beam trawl was comprised of a fishing net attached to steel boom with skies (shoes) attached at either end. The beam trawl is 1.5 metres wide with the head of the net attached to the beam which 0.5m above the base of the skies (shoes). A 1.5m beam trawl net was comprised of 10mm mesh and 5mm cod end liner with 75mm discs on the fishing (ground) line.

Once the vessel had arrived at the study area the proposed trawl path at each site was scouted for obstructions prior to deploying the trawl. Once at the location, the vessel continued at a steady rate (2 knots) along the direction of the tide and the 1.5m beam trawl was lowered over the side of the vessel to the surface using the winch, the winch then paid out the warp until the trawl hit the seabed. Depending on the water depth, additional trawl warp was paid out until the length of warp was greater or equal to 3 ½ times the depth. Once the required length of warp had been paid out the winch was locked and the start point for each trawl commenced from the point at which the winch was locked and the trawl towed for approximately 200m. Upon completion of the 200m run, the trawl was hauled to the surface and the cod end retrieved and the sample recovered. The cod end was then opened over a stainless steel hopper to contain the whole catch, with the net checked for any remaining epifauna and fish, before the cod end was fastened prior to redeployment at the next station. The total volume of the catch was measured and the catch sorted with the fish species separated from the epifaunal invertebrates. A survey log was maintained at all times. The location, direction and path of all trawls was logged by the vessels GPS and uploaded to GIS software to illustrate the actual route of the trawl.

The fish and epifaunal invertebrates were separated to species when possible and enumerated with examples of each species retained for a reference collection. Where species could not be identified in the field (Polychaeta, Crustacea, Bryozoa, Hydrozoa, Echinodermata etc.) samples were retained for laboratory analysis. The beam trawl survey was undertaken on the 6th June 2013 and any notable observations from individual trawls were recorded on the survey log.

2.3.2 Seine Net Surveys

As outlined in the MEMMP seine net surveys were undertaken at eight locations on the south bank of the Humber with four sites in the vicinity of the development (Impact area) and four sites further north (upstream) to act as controls. The seine net surveys were undertaken using a shallow draft catamaran (Lizzard) or 4m rigid inflatable dinghy (RIB) as deployment vessels to deploy and recover the seine net which allowed access into the shallow intertidal area. In addition the 12m survey catamaran Precision 1, owned and operated by Precision Marine Survey Limited, was also available for use as a base vessel for the survey operations as required. Special dispensation to survey was requested from the Marine Management Organisation (MMO) and the North Eastern Inshore Fisheries and Conservation Authority (NEIFCA). Following further discussion with the MMO it was determined that dispensation was not required as the vessel was a survey boat and not a fishing vessel, dispensation was required by the NEIFCA, which was issued prior to the commencement of the survey.

The seine net was comprised of a 100m net standing 3m high from the leaded base line to the buoyed headline. The mesh size in the outer panels was 10mm reducing to 3mm in the cod end. In order to safely access the intertidal zone investigate the fish assemblage within the intertidal zone and in close proximity to the development zone and control stations upstream of the impact area, the seine net was deployed from a RIB. The methodology followed that prescribed by the Environment Agency for the Water Framework Directive’s transitional fish surveillance (EA, 2013).

Recommendations within the guidelines dictate that at least two hauls should be undertaken within site area, ideally at low slack although high slack may be needed at shallow upstream sites (EA, 2013). Standard seine nets of 100m in length and 3m high were used to ensure the compatibility of sampling gears with those likely used during EA WFD surveys in the Humber.

At each survey site the vessel crew deployed one end of the seine net and with the net loaded onto the bow end of the deployment vessel which reversed away from the mudflat tide mark, ensuring that the net deployed smoothly from the boat. The deployment vessel paid out the net in a horseshoe shape across the intertidal zone, migrating back to the point of origin i.e. to the seine net anchor point. At this point the deployment vessels engine was shut off and the seine net was hauled back to the tide mark, with surveyors ensuring that the lead line maintained bottom contact and that the head line did not sink below the surface. As the net is hauled the surveyors move closer to one another to create a “purse” shape.

Once the net had been recovered, the cod end was emptied into a sample container and the net was checked for any remaining epifauna and fish. The sample was handed to crew aboard the main survey vessel for fixing prior to deployment to the next sampling station to continue the survey. The seine net surveys were undertaken over two days on the 5th and 21st June 2013 and any notable observations from individual trawls were recorded on the survey log.

The results of the intertidal fish surveys and locations of survey sites are provided in Section 5.

2.4 Laboratory Analysis

All laboratory methodologies were based on best practice and followed tried and tested method statements widely acknowledged within the industry (Ware & Kenny, 2011; Worsfold & Hall, 2010; Cooper & Rees 2002; Rees, 1999; Barnett, 1993; Rees et al, 1990). PMSL are members of the National Marine Biological and Analytical Quality Control scheme (NMBAQC).

Two experienced members of PMSL undertook the sample sorting, conducting all the sieving, sorting work and sample description with a further member of staff carrying out standard sorting quality control. Experienced taxonomists carried out the identification of the sorted fauna, with an additional member of staff carrying out quality control for faunal identification. A standard sample tracking procedure was followed throughout the analysis period.

2.5 Sorting of Invertebrate Samples

Each sample was sieved in freshwater water and then rinsed with running tap water through a 0.5mm stainless steel sieve with a nest of 20cm diameter 5mm and 1mm sieves used as required for any coarser material. The sieve contents were backwashed over a white tray to catch any potential spillage, into pre-labelled plastic storage buckets. A borax buffered 4% saline formalin solution was then added to the samples. The samples were then well mixed and stored for at least 48 hours to ensure adequate preservation and shaken once during the period.

Prior to identification each sample was washed through a nest of sieves, with the smallest mesh aperture of 0.5mm, to remove the preservative and partition the sample for ease of sorting. The residue from each sieve was then gently washed into separate white trays. Water was added to the trays and the contents agitated. Immediately after agitation, the light fraction was decanted to another tray. This procedure was repeated up to 3 times, and each tray of light fractions examined as a sub-sample of the heavy fraction. The trays were marked with the appropriate sample code (relating to the client, date, specific site, sample and replicate number). All fractions were then decanted into separate 100mm Petri dishes and examined under a stereoscopic microscope with 20x eyepieces giving a maximum magnification of up to 80x. The fauna derived was added to the retained containers, preserved and stored ready for identification. Each petri dish was checked for a final time by another member of staff.

2.6 Taxonomic Identification

Identification was carried out using Olympus SZ40 zoom microscopes with 10x and 20x eyepieces, giving a maximum magnification of up to 80x. An additional 2x objective was occasionally used to increase the potential magnification to 160x. Olympus BX41 compound microscopes were used for further magnification, up to 800x.

Identification of infaunal samples was to the lowest possible taxonomic level (i.e. species), and during identification, all individuals were initially separated into families, with part animals being assigned to families where possible. The macrofaunal specimens were identified to species level using standard taxonomic keys, low and high power stereoscopic microscopes and dissection when necessary, for identification. Incomplete animals without anterior ends are not recorded as individuals to be included in the quantitative dataset. However, they were identified where possible and recorded as present. Similarly, motile and colonial sessile epibenthic taxa and meiofauna were only recorded as present and not included within the infaunal quantitative data set.

Fish species collected were identified using Wheeler, (1969) and Whitehead *et al.* (1989) and length frequency analysis of key species undertaken as required.

As part of the standard quality assessment (QA) procedure, regular cross-reference identification was carried out. Each sample residue was described textually with the residue retained for possible further analysis and Analytical Quality Control (AQC). All fauna will be retained under the standard codes for 2 years or returned to the clients representative for further analysis and AQC should this be required.

The taxonomic literature used is essentially as given in Rees et al (1990) and reporting nomenclature was based on that of the Species Directory of the Marine Fauna and Flora of the British Isles and Surrounding Seas (Howson & Picton, 1997), with updated nomenclature as required following WoRMS standards (Appletans *et al*., 2010).

2.7 Biomass of Invertebrates

Biomass analysis was performed by wet weight (tissue blotted) and carried out for individual species in each sample. Each taxa was placed on blotting paper for 30 seconds to allow absorption of preservative into the blotting paper. Following this time period the individuals were placed on the microbalance and the reading taken. The macrofaunal organisms were then placed back in their respective pots and stored. Biomass calculations include all identifiable fragments and calculated to ± 0.0001g, all biomass data was recorded in grams or fractions thereof. Following collation of wet weight biomass data conversions to Ash Free Dry Weight Biomass were undertaken using coefficients derived from Rumohr et al. (1987) and Ricciardi and Bourget (1998) for comparison with targets. Following analysis each specimen was returned to its sample pot and stored in 70% IMS (Industrial Methylated Spirits).

2.8 Particle Size Analysis (PSA)

The particle size analysis was carried out by a combination of dry sieving and laser particle size analysis (for the fraction <1mm) using a Malvern Mastersizer 3000. Prior to analysis, photographs were taken of all samples. The sediment samples were then split with one sub-sample being passed through a 1mm sieve to remove the larger size classes of sediment if required. The <1mm fraction of the sample was then analysed using the Malvern Mastersizer 3000 and the >1mm fraction discarded. The second sub-sample of coarser material (if present) was passed through a nest of sieves at 0.5 phi intervals. Each fraction, including the <1mm fraction, was then oven dried at 85°C for 24 hours and weighed. Data generated from these methods was analysed separately but for visualisation purposes the finer fractions were also merged to the coarse fraction (if present) to provide an overall grain size distribution for each sample – although it is acknowledged that merging of such datasets can be problematic due to differing techniques. The data derived from PSA was then used to derive statistics such as mean grain size, bulk sediment classes (% silt, sand & gravel), skewness and sorting coefficient using the program Gradistat. These methods are consistent with the procedures identified at the NMBAQC PSA workshop on laboratory methods, which was held at the Cefas Lowestoft laboratory in July 2009.

Estimates of total organic carbon were determined by loss on ignition. Each sample was oven dried at 105ºC until the weight stabilises (± 0.01g). The weight of the sample was recorded and the sample was then placed into a kiln at 480ºC for six hours. Once the sample had cooled the sample was then re-weighed and the difference between the two weights expressed as the percentage loss on ignition (% LOI).

3. Intertidal Benthic Survey Results

As described in Section 2 In total 108 samples were collected from 36 sites on 12 transects at North Killingholme whilst 84 samples were collected from Cherry Cobb Sands at 28 sites on 9 transects. The Cherry Cobb Sands survey included three extra samples at an additional mid shore site on the southernmost transect in the vicinity of an area with increased abundance of *Arenicola marina*. The location of sampling sites surveyed during the intertidal survey is provided in Figure 1.

3.1 Sedimentary Parameters

3.1.1 North Killingholme

A summary of sedimentary parameters from survey sites at North Killingholme are provided in Table 1 with the full data provided in Appendix 1. Maps showing sediment composition, sediment type and median phi grain size are given in Figures 2 to 4. Sediments at North Killingholme were relatively uniform and almost entirely comprised of sandy mud with the exception of site CN3U which was classified as mud. Mud content ranged from 51% to 92% with the majority of sites having over 80% mud and one site (CN3U) having a mud content in excess of 90%. Certain sites had somewhat lower mud content (and conversely higher sand content) e.g. sites IS1L and IS2L. All sites were characterised by sediments which were poorly sorted whilst skewness was highly variable and ranged from coarse skewed to very fine skewed. Levels of organic content (% LOI) were low to moderate with values ranging from 5% to 11.7% with higher values generally at upper shore sites and particularly those adjacent to saltmarsh.

3.1.2 Cherry Cobb Sands

A summary of sedimentary parameters from survey sites at Cherry Cobb Sands are provided in Table 2 with the full data provided in Appendix 2. Maps showing sediment composition, sediment type and median phi grain size are given in Figures 2 to 4. Sediments at Cherry Cobb Sands were quite heterogeneous and exhibited much more variability than at North Killingholme with sediments including sands, muddy sands and sandy mud. Mud content ranged from 2% to 88% and whilst the majority of sites had mud contents in excess of 60% (sandy mud) a number of sites primarily on the low shore (such as sites CN1L, CN2L, CN3L, SC3M, CS3L, and I3L) exhibited mud content from 15% to 50% (muddy sand). Four sites on the low shore had a low mud content (<10%) with predominantly sandy sediments (sites CS1L, CS2L, I1L and I2L). The majority of sites exhibited poorly sorted sediments with the exception of those with characterised by sands which were moderately sorted. Skewness was variable with sediments ranging from very fine skewed to symmetrical. Levels of organic matter as expressed by % LOI in the sediment were similar to that at North Killingholme but usually slightly lower (and particularly at sandy sites) with values ranging from 1.4% to 9.75%. As at North Killingholme higher levels of organic matter tended to be recorded at the muddier areas particularly on the upper shore.

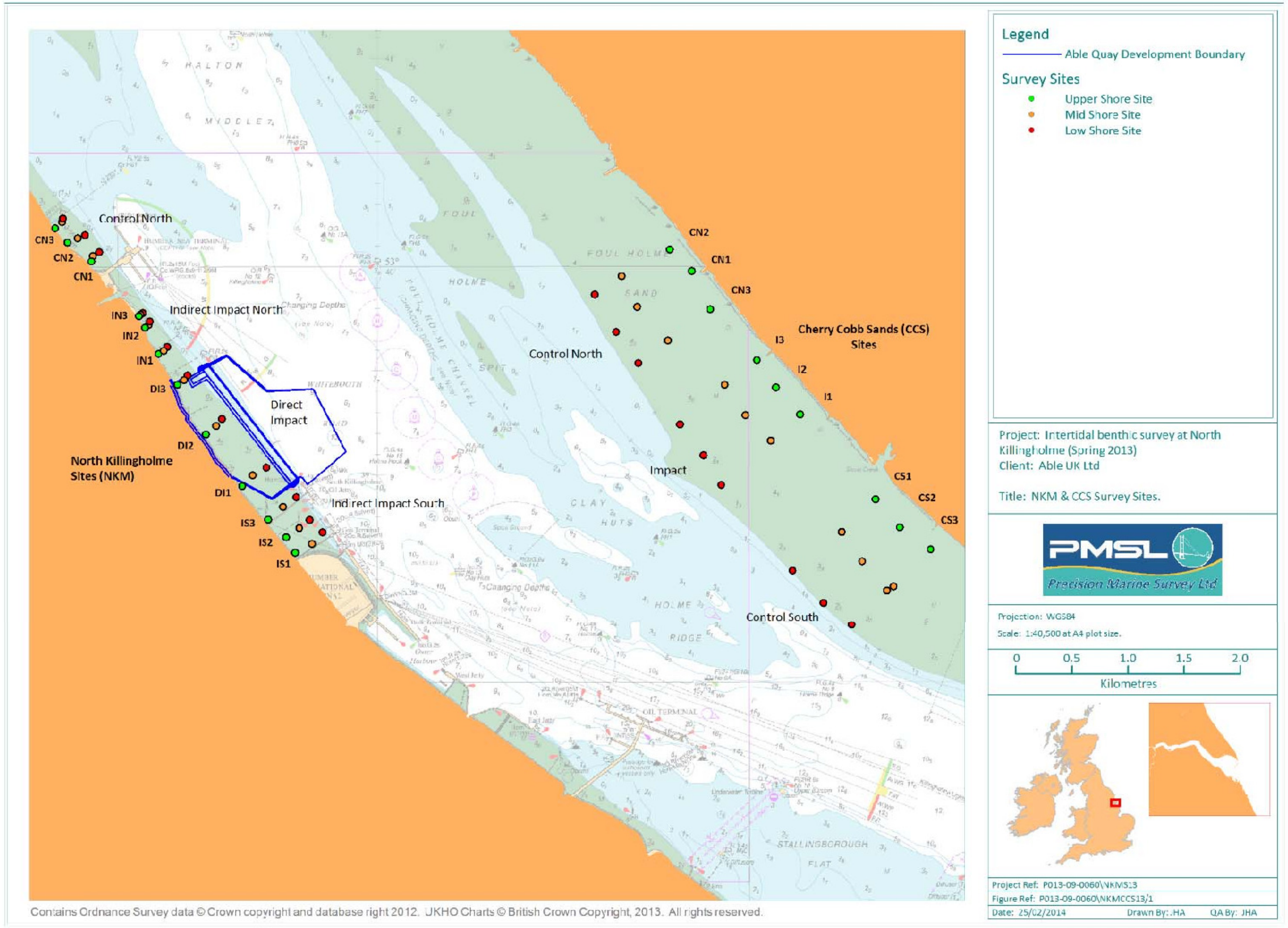

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Figure 1. Location of survey sites at North Killingholme (NKM) and Cherry Cobb Sands (CCS).

Table 1. Summary of sedimentary parameters at North Killingholme.

AREA	SAMPLE	TEXTURAL GROUP	MEDIAN PHI GRAIN SIZE	MEAN PHI GRAIN SIZE	SORTING		SKEWNESS		% GRAVEL	% SAND	% MUD	% LOI
Indirect Impact South	IS2U	Sandy Mud	5.74	5.65	1.92	Poorly Sorted	-0.14	Coarse Skewed	0.00	18.66	81.34	9.74
	IS1L	Sandy Mud	4.05	4.53	1.73	Poorly Sorted	0.39	Very Fine Skewed	0.00	48.46	51.54	5.36
	IS1M	Sandy Mud	5.48	5.58	1.73	Poorly Sorted	0.04	Symmetrical	0.00	17.83	82.17	8.99
	IS1U	Sandy Mud	6.21	6.11	1.67	Poorly Sorted	-0.14	Coarse Skewed	0.00	11.71	88.29	11.73
	IS2L	Sandy Mud	4.47	4.88	1.73	Poorly Sorted	0.32	Very Fine Skewed	0.00	36.37	63.63	5.77
	IS2M	Sandy Mud	6.26	6.17	1.66	Poorly Sorted	-0.12	Coarse Skewed	0.00	11.13	88.87	10.00
	IS3L	Sandy Mud	5.88	5.83	1.74	Poorly Sorted	-0.06	Symmetrical	0.00	16.48	83.52	7.73
	IS3M	Sandy Mud	5.72	5.74	1.73	Poorly Sorted	-0.01	Symmetrical	0.00	16.66	83.34	8.97
	IS3U	Sandy Mud	6.29	6.18	1.67	Poorly Sorted	-0.16	Coarse Skewed	0.00	11.20	88.80	9.68
Indirect Impact North	IN3U	Sandy Mud	5.82	5.82	1.69	Poorly Sorted	-0.03	Symmetrical	0.00	15.10	84.90	8.89
	IN3M	Sandy Mud	5.81	5.83	1.66	Poorly Sorted	-0.01	Symmetrical	0.00	14.49	85.51	7.92
	IN3L	Sandy Mud	5.19	5.45	1.76	Poorly Sorted	0.18	Fine Skewed	0.00	22.40	77.60	5.85
	IN2U	Sandy Mud	5.93	5.92	1.72	Poorly Sorted	-0.04	Symmetrical	0.00	14.15	85.85	8.37
	IN2M	Sandy Mud	5.97	5.95	1.64	Poorly Sorted	-0.04	Symmetrical	0.00	12.80	87.20	7.56
	IN2L	Sandy Mud	5.57	5.71	1.65	Poorly Sorted	0.10	Symmetrical	0.00	15.33	84.67	6.89
	IN1U	Sandy Mud	6.07	5.96	1.81	Poorly Sorted	-0.14	Coarse Skewed	0.00	15.25	84.75	9.94
	IN1M	Sandy Mud	5.38	5.56	1.69	Poorly Sorted	0.13	Fine Skewed	0.00	17.99	82.01	6.94
	IN1L	Sandy Mud	5.25	5.44	1.73	Poorly Sorted	0.15	Fine Skewed	0.00	22.90	77.10	6.65
Direct Impact	DI3U	Sandy Mud	5.60	5.66	1.74	Poorly Sorted	0.01	Symmetrical	0.00	17.35	82.65	8.47
	DI3M	Sandy Mud	5.27	5.47	1.72	Poorly Sorted	0.15	Fine Skewed	0.00	20.94	79.06	7.01
	DI3L	Sandy Mud	5.56	5.61	1.67	Poorly Sorted	0.04	Symmetrical	0.00	18.07	81.93	8.05
	DI2U	Sandy Mud	5.77	5.82	1.69	Poorly Sorted	0.01	Symmetrical	0.00	14.70	85.30	8.65
	DI2M	Sandy Mud	5.30	5.51	1.76	Poorly Sorted	0.15	Fine Skewed	0.00	21.04	78.96	6.77
	DI2Lb	Sandy Mud	5.62	5.63	1.73	Poorly Sorted	0.01	Symmetrical	0.00	19.57	80.43	7.46
	DI1U	Sandy Mud	5.85	5.75	1.81	Poorly Sorted	-0.13	Coarse Skewed	0.00	16.97	83.03	10.38
	DI1M	Sandy Mud	5.55	5.60	1.70	Poorly Sorted	0.02	Symmetrical	0.00	17.88	82.12	9.09
	DI1L	Sandy Mud	5.82	5.82	1.74	Poorly Sorted	0.00	Symmetrical	0.00	16.84	83.16	7.11
Control North	CN3U	Mud	6.36	6.29	1.52	Poorly Sorted	-0.10	Coarse Skewed	0.00	7.74	92.26	9.82
	CN3M	Sandy Mud	5.48	5.67	1.71	Poorly Sorted	0.14	Fine Skewed	0.00	16.93	83.07	6.21
	CN3L	Sandy Mud	5.95	5.95	1.66	Poorly Sorted	-0.03	Symmetrical	0.00	12.68	87.32	8.18
	CN2U	Sandy Mud	5.99	5.96	1.63	Poorly Sorted	-0.06	Symmetrical	0.00	12.35	87.65	10.00
	CN2M	Sandy Mud	5.15	5.40	1.73	Poorly Sorted	0.19	Fine Skewed	0.00	23.30	76.70	5.24
	CN2L	Sandy Mud	5.35	5.51	1.75	Poorly Sorted	0.12	Fine Skewed	0.00	21.26	78.74	6.21
	CN1U	Sandy Mud	5.27	5.49	1.68	Poorly Sorted	0.16	Fine Skewed	0.00	18.63	81.37	7.16
	CN1M	Sandy Mud	4.82	5.20	1.73	Poorly Sorted	0.30	Fine Skewed	0.00	27.27	72.73	5.01
	CN1L	Sandy Mud	5.71	5.73	1.67	Poorly Sorted	0.01	Symmetrical	0.00	16.56	83.44	6.35

Table 2. Summary of sedimentary parameters at Cherry Cobb Sands.

AREA	SAMPLE	TEXTURAL GROUP	MEDIAN PHI GRAIN SIZE	MEAN PHI GRAIN SIZE	SORTING		SKEWNESS		% GRAVEL	% SAND	% MUD	% LOI
Control North	CN1L	Muddy Sand	3.71	4.32	1.79	Poorly Sorted	0.49	Very Fine Skewed	0.00	58.94	41.06	3.69
	CN1M	Sandy Mud	5.16	5.39	1.70	Poorly Sorted	0.15	Fine Skewed	0.00	20.37	79.63	6.23
	CN1U	Sandy Mud	5.99	5.99	1.68	Poorly Sorted	-0.01	Symmetrical	0.00	12.57	87.43	8.10
	CN2L	Muddy Sand	3.71	4.17	1.59	Poorly Sorted	0.48	Very Fine Skewed	0.00	61.94	38.06	3.46
	CN2M	Sandy Mud	5.44	5.62	1.80	Poorly Sorted	0.10	Fine Skewed	0.00	18.57	81.43	7.89
	CN2U	Sandy Mud	5.65	5.62	1.86	Poorly Sorted	-0.06	Symmetrical	0.00	19.98	80.02	9.75
	CN3L	Muddy Sand	3.34	3.42	1.08	Poorly Sorted	0.38	Very Fine Skewed	0.00	80.88	19.12	2.26
	CN3M	Sandy Mud	5.07	5.40	1.73	Poorly Sorted	0.24	Fine Skewed	0.00	22.08	77.92	7.03
	CN3U	Sandy Mud	5.87	5.93	1.67	Poorly Sorted	0.00	Symmetrical	0.00	12.24	87.76	9.52
Control South	CS1L	Sand	2.88	2.92	0.93	Moderately Sorted	0.26	Fine Skewed	0.00	91.34	8.66	1.55
	CS1M	Sandy Mud	4.79	5.17	1.73	Poorly Sorted	0.29	Fine Skewed	0.00	28.00	72.00	5.06
	CS1U	Sandy Mud	4.54	4.93	1.66	Poorly Sorted	0.34	Very Fine Skewed	0.00	33.02	66.98	5.00
	CS2L	Sand	2.47	2.49	0.55	Moderately Well Sorted	0.05	Symmetrical	0.00	97.45	2.55	1.41
	CS2M	Sandy Mud	4.44	4.97	1.81	Poorly Sorted	0.39	Very Fine Skewed	0.00	38.23	61.77	4.50
	CS2U	Sandy Mud	4.55	4.91	1.55	Poorly Sorted	0.36	Very Fine Skewed	0.00	31.27	68.73	4.84
	CS3L	Muddy Sand	2.79	3.03	1.40	Poorly Sorted	0.47	Very Fine Skewed	0.00	83.36	16.64	2.67
	CS3M	Muddy Sand	3.32	3.35	0.95	Moderately Sorted	0.31	Very Fine Skewed	0.00	83.63	16.37	2.05
	CS3M2	Muddy Sand	3.32	3.38	1.03	Poorly Sorted	0.31	Very Fine Skewed	0.00	80.72	19.28	1.57
	CS3U	Sandy Mud	4.31	4.64	1.61	Poorly Sorted	0.34	Very Fine Skewed	0.00	40.29	59.71	4.53
Impact	I1L	Sand	3.12	3.15	0.62	Moderately Well Sorted	0.09	Symmetrical	0.00	92.81	7.19	1.72
	I1M	Sandy Mud	5.37	5.56	1.77	Poorly Sorted	0.12	Fine Skewed	0.00	19.96	80.04	6.47
	I1U	Sandy Mud	4.84	5.15	1.64	Poorly Sorted	0.26	Fine Skewed	0.00	25.24	74.76	4.95
	I2L	Sand	3.24	3.25	0.60	Moderately Well Sorted	0.06	Symmetrical	0.00	90.86	9.14	1.86
	I2M	Sandy Mud	5.22	5.45	1.72	Poorly Sorted	0.16	Fine Skewed	0.00	20.32	79.68	6.37
	I2U	Sandy Mud	5.43	5.62	1.63	Poorly Sorted	0.14	Fine Skewed	0.00	15.49	84.51	6.57
	I3L	Muddy Sand	3.53	4.20	1.75	Poorly Sorted	0.56	Very Fine Skewed	0.00	66.15	33.85	4.14
	I3M	Sandy Mud	5.25	5.48	1.68	Poorly Sorted	0.17	Fine Skewed	0.00	19.19	80.81	6.53
	I3U	Sandy Mud	5.49	5.65	1.72	Poorly Sorted	0.09	Symmetrical	0.00	16.89	83.11	7.14

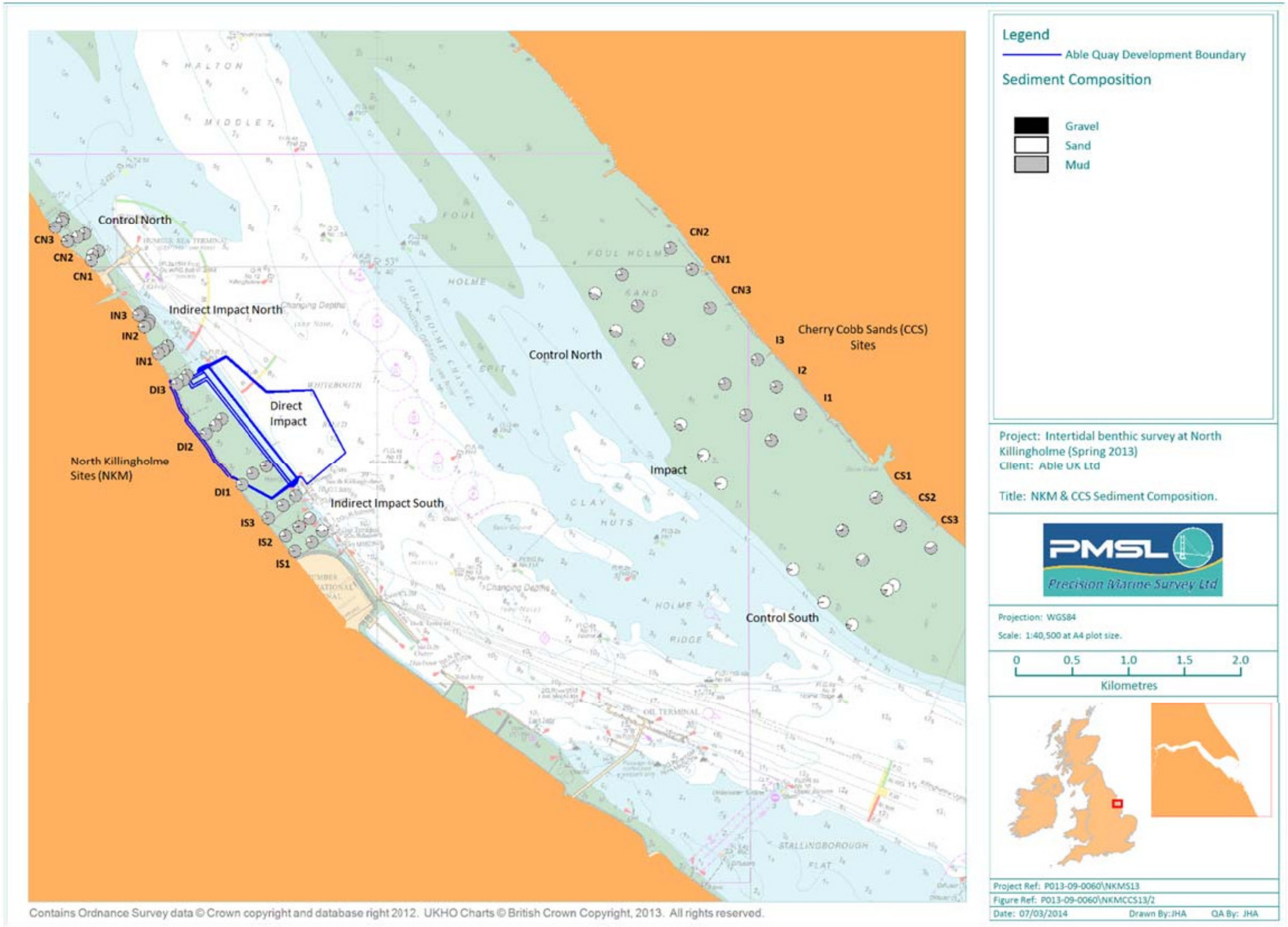

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Figure 2. Sediment composition at survey sites.

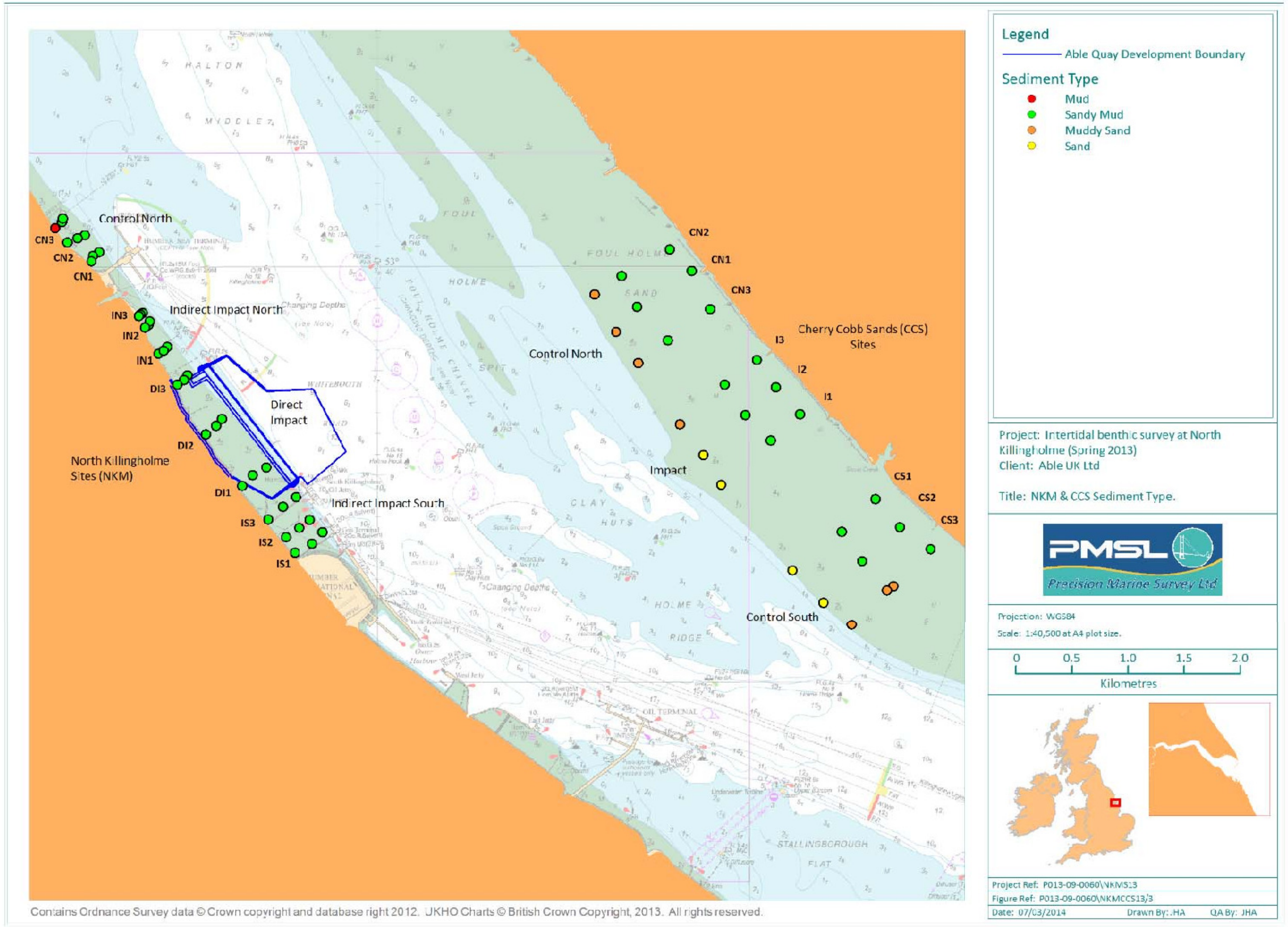


Figure 3. Sediment type at survey sites.

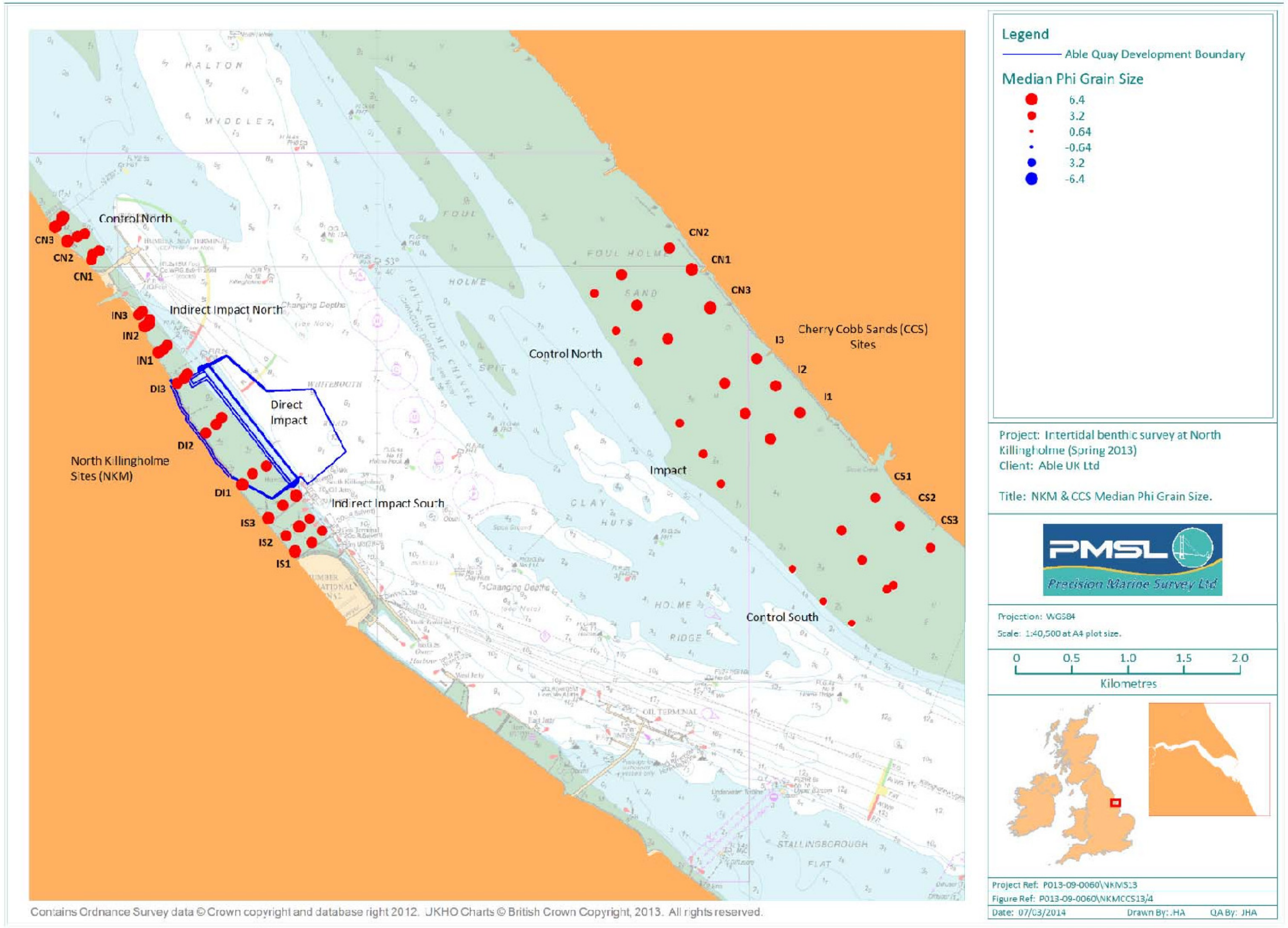


Figure 4. **Median phi grain size at survey sites.**

3.2 Biological Parameters

A number of primary and derived biological parameters values were calculated from the species data tabulated and input into GIS. Standard biological parameters utilised for benthic analysis include the following:

- The total number of taxa at each site/replicate (S)
- The total number of individuals (abundance) at each site/replicate (N)
- The total biomass (in grams AFDW) at each site/replicate (B).
- Margalef's index of species richness (d)
- Shannon's diversity index (H')

This index is a univariate measure of diversity which incorporates both the number of species and the distribution or equitability of individuals between species. High values of H' indicate a more diverse community whilst low values indicate low diversity.

- Pielou's evenness (J)

This index is a univariate measure of evenness or equitability which describes the distribution of individuals between species. High values of J (approaching 1) indicate that the abundance of animals are evenly spread between species whilst low values of J (approaching 0) indicate that the majority of animals are comprised of a few species, a situation which often occurs in low diversity areas subject to disturbance or organic enrichment.

In addition, the PRIMER package developed by Primer-E (Clarke and Gorley, 2006) was used to derive Abundance Biomass Comparison (ABC) plots (Warwick, 1986) for each replicate and per site. These show the cumulative % dominance of abundance and biomass per species rank and have been used to detect stress in benthic communities. In healthy communities the biomass curve is usually elevated above the abundance curve whilst in transitional or disturbed communities the abundance curves intersects the biomass curves or is elevated above it as the community is characterised by numerous small-bodied opportunist species. In naturally stressed environments such as estuaries some communities naturally exhibit curves indicative of chronic levels of disturbance e.g. due to salinity fluctuations or sediment disturbance although the curves still provide a useful graphical description of community structure and the contribution of larger bodied animals which may for example be an important food source for other groups of animals such as birds/fish. The ABC plots produced by PRIMER also provide the w statistic, which is a univariate descriptor of the ABC plots and measures the extent to which the biomass curve lies above the abundance curve (positive values for relatively undisturbed communities and negative values for potentially disturbed communities) and this was subsequently used as an additional biological parameter.

A summary of the biological parameters at each site is provided in Tables 3 and 4 which gives average values per 0.01m^2 for North Killingholme and Cherry Cobb Sands respectively whilst the values of biological parameters from the individual replicates are provided in Appendices

3 and 4. Replicate samples have also been combined to provide summaries of overall ABC structure per site and these are provided in Appendices 5 and 6. A series of summary graphs/tables showing average values (and standard error) for each zone/shore level have also been derived from using the replicate data from each area to gives mean parameters per $0.01m^2$ (Figures 5 and 6) and the spatial variation in these parameters is highlighted in Figures 7 to 13.

3.2.1 North Killingholme

Values of biological parameters appear to be typical for mid estuary muddy intertidal habitats and generally in line with values recorded elsewhere in the middle Humber estuary. Total numbers of taxa tend to be relatively low ranging from two to twelve taxa per site with mean values ranging from 1 to 7 animals per $0.01m^2$ whilst the total numbers of individuals was quite variable with very low numbers <10 animals per core in some areas, predominantly lower shore sites with abundances ranging from 1 to 388 individuals per $0.01m^2$. Biomass was similarly variable with average AFDW biomass values ranging from 0.00003g to 0.26g per core. Total abundances and biomass scaled up to values per metre square range from 167 to 38800 animals per m^2 and 0.0027g to 25.67g AFDW biomass per m^2.

Some spatial patterns in biological patterns were evident (Figures 2 to 9) largely in relation to position on the shore. Numbers of taxa were relatively similar across the survey area although sites from the indirect impact areas tended to have very slightly lower values with mean numbers of taxa within the southern indirect impact area for example having mean numbers of taxa from ranging from 1 to 5 taxa per $0.01m^2$ whilst the direct impact and northern control area had mean numbers of taxa ranging from 3 to 7 taxa per $0.01m^2$. Numbers of individuals and biomass tended to show more distinct patterns in relation to shore position with generally lower values on the lower shore and increased numbers or biomass on the mid or upper shore. Biomass and numbers of individuals was relatively variable with sporadic sites with particularly high or low values occurring throughout the area but in general the direct impact area and the control area tended to be broadly comparable with slightly lower values often recorded at the indirect impact sites. Values for diversity indices such as Margalef's d and Shannon's H tended to be moderate to low as is commonly the case in estuarine conditions whilst values of Pielou's evenness J were moderate. Relatively few clear cut spatial patterns in these parameters were evident.

The mean values of the ABC w statistic in Table 3 and ABC plots per site given in Appendix 5 indicated that the majority of sites had biomass curves elevated above the abundance curve indicating normal communities although a few sites exhibited plots in which the curves intersected and mean w statistics of close to or just below zero which although this is typical in naturally stressed estuarine habitats and in such areas this tends to be due to increased dominance by taxa such as *Corophium volutator* or *Tubificoides* spp. and no communities particularly indicative of organic enrichment or anthropogenic disturbance were observed. No particular spatial pattern was evident in terms of ABC curves and resultant w statistics and each survey areas having examples of high and low values the direct impact (development) area and the northern control area generally included fewer low values whilst the southern indirect impact area tended to have higher numbers of sites with lower values close to or below zero and ABC curves which intersected.

3.2.2 Cherry Cobb Sands

The mean biological parameters derived from Cherry Cobb Sands dataset are shown in Table 4 whilst the replicate data is given in Appendix 4 and graphs showing mean values per $0.01m^2$ for each survey area and shore level are given in Figure 6. The spatial distribution of mean biological parameters per site are provided in Figures 7 to 13. The results of the CCS survey indicate that numbers of taxa were broadly similar to NKM with mean values per site ranging from 1 to 10 taxa per $0.01m^2$ and lower numbers of taxa tended to occur on the lower shore sites particularly in sandier areas. The mean numbers of individuals at CCS were also broadly similar to the NKM sites (ranging from <1 to 373 per $0.01m^2$) whilst mean AFDW biomass ranged from 0.005g to 0.22g per $0.01m^2$. Total abundances and biomass scaled up to values per metre square range from 67 to 37333 animals per m^2 and 0.045g to 22g AFDW biomass per m^2 and generally correspond to other surveys in the middle Humber with lower values tending to be recorded in lower shore areas presumably reflecting the more dynamic sedimentary environment. Diversity parameters were variable but with many sites exhibiting low to moderate levels of diversity (as recorded for NKM) and ABC plots per replicate (or per site - Appendix 6) indicated that the majority of sites exhibited curves with biomass curves above abundance curves (higher w values) although occasional sites (usually on upper or mid shore muddy habitats) had intersecting curves with w values around zero.

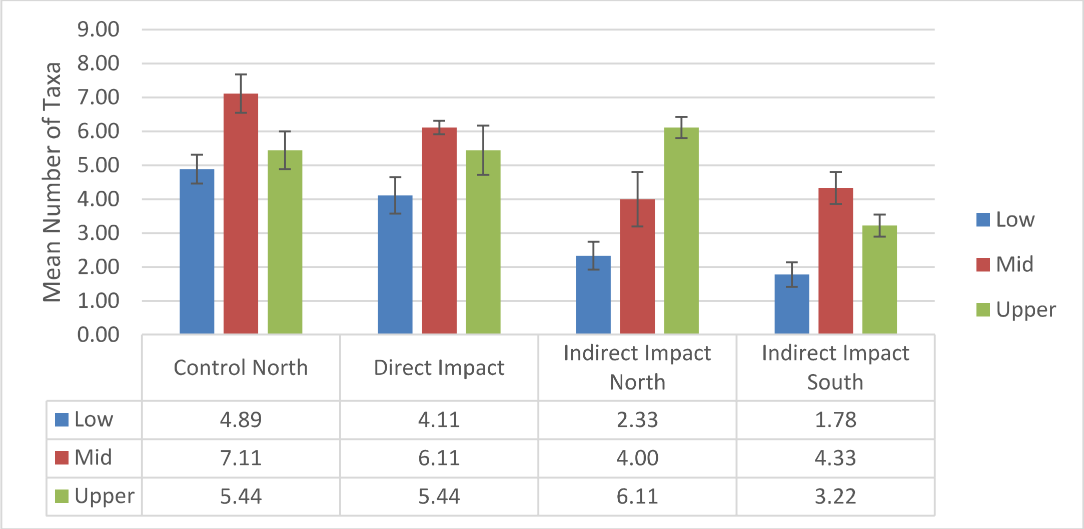
An assessment of spatial variation indicates relatively few differences in terms of the numbers of taxa between NKM and CCS although a higher total number of taxa were recorded at CCS which presumably reflects the wider range of sediment types in this area. Numbers of individuals and biomass were highly variable and CCS sites tended to exhibit lower values than NKM on the low shore (and to a lesser extent at the northern CCS control sites). Diversity parameters were similarly variable with occasional lower values recorded at low shore CCS sites or in the case of the ABC w statistic at certain mid or upper shore CCS sites. The lower values of these parameters at CCS (with the exception of ABC w statistic) tend to occur in sandier sediments although some similarly low values were also recorded at NKM in the southern indirect impact area. The remainder of the upper and mid shore CCS sites however tended to have somewhat higher total numbers of individuals and biomass than recorded at the NKM sites.

Table 3. Mean values of biological parameters for each site ($0.01m^2$) at North Killingholme.

Area	Shore	Site	Mean Numbers of Taxa	Mean Numbers of Individuals		Mean Biomass (AFDW g)		Mean Margalef's d	Mean Pielou's J	Mean Shannon's H'	Mean AFDW ABC w stat
				per 0.01 m^2	per 1 m^2	per 0.01 m^2	per 1 m^2				
Control North	Low	CN1L	4.00	14.67	1467	0.0007	0.0737	1.18	0.87	1.71	0.41
	Mid	CN1M	7.00	56.00	5600	0.0153	1.5288	1.43	0.70	1.85	0.18
	Upper	CN1U	7.33	37.67	3767	0.0690	6.9045	1.76	0.78	2.22	0.37
	Low	CN2L	5.00	107.33	10733	0.0187	1.8671	0.86	0.52	1.19	0.13
	Mid	CN2M	7.00	131.33	13133	0.0302	3.0170	1.23	0.46	1.27	0.04
	Upper	CN2U	5.33	388.00	38800	0.1690	16.8963	0.74	0.30	0.72	0.00
	Low	CN3L	5.67	129.00	12900	0.0276	2.7588	0.97	0.43	1.07	0.11
	Mid	CN3M	7.33	98.00	9800	0.0143	1.4275	1.39	0.66	1.91	0.19
	Upper	CN3U	3.67	47.67	4767	0.0515	5.1520	0.70	0.63	1.19	0.32
Direct Impact	Low	DI1L	3.33	13.00	1300	0.0110	1.0998	1.00	0.79	1.25	0.32
	Mid	DI1M	6.67	69.67	6967	0.0307	3.0737	1.18	0.52	1.35	-0.01
	Upper	DI1U	6.67	81.00	8100	0.2567	25.6722	1.29	0.71	1.92	0.34
	Low	DI2L	4.67	26.67	2667	0.0045	0.4531	1.11	0.75	1.64	0.28
	Mid	DI2M	6.00	101.67	10167	0.0243	2.4282	0.95	0.78	1.87	0.12
	Upper	DI2U	2.67	56.67	5667	0.0813	8.1309	0.41	0.69	0.96	0.33
	Low	DI3L	4.33	29.67	2967	0.0007	0.0727	0.96	0.84	1.59	0.21
	Mid	DI3M	5.67	113.33	11333	0.0317	3.1743	0.99	0.66	1.66	0.04
	Upper	DI3U	7.00	294.33	29433	0.0960	9.6021	1.06	0.61	1.72	0.11
Indirect Impact North	Low	IN1L	3.33	9.67	967	0.0053	0.5272	1.35	0.89	1.53	0.63
	Mid	IN1M	4.00	81.67	8167	0.0167	1.6716	0.61	0.64	1.18	0.13
	Upper	IN1U	7.00	72.00	7200	0.0689	6.8908	1.40	0.81	2.29	0.42
	Low	IN2L	1.67	1.67	167	0.0017	0.1746	0.72	0.81	0.27	0.21
	Mid	IN2M	6.33	88.00	8800	0.0213	2.1275	1.19	0.59	1.52	0.12
	Upper	IN2U	6.00	66.67	6667	0.0352	3.5247	1.20	0.70	1.80	0.20
	Low	IN3L	2.00	2.33	233	0.0040	0.3974	1.86	0.96	0.64	0.26
	Mid	IN3M	1.67	6.33	633	0.0051	0.5089	0.69	0.91	0.76	0.68
	Upper	IN3U	5.33	67.00	6700	0.0267	2.6670	0.97	0.45	1.04	-0.05
Indirect Impact South	Low	IS1L	1.00	1.00	100	0.0047	0.4665	1.44	1.00	0.33	0.48
	Mid	IS1M	4.00	95.00	9500	0.0233	2.3253	0.65	0.35	0.68	-0.35
	Upper	IS1U	2.67	22.00	2200	0.0026	0.2639	0.57	0.63	0.82	-0.06
	Low	IS2L	1.33	2.33	233	0.0000	0.0027	0.36	0.81	0.27	-0.16
	Mid	IS2M	5.33	283.67	28367	0.0391	3.9149	0.77	0.21	0.51	-0.18
	Upper	IS2U	3.67	18.33	1833	0.0060	0.5974	1.04	0.81	1.46	0.33
	Low	IS3L	3.00	12.33	1233	0.0019	0.1913	1.13	0.78	1.23	0.21
	Mid	IS3M	3.67	12.33	1233	0.0175	1.7482	1.10	0.75	1.39	0.20
	Upper	IS3U	3.33	63.00	6300	0.0017	0.1689	0.93	0.75	1.07	0.25

Table 4. Mean values of biological parameters for each site (0.01m^2) at Cherry Cobb Sands.

Area	Shore	Site	Mean Numbers of Taxa	Mean Numbers of Individuals		Mean Biomass (AFDW g)		Mean Margalef's d	Mean Pielou's J	Mean Shannon's H'	Mean AFDW ABC w stat
				per 0.01 m^2	per 1 m^2	per 0.01 m^2	per 1 m^2				
Control North	Low	CN1L	1.00	3.33	333.33	0.01	0.65	0.00	-	0.00	0.00
	Mid	CN1M	4.67	69.33	6933.33	0.03	2.78	0.89	0.76	1.59	0.41
	Upper	CN1U	5.00	40.33	4033.33	0.09	9.18	1.08	0.73	1.61	0.38
	Low	CN2L	3.00	4.67	466.67	0.00	0.25	1.54	0.93	1.12	0.44
	Mid	CN2M	7.67	165.00	16500.00	0.04	4.39	1.31	0.55	1.59	0.08
	Upper	CN2U	8.33	373.33	37333.33	0.12	12.48	1.24	0.50	1.51	0.12
	Low	CN3L	2.67	3.67	366.67	0.01	0.89	0.90	0.91	0.96	0.44
	Mid	CN3M	6.67	85.67	8566.67	0.05	4.83	1.27	0.64	1.75	0.13
	Upper	CN3U	4.00	55.67	5566.67	0.05	5.05	0.86	0.72	1.45	0.42
Control South	Low	CS1L	2.33	3.33	333.33	0.00	0.34	1.28	0.97	1.03	0.64
	Mid	CS1M	7.00	225.33	22533.33	0.14	14.15	1.11	0.49	1.38	0.08
	Upper	CS1U	7.33	239.67	23966.67	0.22	21.99	1.16	0.49	1.40	0.06
	Low	CS2L	0.67	0.67	66.67	0.00	0.06	-	-	0.00	0.00
	Mid	CS2M	10.33	106.00	10600.00	0.09	8.68	2.00	0.56	1.87	0.17
	Upper	CS2U	8.33	214.00	21400.00	0.20	20.48	1.30	0.49	1.45	0.05
	Low	CS3L	1.00	1.00	100.00	0.00	0.05	1.44	1.00	0.33	0.49
	Mid	CS3M	5.33	20.33	2033.33	0.03	2.67	1.44	0.77	1.85	0.22
	Mid	CS3M2	5.33	19.67	1966.67	0.05	4.69	1.46	0.78	1.84	0.29
	Upper	CS3U	7.00	169.67	16966.67	0.18	17.89	1.17	0.65	1.79	0.24
Impact	Low	I1L	2.67	3.33	333.33	0.00	0.41	1.20	0.93	1.10	0.75
	Mid	I1M	8.00	348.00	34800.00	0.21	21.28	1.20	0.60	1.80	0.15
	Upper	I1U	7.67	365.00	36500.00	0.10	9.51	1.13	0.45	1.34	-0.05
	Low	I2L	2.00	2.67	266.67	0.01	1.12	0.91	0.96	0.83	0.16
	Mid	I2M	8.00	331.33	33133.33	0.13	12.92	1.21	0.62	1.85	0.11
	Upper	I2U	6.00	15.00	1500.00	0.02	2.17	1.86	0.88	2.28	0.55
	Low	I3L	4.33	5.33	533.33	0.00	0.49	2.04	0.96	1.99	0.57
	Mid	I3M	7.33	294.67	29466.67	0.11	10.73	1.11	0.59	1.70	0.09
	Upper	I3U	7.00	210.67	21066.67	0.13	13.33	1.12	0.63	1.75	0.18



	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	4.89	4.11	2.33	1.78
🟥 Mid	7.11	6.11	4.00	4.33
🟩 Upper	5.44	5.44	6.11	3.22

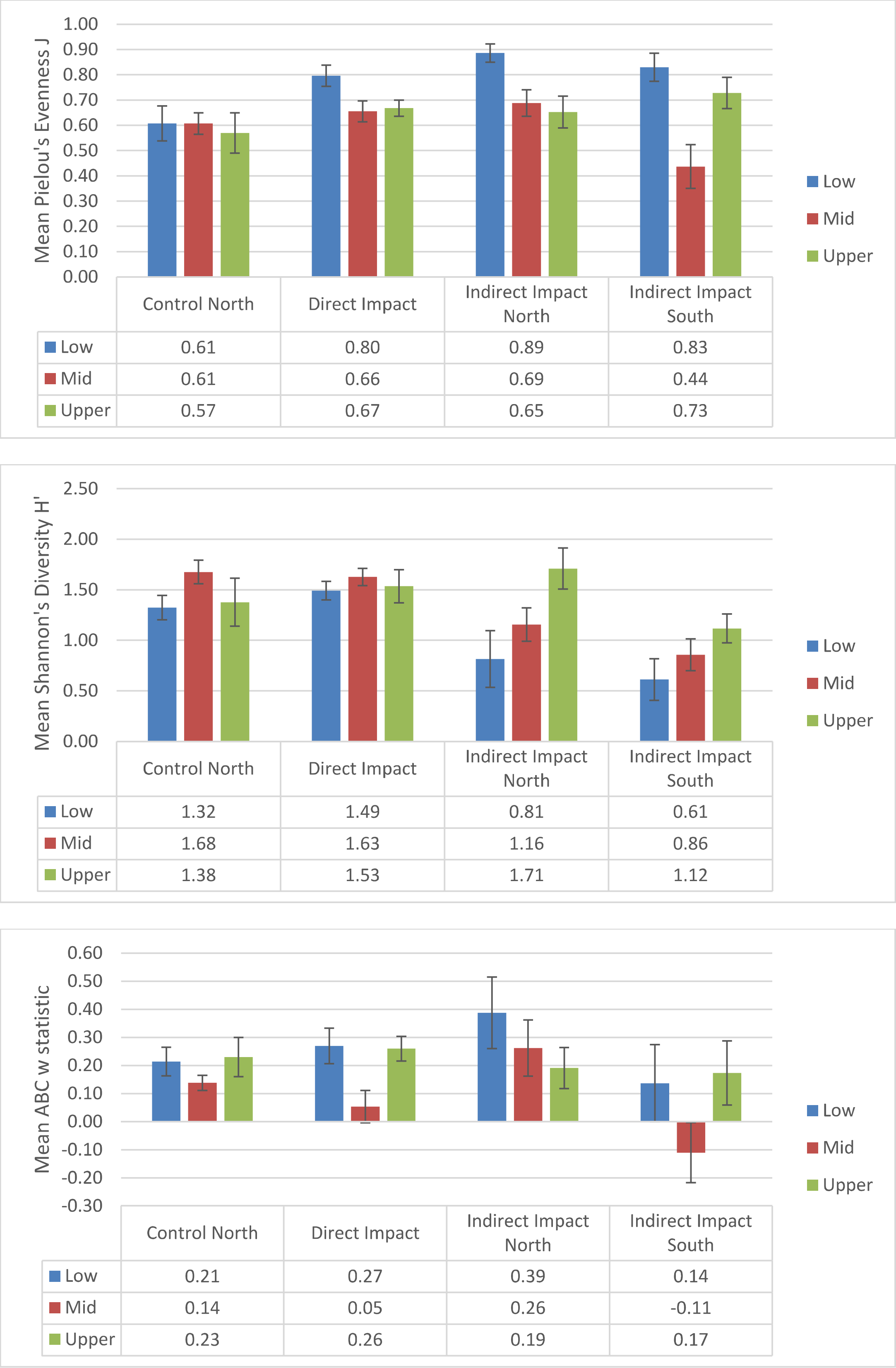
Figure 5. Average values (with standard error) of biological parameters (per 0.01m^2) for each survey area at North Killingholme.

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	83.67	23.11	4.56	5.22
🟥 Mid	95.11	94.89	58.67	130.33
🟩 Upper	157.78	144.00	68.56	34.44

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	0.016	0.005	0.004	0.002
🟥 Mid	0.020	0.029	0.014	0.027
🟩 Upper	0.097	0.145	0.044	0.003

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	1.00	1.02	1.33	0.93
🟥 Mid	1.35	1.04	0.85	0.84
🟩 Upper	1.06	0.92	1.19	0.85

Figure 5 (cont.). **Average values (with standard error) of biological parameters (per 0.01m²) for each survey area at North Killingholme.**

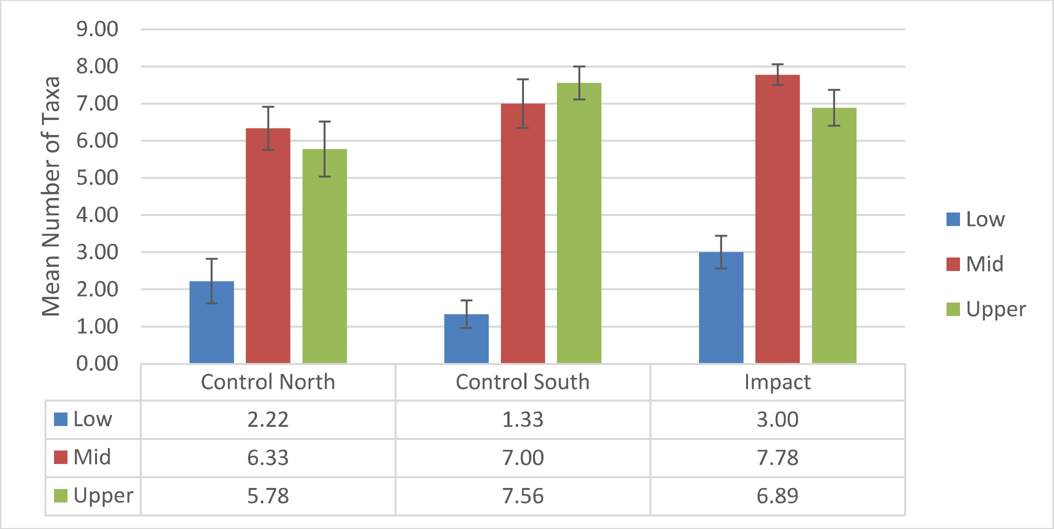


	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	0.61	0.80	0.89	0.83
🟥 Mid	0.61	0.66	0.69	0.44
🟩 Upper	0.57	0.67	0.65	0.73

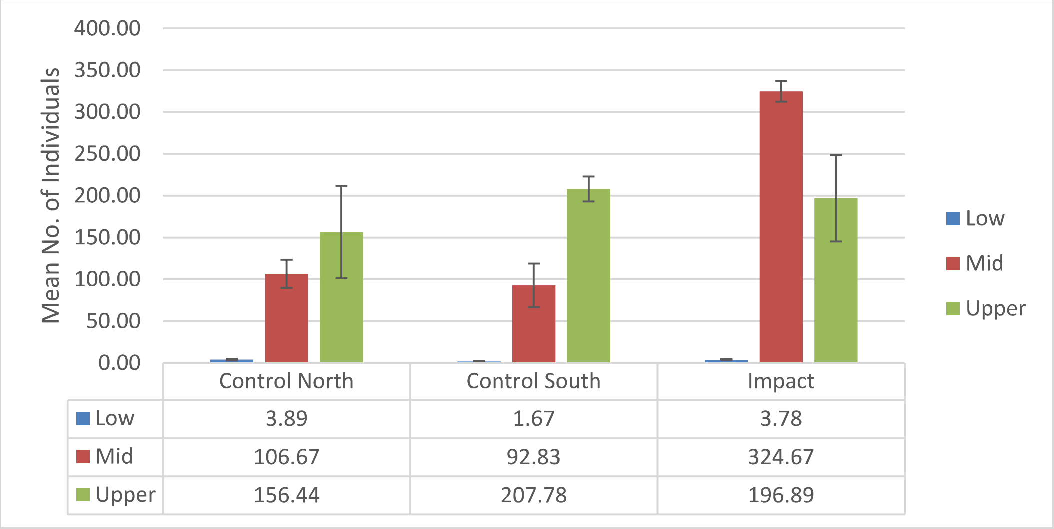
	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	1.32	1.49	0.81	0.61
🟥 Mid	1.68	1.63	1.16	0.86
🟩 Upper	1.38	1.53	1.71	1.12

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
🟦 Low	0.21	0.27	0.39	0.14
🟥 Mid	0.14	0.05	0.26	-0.11
🟩 Upper	0.23	0.26	0.19	0.17

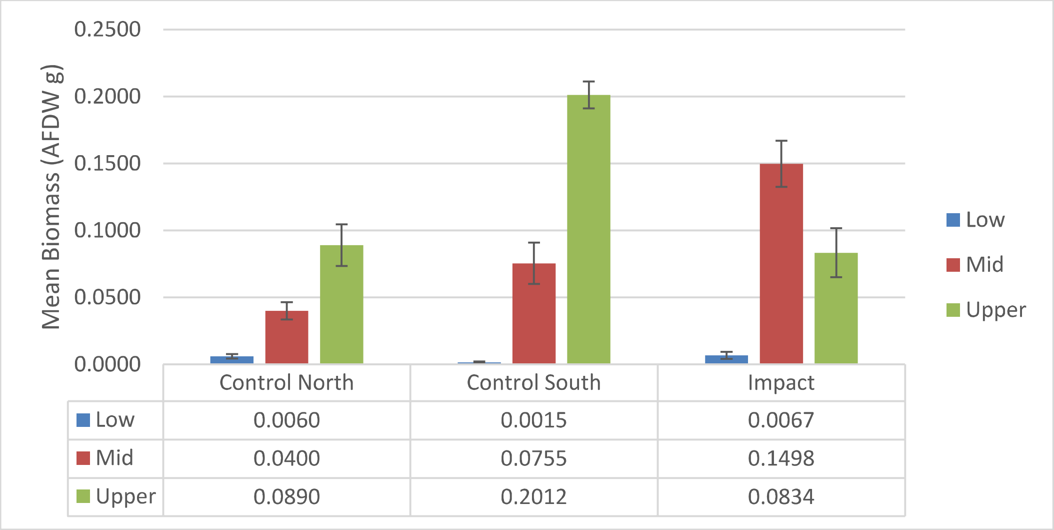
Figure 5 (cont.). **Average values (with standard error) of biological parameters (per 0.01m^2) for each survey area at North Killingholme.**



	Control North	Control South	Impact
🟦 Low	2.22	1.33	3.00
🟥 Mid	6.33	7.00	7.78
🟩 Upper	5.78	7.56	6.89

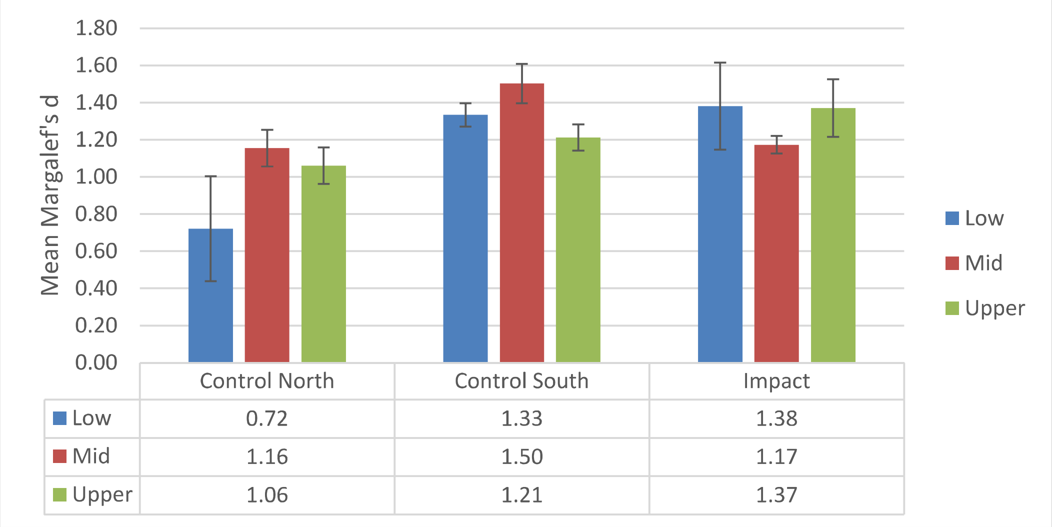


	Control North	Control South	Impact
🟦 Low	3.89	1.67	3.78
🟥 Mid	106.67	92.83	324.67
🟩 Upper	156.44	207.78	196.89

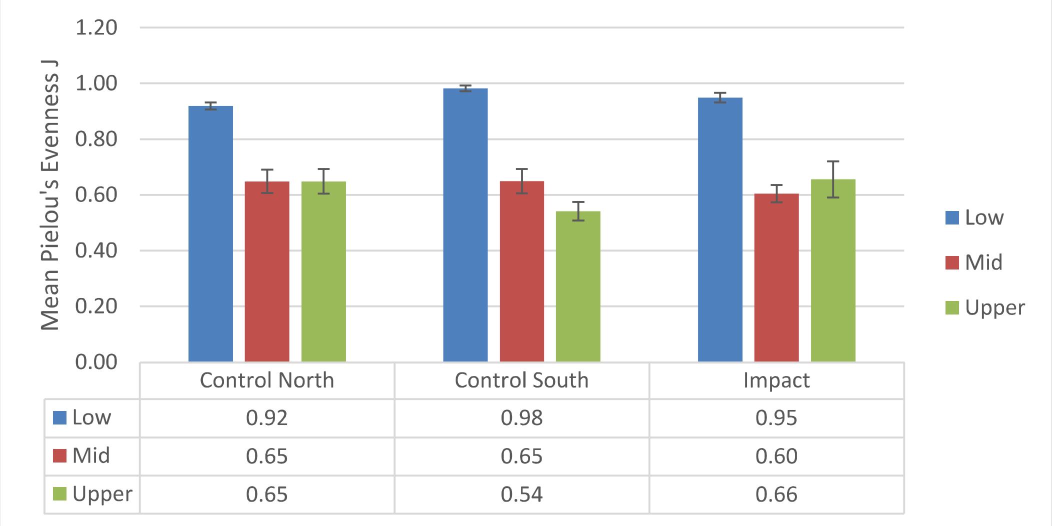


	Control North	Control South	Impact
🟦 Low	0.0060	0.0015	0.0067
🟥 Mid	0.0400	0.0755	0.1498
🟩 Upper	0.0890	0.2012	0.0834

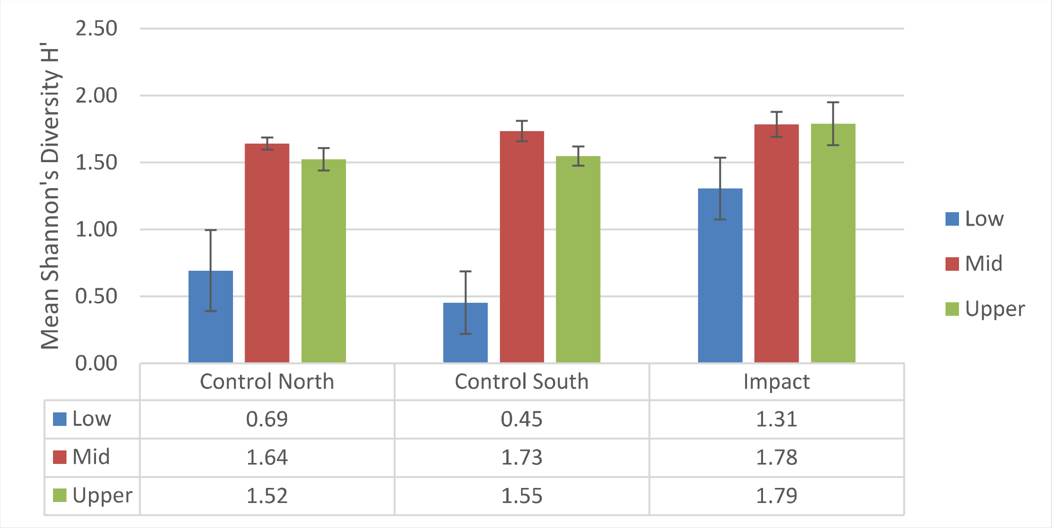
Figure 6. Average values (with standard error) of biological parameters (per 0.01m^2) for each survey area at Cherry Cobb Sands.



	Control North	Control South	Impact
🟦 Low	0.72	1.33	1.38
🟥 Mid	1.16	1.50	1.17
🟩 Upper	1.06	1.21	1.37

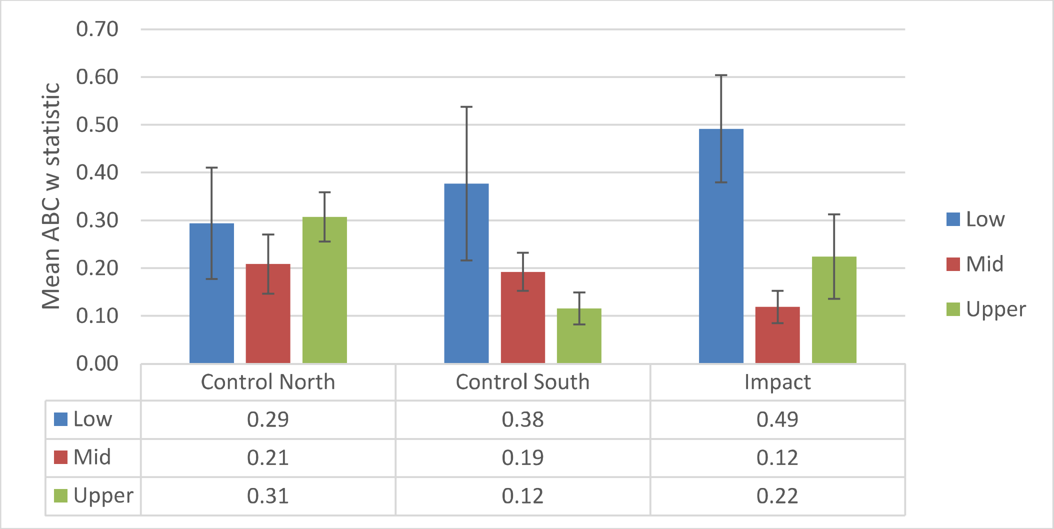


	Control North	Control South	Impact
🟦 Low	0.92	0.98	0.95
🟥 Mid	0.65	0.65	0.60
🟩 Upper	0.65	0.54	0.66



	Control North	Control South	Impact
🟦 Low	0.69	0.45	1.31
🟥 Mid	1.64	1.73	1.78
🟩 Upper	1.52	1.55	1.79

Figure 6 (cont.). Average values (with standard error) of biological parameters (per 0.01m2) for each survey area at Cherry Cobb Sands.



	Control North	Control South	Impact
🟦 Low	0.29	0.38	0.49
🟥 Mid	0.21	0.19	0.12
🟩 Upper	0.31	0.12	0.22

Figure 6 (cont.). **Average values (with standard error) of biological parameters (per 0.01m2) for each survey area at Cherry Cobb Sands.**

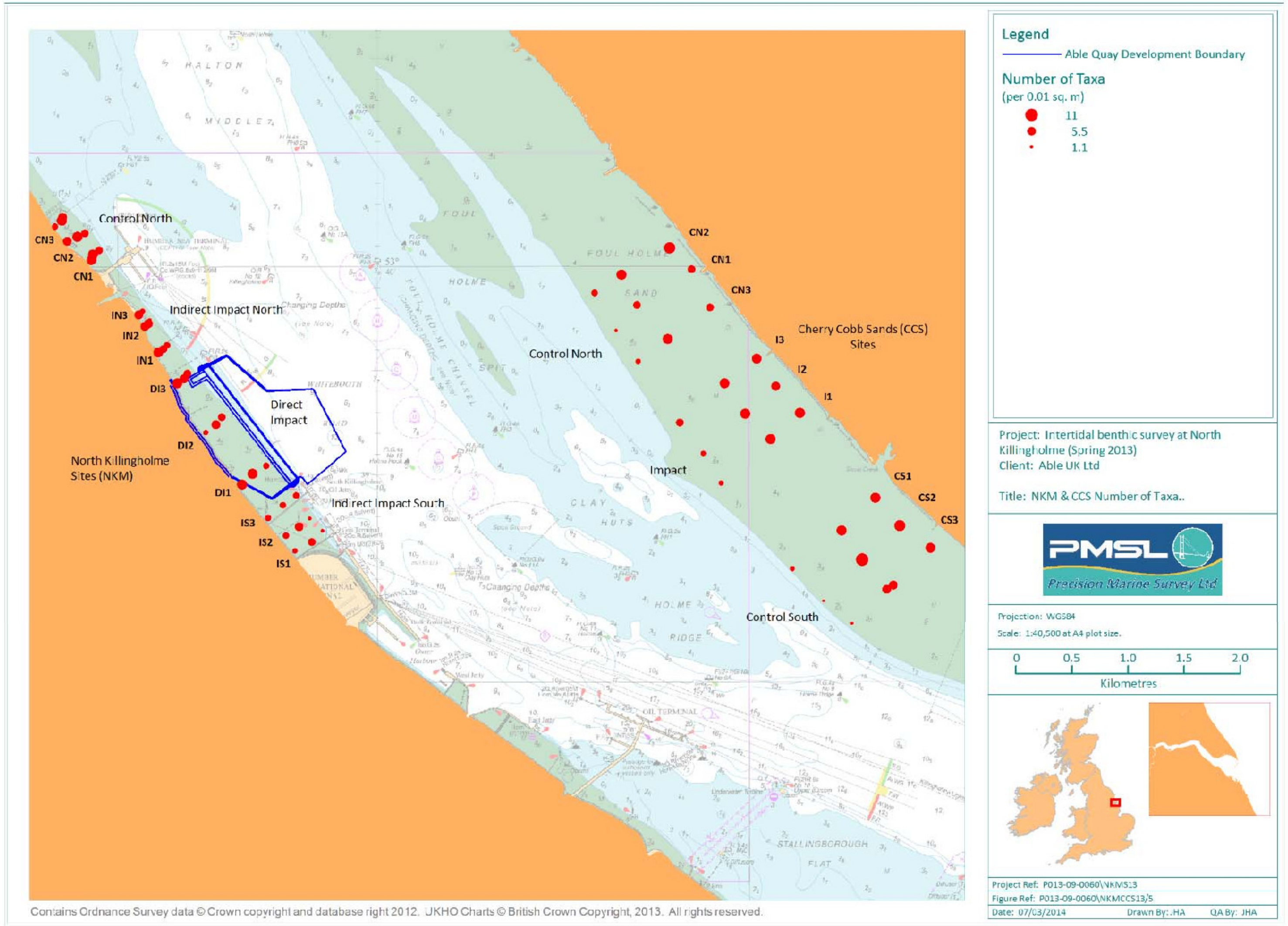


Figure 7. **Number of taxa per $0.01m^2$ at the survey sites.**

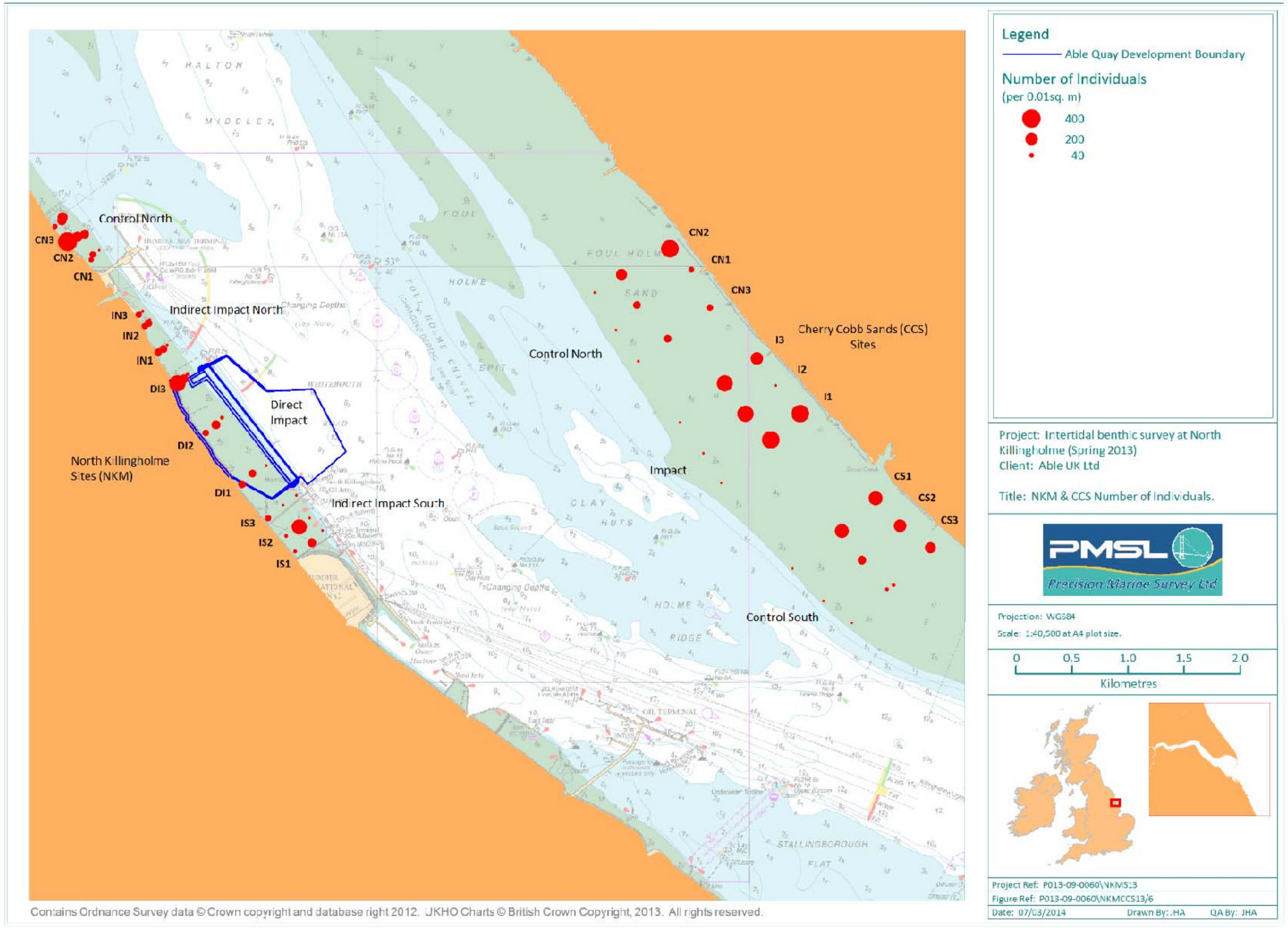


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Figure 8. **Numbers of individuals per 0.01m^2 at the survey sites.**

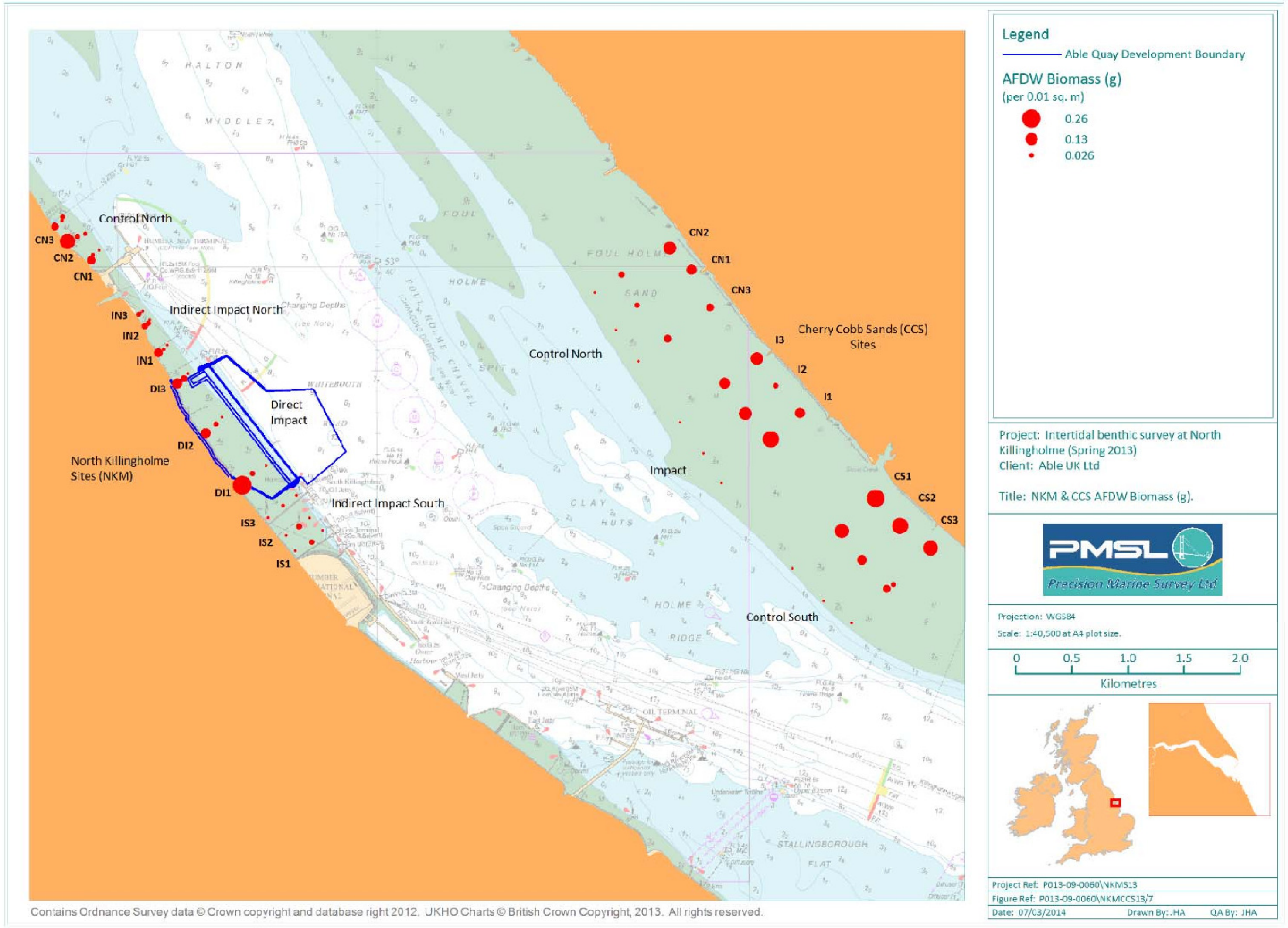

Figure 9. AFDW Biomass (g per 0.01m^2) at the survey sites.

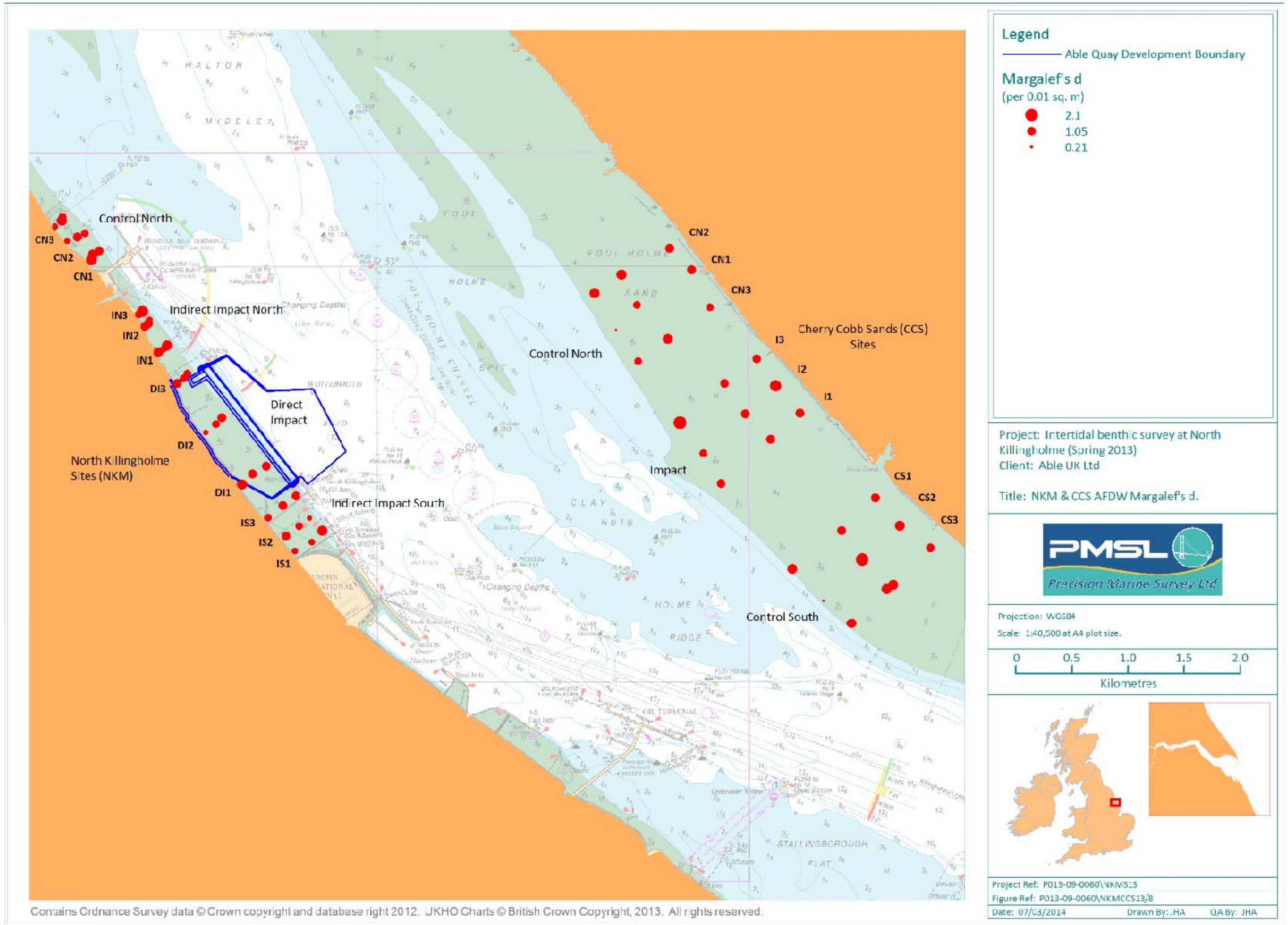

Figure 10. Margalef's d at the survey sites (per 0.01m^2).

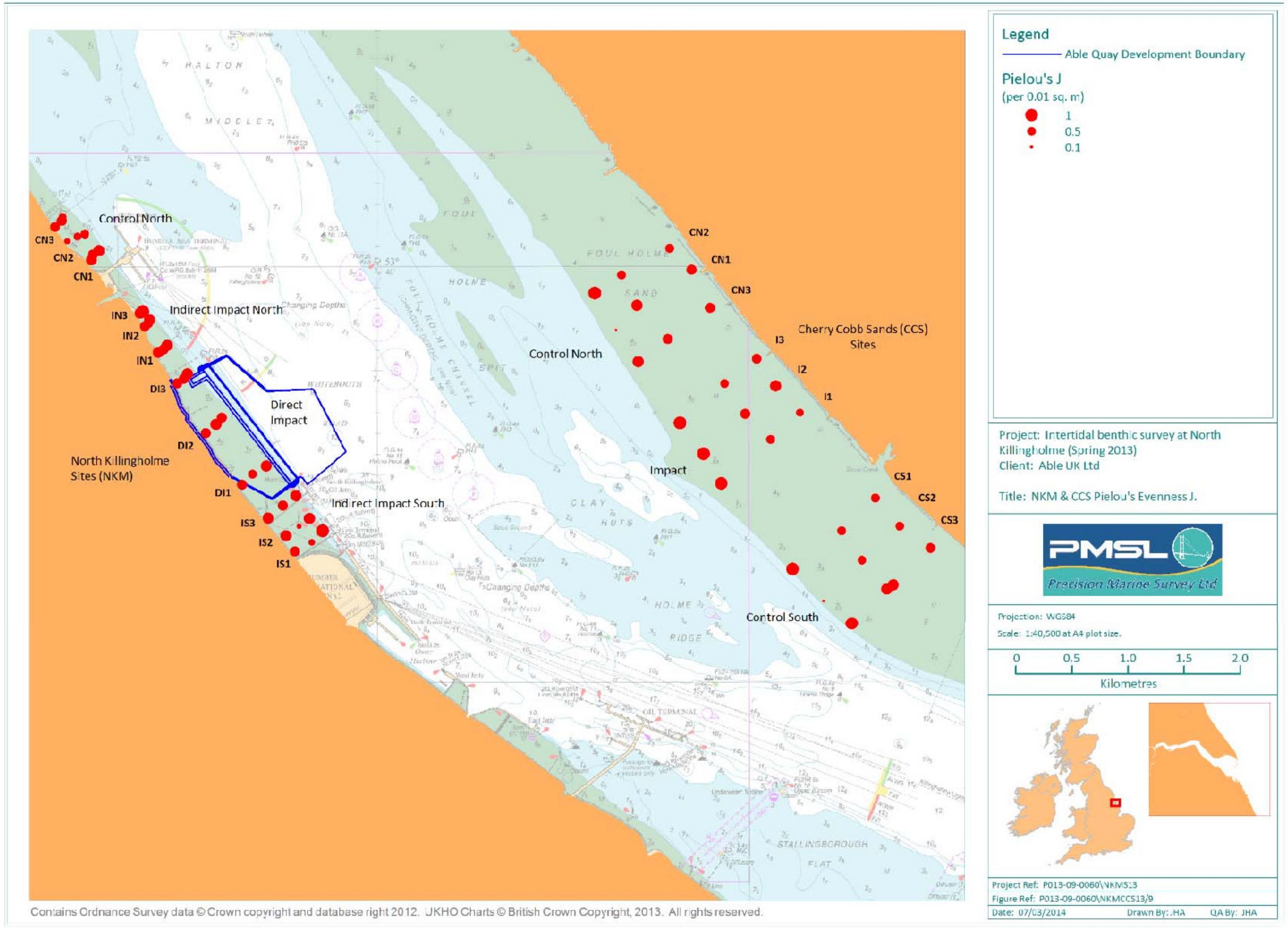

Figure 11. Pielou's evenness J at the survey sites (per 0.01m^2).

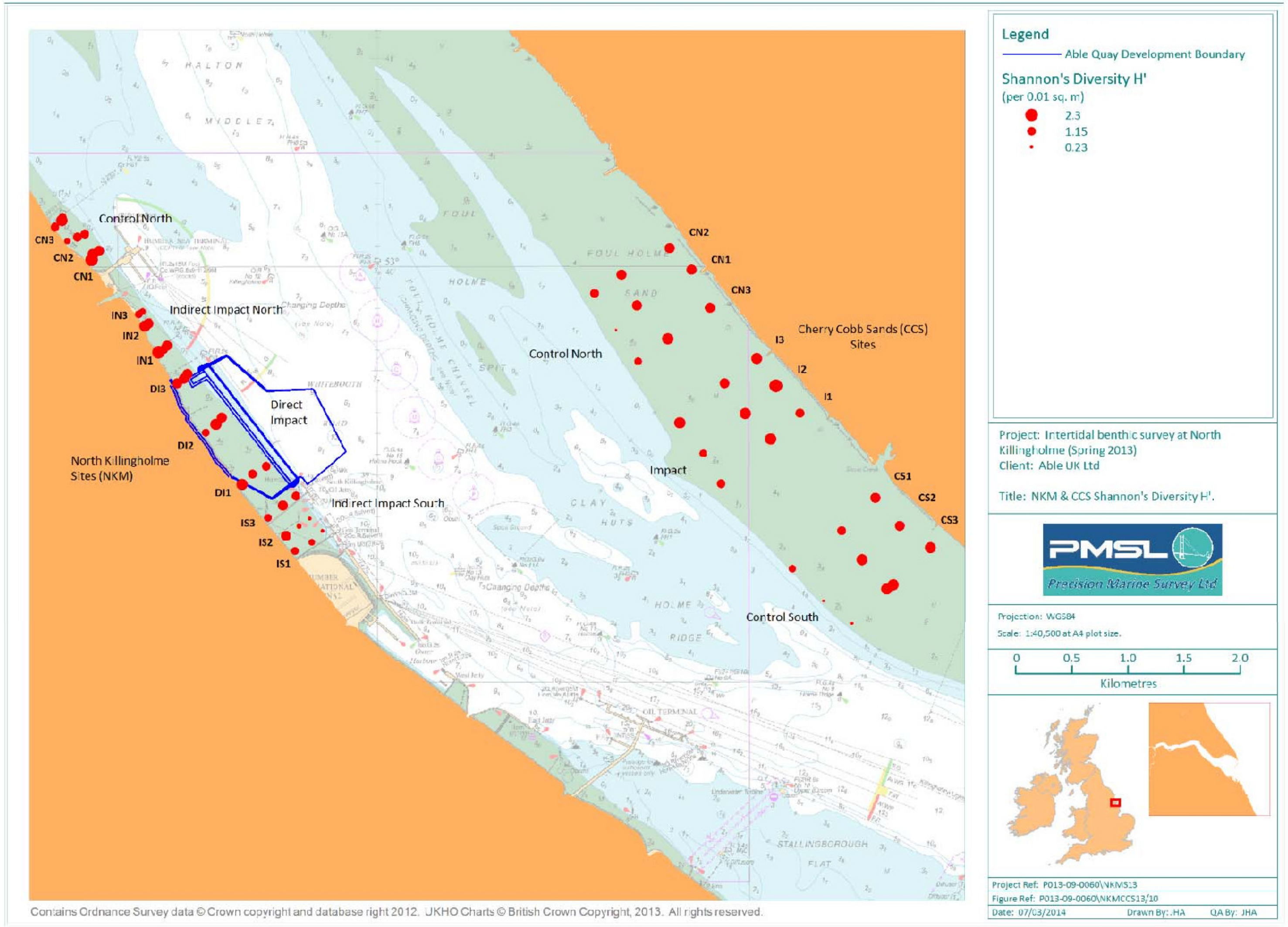

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Figure 12. Shannon's diversity H' at the survey sites (per 0.01m^2).

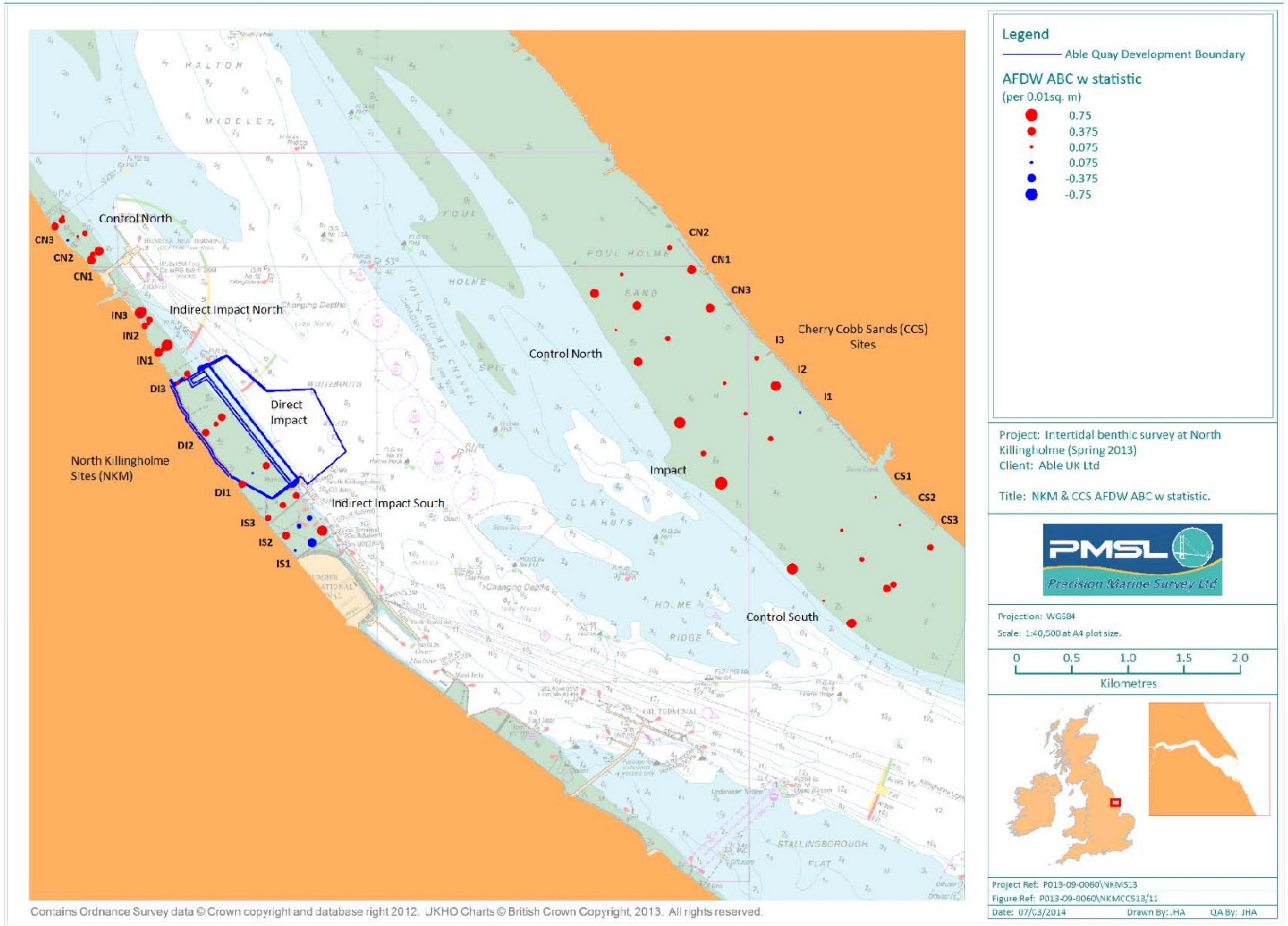

Figure 13. ABC w statistic at the survey sites (per 0.01m^2).

3.3 Species composition at the survey areas

3.3.1 North Killingholme

A summary of the dominant taxa by abundance and biomass has been provided based on pooled data at each site. The average abundances and AFDW biomass per site have been scaled up to numbers and weights per m^2 across the entire survey area and these are provided in Table 5. In total 25 taxa were recorded during the survey including a number of terrestrial (insect) taxa which have been included as they were particularly indicative of upper shore areas adjacent to saltmarsh.

In terms of total abundance the most dominant taxa were *Tubificoides benedii* and *Corophium volutator* which accounted for over 60% of the total abundance and were recorded at the majority of sites (94% and 83% respectively). Moderate numbers of other oligochaetes (*Tubificoides* agg. and Enchytraeidae sp.) were also recorded at a lower number of sites. *Hediste diversicolor* was also common and recorded at over 60% of the sites whilst *Streblospio shrubsolii* and *Macoma balthica* were also widely recorded in somewhat lower numbers. In terms of biomass larger species such as *Hediste diversicolor, Corophium volutator* and *Macoma balthica* accounted for the majority of the biomass (92% of total).

Table 5. Ranked average abundance and biomass for the full survey area at North Killingholme (per m^2).

Taxa	Mean Abundance per m^2	% of sites	% of Total	Taxa	Mean AFDW Biomass (g) per m^2	% of sites	% of Total
Tubificoides benedii	2474	94	32.98	Hediste diversicolor	2.13816	64	63.35
Corophium volutator	2030	83	60.03	Corophium volutator	0.72083	83	84.71
Tubificoides agg. (pseudogaster)	894	36	71.94	Macoma balthica	0.25360	78	92.22
Hediste diversicolor	578	64	79.64	Tubificoides benedii	0.13608	94	96.26
Streblospio shrubsolii	535	72	86.77	Tubificoides agg. (pseudogaster)	0.05476	36	97.88
Enchytraeidae	319	28	91.02	Streblospio shrubsolii	0.02961	72	98.76
Nematoda	306	72	95.09	Enchytraeidae	0.01452	28	99.19
Collembola sp.	177	17	97.45	Nephtys hombergii	0.01069	6	99.50
Macoma balthica	77	78	98.47	Diptera sp.	0.00882	19	99.76
Tubificoides swirencoides	31	8	98.89	Lekanesphaera hookeri	0.00209	3	99.83
Pygospio elegans	28	36	99.26	Coleoptera sp.	0.00173	6	99.88
Diptera sp.	19	19	99.51	Tharyx sp.	0.00119	14	99.91
Manayunkia aestuarina	17	17	99.73	Nematoda	0.00111	72	99.95
Tharyx sp.	9	14	99.85	Collembola sp.	0.00058	17	99.96
Nephtys hombergii	3	6	99.89	Tubificoides swirencoides	0.00043	8	99.98
Coleoptera sp.	3	6	99.93	Pygospio elegans	0.00035	36	99.99
Nemertea	1	3	99.94	Nemertea	0.00029	3	99.99
Eteone longa/flava agg.	1	3	99.95	Manayunkia aestuarina	0.00012	17	100.00
Naididae	1	3	99.96	Tellinacea juv.	0.00004	3	100.00
Polydora cornuta	1	3	99.98	Spionidae sp.	0.00001	3	100.00
Lekanesphaera hookeri	1	3	99.99	Polydora cornuta	0.00001	3	100.00
Tellinacea juv.	1	3	100.00	Eteone longa/flava agg.	0.00001	3	100.00
Spionidae sp.	P	3		Naididae	0.00000	3	100.00

3.3.2 Cherry Cobb Sands

In terms of characteristic species from the CCS survey the dominant taxa across the survey area (mean abundance and AFDW biomass per m^2) are given in Table 6. A similar range of taxa were recorded at CCS in comparison to NKM with the exception of *Corophium volutator* which is largely absent in this area although the total number of taxa recorded (33 taxa) is greater which reflects wider range of habitats present. The dominant taxa at CCS (in terms of numbers of individuals) are *Tubificoides benedii,* Nematoda*, Macoma balthica, Tubificoides agg. (pseudogaster), Hediste diversicolor and Pygospio elegans* which account for 90% of the total abundance. In terms of biomass *Macoma balthica* and *Hediste diversicolor* account for over 90% of the total.

Table 6. Ranked average abundance and biomass for the full survey area at Cherry Cobb Sands (per m^2).

Taxa	Mean Abundance per m^2	% of sites	% of Total	Taxa	Mean AFDW Biomass (g) per m^2	% of sites	% of Total
Tubificoides benedii	6047.62	78.57	50.15	Macoma balthica	3.8173	82.14	52.54
Nematoda	1598.81	71.43	63.41	Hediste diversicolor	2.7845	67.86	90.86
Macoma balthica	1154.76	82.14	72.98	Tubificoides benedii	0.3366	78.57	95.49
Tubificoides agg. (pseudogaster)	990.48	14.29	81.19	Nephtys hombergii	0.1040	28.57	96.92
Hediste diversicolor	596.43	67.86	86.14	Hydrobia ulvae	0.0966	64.29	98.25
Pygospio elegans	569.05	71.43	90.86	Tubificoides agg. (pseudogaster)	0.0341	14.29	98.72
Hydrobia ulvae	403.57	64.29	94.21	Pygospio elegans	0.0218	71.43	99.02
Enchytraeidae	369.05	53.57	97.27	Eteone longa/flava agg.	0.0168	35.71	99.25
Manayunkia aestuarina	123.81	39.29	98.29	Diptera sp.	0.0157	21.43	99.47
Diptera sp.	48.81	21.43	98.70	Nematoda	0.0119	71.43	99.63
Eteone longa/flava agg.	27.38	35.71	98.92	Abra tenuis	0.0080	10.71	99.74
Nephtys hombergii	27.38	28.57	99.15	Corophium volutator	0.0050	7.14	99.81
Streblospio shrubsolii	20.24	28.57	99.32	Bathyporeia sarsi	0.0038	3.57	99.86
Bathyporeia sarsi	19.05	3.57	99.48	Scoloplos armiger	0.0020	3.57	99.89
Corophium volutator	13.10	7.14	99.59	Enchytraeidae	0.0017	53.57	99.91
Collembola sp.	11.90	10.71	99.68	Manayunkia aestuarina	0.0010	39.29	99.93
Abra tenuis	5.95	10.71	99.73	Abra sp.	0.0010	3.57	99.94
Tharyx sp.	5.95	3.57	99.78	Spionidae sp.	0.0010	3.57	99.95
Cyathura carinata	4.76	14.29	99.82	Tharyx sp.	0.0009	3.57	99.97
Mytilidae juv.	4.76	10.71	99.86	Retusa obtusa	0.0006	3.57	99.98
Alderia modesta	2.38	7.14	99.88	Scrobicularia plana	0.0005	3.57	99.98
Acarina sp.	2.38	7.14	99.90	Nereididae sp.	0.0004	3.57	99.99
Dalyelliidae sp.	2.38	3.57	99.92	Cyathura carinata	0.0003	14.29	99.99
Caulleriella killariensis	2.38	3.57	99.94	Collembola sp.	0.0002	10.71	99.99
Nemertea	1.19	3.57	99.95	Streblospio shrubsolii	0.0002	28.57	100.00
Sphaerodoropsis baltica	1.19	3.57	99.96	Alderia modesta	0.0000	7.14	100.00
Scoloplos armiger	1.19	3.57	99.97	Acarina sp.	0.0000	7.14	100.00
Retusa obtusa	1.19	3.57	99.98	Dalyelliidae sp.	0.0000	3.57	100.00
Abra sp.	1.19	3.57	99.99	Nemertea	0.0000	3.57	100.00
Scrobicularia plana	1.19	3.57	100.00	Sphaerodoropsis baltica	0.0000	3.57	100.00
Nereididae sp.	P	3.57		Caulleriella killariensis	0.0000	3.57	100.00
Spionidae sp.	P	3.57		Mytilidae juv.	0.0000	10.71	100.00
Ascidiacea sp.	P	3.57		Ascidiacea sp.	P	3.57	

3.3.3 Spatial Trends

The summaries of dominant taxa (mean abundance and AFDW biomass per m^2) within the different shore levels in each survey area are provided in Tables 7 to 9 for NKM and 10 to 12 for CCS and the spatial distribution of key taxa (*Hediste diversicolor*, *Macoma balthica*, *Corophium volutator, Streblospio shrubsolii, Pygospio elegans* and oligochaetes) in terms of mean numbers per m^2 at each site are provided in a series of charts in Figures 14 to 19. These results highlight the influence of shore level on the distribution of infauna with differences between specific survey areas less pronounced for NKM but more so for CCS where a much larger variation in sediment types is reflected in species distribution. For example at NKM taxa such as *Corophium volutator*, *Tubificoides* spp. and *Streblospio shrubsolii* generally dominate in varying degrees in all areas although species such as *Streblospio shrubsolii* were generally more prevalent on the low shore whilst *Hediste diversicolor* is more common in upper shore sites. The maps shown in Figures 14 to 19 highlight also the widespread coverage by *Corophium volutator*, particularly in the northern indirect impact area and control area whilst *Macoma balthica* is widely distributed in varying densities throughout the area with perhaps a slight increase in numbers on the mid shore and in the direct impact zone. Upper shore sites at NKM adjacent to saltmarsh with greater elevation e.g. at the control area and southern indirect impact area tended to have higher numbers of *Tubificoides* agg. (*pseudogaster*) and terrestrial insect taxa with relatively impoverished communities. As expected *Hediste diversicolor*, *Macoma balthica*, *Corophium volutator* and *Tubificoides* spp. dominate in terms of biomass across all the areas at NKM.

At CCS more pronounced spatial differences were evident reflecting the variation in sedimentary regime with some differences in key taxa between CCS and NKM. Modest numbers of taxa were present at low shore areas (particularly at the southern control area) with *Macoma balthica* and *Nephtys hombergii* characteristic whilst on the mid shore oligochaetes such as *Tubificoides benedii* tended to dominate along with Hediste diversicolor and *Macoma balthica* although the latter were more prevalent in the southern control area and less abundant in the northern control area. The upper shore was also strongly dominated by *Tubificoides* spp. with *Tubificoides* agg. (*pseudogaster*) in saltmarsh influenced areas to the north along with Enchytraeidae and *Hediste diversicolor* whilst the impact and southern control areas had *Tubificoides benedii* with *Hediste diversicolor*, *Hydrobia ulvae* (in the impact area), *Pygospio elegans* and *Macoma balthica* with the latter more common in the southern area. Whilst a similar range of taxa were recorded at CCS in comparison to NKM some differences are apparent and Figures 14 to 19 highlight the relative absence of *Corophium volutator* at CCS whilst it is often abundant at NKM (and particularly north/upstream of the development site) which may reflect sedimentological differences although the distribution of *Corophium volutator* in the Humber is known to exhibit high levels of temporal and spatial variability. Similar numbers of *Hediste diversicolor* were recorded at NKM and CCS albeit with a slightly wider distribution at CCS whilst *Macoma balthica* tended to occur in higher numbers at CCS on the upper and mid shore and particularly at the southern control and impact transects.

Table 7. Average ranked abundance and biomass (per 1m^2) for the low shore sites at North Killingholme.

Control North Low Shore			**Direct Impact Low Shore**			**Indirect Impact North Low Shore**			**Indirect Impact South Low Shore**		
Taxa	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**
Corophium volutator	589	100	Streblospio shrubsolii	101	100	Streblospio shrubsolii	22	100	Tubificoides swirencoides	20	33
Streblospio shrubsolii	173	100	Nematoda	56	67	Tubificoides benedii	14	100	Streblospio shrubsolii	16	33
Nematoda	33	100	Tubificoides benedii	37	100	Macoma balthica	6	100	Tubificoides benedii	9	100
Tubificoides benedii	28	100	Tubificoides swirencoides	18	67	Nematoda	1	33	Corophium volutator	3	67
Macoma balthica	6	100	Macoma balthica	9	100	Corophium volutator	1	33	Macoma balthica	2	67
Hediste diversicolor	2	67	Pygospio elegans	3	67	Tellinacea juv.	1	33	Nephtys hombergii	2	33
Pygospio elegans	2	67	Corophium volutator	2	67	Spionidae sp.	P	33			
Tubificoides agg. (pseudogaster)	1	33	Tharyx sp.	2	33						
Enchytraeidae	1	33	Hediste diversicolor	1	33						
Polydora cornuta	1	33	Nephtys hombergii	1	33						
			Diptera sp.	1	33						

Control North Low Shore			**Direct Impact Low Shore**			**Indirect Impact North Low Shore**			**Indirect Impact South Low Shore**		
Taxa	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**
Corophium volutator	1.4011	100	Macoma balthica	0.2445	100	Macoma balthica	0.3502	100	Macoma balthica	0.1520	67
Streblospio shrubsolii	0.1243	100	Hediste diversicolor	0.1419	33	Streblospio shrubsolii	0.0094	100	Nephtys hombergii	0.0576	33
Macoma balthica	0.0220	100	Nephtys hombergii	0.0708	33	Tubificoides benedii	0.0056	100	Corophium volutator	0.0041	67
Hediste diversicolor	0.0088	67	Streblospio shrubsolii	0.0453	100	Tellinacea juv.	0.0005	33	Tubificoides swirencoides	0.0033	33
Tubificoides benedii	0.0080	100	Corophium volutator	0.0251	67	Corophium volutator	0.0004	33	Streblospio shrubsolii	0.0023	33
Nematoda	0.0018	100	Tubificoides benedii	0.0102	100	Nematoda	0.0002	33	Tubificoides benedii	0.0010	100
Pygospio elegans	0.0002	67	Tubificoides swirencoides	0.0019	67	Spionidae sp.	0.0002	33			
Polydora cornuta	0.0002	33	Nematoda	0.0014	67						
Tubificoides agg. (pseudogaster)	0.0001	33	Pygospio elegans	0.0004	67						
Enchytraeidae	0.0001	33	Tharyx sp.	0.0004	33						
			Diptera sp.	0.0002	33						

Table 8. Average ranked abundance and biomass (per 1m^2) for the mid shore sites North Killingholme.

Control North Mid Shore			Direct Impact Mid Shore			Indirect Impact North Mid Shore			Indirect Impact South Mid Shore		
Taxa	Mean Abundance per m^2	% of sites	Taxa	Mean Abundance per m^2	% of sites	Taxa	Mean Abundance per m^2	% of sites	Taxa	Mean Abundance per m^2	% of sites
Corophium volutator	538	100	Tubificoides benedii	538	100	Corophium volutator	283	100	Tubificoides benedii	1167	100
Tubificoides benedii	233	100	Corophium volutator	190	100	Tubificoides benedii	254	100	Streblospio shrubsolii	44	67
Nematoda	68	100	Streblospio shrubsolii	127	100	Streblospio shrubsolii	17	33	Hediste diversicolor	36	100
Streblospio shrubsolii	31	100	Nematoda	49	100	Nematoda	9	67	Corophium volutator	19	100
Enchytraeidae	30	100	Macoma balthica	34	100	Hediste diversicolor	7	100	Nematoda	16	67
Pygospio elegans	20	100	Tharyx sp.	7	67	Diptera sp.	7	67	Manayunkia aestuarina	13	33
Macoma balthica	14	100	Pygospio elegans	2	67	Macoma balthica	6	67	Macoma balthica	4	100
Hediste diversicolor	10	100	Tubificoides agg. (pseudogaster)	2	33	Tharyx sp.	2	33	Pygospio elegans	2	67
Tubificoides agg. (pseudogaster)	2	33	Hediste diversicolor	P	67	Coleoptera sp.	2	33	Tubificoides agg. (pseudogaster)	2	33
Nemertea	1	33									
Manayunkia aestuarina	1	33									
Naididae	1	33									
Coleoptera sp.	1	33									
Tharyx sp.	P	33									

Control North Mid Shore			Direct Impact Mid Shore			Indirect Impact North Mid Shore			Indirect Impact South Mid Shore		
Taxa	Mean AFDW Biomass (g) per m^2	% of sites	Taxa	Mean AFDW Biomass (g) per m^2	% of sites	Taxa	Mean AFDW Biomass (g) per m^2	% of sites	Taxa	Mean AFDW Biomass (g) per m^2	% of sites
Corophium volutator	1.3177	100	Macoma balthica	1.3550	100	Corophium volutator	0.9563	100	Hediste diversicolor	1.6491	100
Macoma balthica	0.3526	100	Corophium volutator	1.0617	100	Tubificoides benedii	0.1781	100	Tubificoides benedii	0.7324	100
Hediste diversicolor	0.2124	100	Tubificoides benedii	0.2863	100	Hediste diversicolor	0.1520	100	Corophium volutator	0.1506	100
Tubificoides benedii	0.0866	100	Hediste diversicolor	0.0998	67	Macoma balthica	0.1090	67	Macoma balthica	0.0987	100
Streblospio shrubsolii	0.0128	100	Streblospio shrubsolii	0.0761	100	Coleoptera sp.	0.0191	33	Streblospio shrubsolii	0.0284	67
Nemertea	0.0034	33	Tharyx sp.	0.0110	67	Streblospio shrubsolii	0.0101	33	Tubificoides agg. (pseudogaster)	0.0022	33
Coleoptera sp.	0.0017	33	Nematoda	0.0018	100	Diptera sp.	0.0077	67	Nematoda	0.0008	67
Nematoda	0.0014	100	Pygospio elegans	0.0002	67	Tharyx sp.	0.0027	33	Manayunkia aestuarina	0.0004	33
Pygospio elegans	0.0010	100	Tubificoides agg. (pseudogaster)	0.0001	33	Nematoda	0.0010	67	Pygospio elegans	0.0002	67
Enchytraeidae	0.0010	100									
Tharyx sp.	0.0002	33									
Manayunkia aestuarina	0.0002	33									
Naididae	0.0001	33									
Tubificoides agg. (pseudogaster)	0.0001	33									

Table 9. Average ranked abundance and biomass (per 1m^2) for the upper shore sites North Killingholme.

Control North Upper Shore			Direct Impact Upper Shore			Indirect Impact North Upper Shore			Indirect Impact South Upper Shore		
Taxa	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**
Tubificoides agg. (pseudogaster)	880	100	Tubificoides benedii	2074	100	Corophium volutator	391	100	Collembola sp.	148	100
Enchytraeidae	321	67	Corophium volutator	1133	100	Hediste diversicolor	127	100	Tubificoides agg. (pseudogaster)	126	100
Hediste diversicolor	179	100	Hediste diversicolor	1107	100	Streblospio shrubsolii	54	100	Tubificoides benedii	31	100
Corophium volutator	72	100	Nematoda	189	67	Tubificoides agg. (pseudogaster)	33	67	Nematoda	14	67
Collembola sp.	62	33	Streblospio shrubsolii	167	67	Tubificoides benedii	32	100	Diptera sp.	11	100
Nematoda	49	100	Tubificoides agg. (pseudogaster)	85	33	Enchytraeidae	29	100	Corophium volutator	7	33
Tubificoides benedii	3	33	Manayunkia aestuarina	11	67	Nematoda	16	100	Streblospio shrubsolii	4	33
Diptera sp.	3	33	Macoma balthica	11	33	Macoma balthica	3	100	Macoma balthica	2	33
Manayunkia aestuarina	2	67	Collembola sp.	7	67				Lekanesphaera hookeri	1	33
Streblospio shrubsolii	2	33	Pygospio elegans	7	33						
Macoma balthica	2	33	Eteone longa/flava agg.	4	33						
Pygospio elegans	1	33	Enchytraeidae	4	33						

Control North Upper Shore			Direct Impact Upper Shore			Indirect Impact North Upper Shore			Indirect Impact South Upper Shore		
Taxa	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**
Hediste diversicolor	8.5097	100	Hediste diversicolor	11.9592	100	Hediste diversicolor	2.9250	100	Macoma balthica	0.0855	33
Tubificoides agg. (pseudogaster)	0.5610	100	Corophium volutator	2.1612	100	Corophium volutator	1.2761	100	Tubificoides agg. (pseudogaster)	0.0748	100
Corophium volutator	0.2215	100	Tubificoides benedii	0.2875	100	Macoma balthica	0.1097	100	Corophium volutator	0.0743	33
Enchytraeidae	0.1715	67	Macoma balthica	0.0302	33	Streblospio shrubsolii	0.0194	100	Diptera sp.	0.0555	100
Macoma balthica	0.1339	33	Streblospio shrubsolii	0.0204	67	Tubificoides benedii	0.0163	100	Lekanesphaera hookeri	0.0251	33
Diptera sp.	0.0425	33	Tubificoides agg. (pseudogaster)	0.0074	33	Tubificoides agg. (pseudogaster)	0.0115	67	Tubificoides benedii	0.0208	100
Collembola sp.	0.0036	33	Nematoda	0.0012	67	Enchytraeidae	0.0017	100	Streblospio shrubsolii	0.0037	33
Streblospio shrubsolii	0.0030	33	Manayunkia aestuarina	0.0005	67	Nematoda	0.0012	100	Collembola sp.	0.0030	100
Pygospio elegans	0.0020	33	Collembola sp.	0.0003	67				Nematoda	0.0006	67
Nematoda	0.0016	100	Eteone longa/flava agg.	0.0002	33						
Manayunkia aestuarina	0.0004	67	Pygospio elegans	0.0001	33						
Tubificoides benedii	0.0002	33	Enchytraeidae	0.0001	33						

Table 10. Average ranked abundance and biomass (per 1m^2) for the low shore sites at Cherry Cobb Sands.

Control North Low Shore			**Impact Low Shore**			**Control South Low Shore**		
Taxa	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**
Macoma balthica	222	100	Macoma balthica	167	100	Nephtys hombergii	67	100
Nematoda	33	33	Nephtys hombergii	44	67	Tubificoides benedii	44	67
Hydrobia ulvae	33	33	Nematoda	44	33	Macoma balthica	33	67
Eteone longa/flava agg.	22	67	Tubificoides benedii	33	100	Mytilidae juv.	22	33
Tubificoides benedii	22	33	Pygospio elegans	33	67	Spionidae sp.	P	33
Enchytraeidae	22	33	Hydrobia ulvae	22	67			
Streblospio shrubsolii	11	33	Hediste diversicolor	11	33			
Manayunkia aestuarina	11	33	Manayunkia aestuarina	11	33			
Mytilidae juv.	11	33	Enchytraeidae	11	33			
Ascidiacea sp.	P	33	Nereididae sp.	P	33			

Control North Low Shore			**Impact Low Shore**			**Control South Low Shore**		
Taxa	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**
Macoma balthica	0.5825	100	Macoma balthica	0.5729	100	Nephtys hombergii	0.0990	100
Hydrobia ulvae	0.0114	33	Nephtys hombergii	0.0756	67	Macoma balthica	0.0377	67
Eteone longa/flava agg.	0.0048	67	Hydrobia ulvae	0.0166	67	Spionidae sp.	0.0089	33
Nematoda	0.0004	33	Nereididae sp.	0.0035	33	Tubificoides benedii	0.0007	67
Tubificoides benedii	0.0004	33	Nematoda	0.0004	33	Mytilidae juv.	0.0001	33
Streblospio shrubsolii	0.0002	33	Pygospio elegans	0.0004	67			
Manayunkia aestuarina	0.0002	33	Tubificoides benedii	0.0002	100			
Enchytraeidae	0.0001	33	Manayunkia aestuarina	0.0002	33			
Mytilidae juv.	0.0001	33	Hediste diversicolor	0.0002	33			
Ascidiacea sp.	P	33	Enchytraeidae	0.0001	33			

Table 11. Average ranked abundance and biomass (per 1m^2) for the mid shore sites at Cherry Cobb Sands.

Control North Mid Shore			**Impact Mid Shore**			**Control South Mid Shore**		
Taxa	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**
Nematoda	4967	100	Tubificoides benedii	20422	100	Tubificoides benedii	4375	100
Tubificoides benedii	3333	67	Nematoda	3733	100	Macoma balthica	2908	100
Hediste diversicolor	611	100	Hediste diversicolor	1911	100	Pygospio elegans	833	100
Enchytraeidae	611	100	Pygospio elegans	1856	100	Nematoda	375	75
Manayunkia aestuarina	333	100	Macoma balthica	1822	100	Hediste diversicolor	200	75
Pygospio elegans	267	100	Hydrobia ulvae	1811	100	Bathyporeia sarsi	133	25
Hydrobia ulvae	256	100	Enchytraeidae	811	100	Nephtys hombergii	108	75
Macoma balthica	100	67	Streblospio shrubsolii	33	67	Corophium volutator	92	50
Streblospio shrubsolii	100	33	Eteone longa/flava agg.	22	67	Eteone longa/flava agg.	50	50
Collembola sp.	78	33	Cyathura carinata	22	67	Hydrobia ulvae	42	75
Abra tenuis	11	33	Diptera sp.	11	33	Enchytraeidae	42	50
			Acarina sp.	11	33	Tharyx sp.	42	25
						Caulleriella killariensis	17	25
						Nemertea	8	25
						Streblospio shrubsolii	8	25
						Sphaerodoropsis baltica	8	25
						Scoloplos armiger	8	25
						Cyathura carinata	8	25
						Retusa obtusa	8	25
						Alderia modesta	8	25
						Mytilidae juv.	8	25

Control North Mid Shore			Impact Mid Shore			Control South Mid Shore		
Taxa	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**
Hediste diversicolor	2.9365	100	Macoma balthica	8.9790	100	Macoma balthica	5.8951	100
Macoma balthica	0.7195	67	Hediste diversicolor	4.2919	100	Hediste diversicolor	0.6878	75
Tubificoides benedii	0.1714	67	Tubificoides benedii	1.1269	100	Nephtys hombergii	0.5972	75
Hydrobia ulvae	0.1000	100	Hydrobia ulvae	0.4687	100	Tubificoides benedii	0.2129	100
Nematoda	0.0409	100	Pygospio elegans	0.0486	100	Corophium volutator	0.0349	50
Abra tenuis	0.0197	33	Nematoda	0.0298	100	Pygospio elegans	0.0325	100
Pygospio elegans	0.0083	100	Eteone longa/flava agg.	0.0153	67	Bathyporeia sarsi	0.0268	25
Manayunkia aestuarina	0.0023	100	Diptera sp.	0.0132	33	Eteone longa/flava agg.	0.0177	50
Collembola sp.	0.0015	33	Enchytraeidae	0.0026	100	Scoloplos armiger	0.0142	25
Enchytraeidae	0.0015	100	Streblospio shrubsolii	0.0004	67	Hydrobia ulvae	0.0136	75
Streblospio shrubsolii	0.0005	33	Cyathura carinata	0.0003	67	Tharyx sp.	0.0065	25
			Acarina sp.	0.0002	33	Retusa obtusa	0.0041	25
						Cyathura carinata	0.0018	25
						Nematoda	0.0012	75
						Nemertea	0.0002	25
						Alderia modesta	0.0001	25
						Enchytraeidae	0.0001	50
						Streblospio shrubsolii	0.0001	25
						Sphaerodoropsis baltica	0.0001	25
						Caulleriella killariensis	0.0001	25
						Mytilidae juv.	0.0000	25

Table 12. Average ranked abundance and biomass (per 1m^2) for the upper shore sites at Cherry Cobb Sands.

Control North Upper Shore			Impact Upper Shore			Control South Upper Shore		
Taxa	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**	**Taxa**	**Mean Abundance per m^2**	**% of sites**
Tubificoides agg. (pseudogaster)	9144	67	Tubificoides benedii	13489	100	Tubificoides benedii	13222	100
Nematoda	2367	100	Nematoda	2289	100	Macoma balthica	4100	100
Enchytraeidae	1544	67	Hydrobia ulvae	1356	100	Pygospio elegans	1378	100
Hediste diversicolor	1178	100	Hediste diversicolor	989	100	Nematoda	989	100
Manayunkia aestuarina	722	67	Pygospio elegans	589	100	Hediste diversicolor	600	100
Diptera sp.	411	67	Macoma balthica	456	100	Eteone longa/flava agg.	133	100
Hydrobia ulvae	100	33	Enchytraeidae	389	100	Hydrobia ulvae	133	67
Pygospio elegans	78	67	Manayunkia aestuarina	67	100	Tubificoides agg. (pseudogaster)	100	67
Tubificoides benedii	44	33	Diptera sp.	22	67	Abra tenuis	44	67
Collembola sp.	33	67	Eteone longa/flava agg.	11	33	Dalyelliidae sp.	22	33
Streblospio shrubsolii	11	33	Streblospio shrubsolii	11	33	Streblospio shrubsolii	11	33
Acarina sp.	11	33	Alderia modesta	11	33	Manayunkia aestuarina	11	33
			Abra sp.	11	33	Cyathura carinata	11	33
						Scrobicularia plana	11	33
						Diptera sp.	11	33

Control North Upper Shore			Impact Upper Shore			Control South Upper Shore		
Taxa	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**	**Taxa**	**Mean AFDW Biomass (g) per m^2**	**% of sites**
Hediste diversicolor	8.4546	100	Hediste diversicolor	4.6821	100	Macoma balthica	14.4060	100
Tubificoides agg. (pseudogaster)	0.3133	67	Macoma balthica	2.4708	100	Hediste diversicolor	4.7066	100
Diptera sp.	0.0796	67	Tubificoides benedii	0.8563	100	Tubificoides benedii	0.7009	100
Hydrobia ulvae	0.0226	33	Hydrobia ulvae	0.2408	100	Eteone longa/flava agg.	0.1077	100
Nematoda	0.0139	100	Diptera sp.	0.0352	67	Pygospio elegans	0.0849	100
Enchytraeidae	0.0098	67	Pygospio elegans	0.0180	100	Abra tenuis	0.0546	67
Manayunkia aestuarina	0.0062	67	Nematoda	0.0174	100	Hydrobia ulvae	0.0235	67
Tubificoides benedii	0.0013	33	Abra sp.	0.0093	33	Diptera sp.	0.0190	33
Pygospio elegans	0.0005	67	Eteone longa/flava agg.	0.0050	33	Nematoda	0.0061	100
Collembola sp.	0.0005	67	Enchytraeidae	0.0015	100	Tubificoides agg. (pseudogaster)	0.0053	67
Streblospio shrubsolii	0.0002	33	Manayunkia aestuarina	0.0005	100	Scrobicularia plana	0.0047	33
Acarina sp.	0.0002	33	Alderia modesta	0.0002	33	Dalyelliidae sp.	0.0003	33
			Streblospio shrubsolii	0.0002	33	Streblospio shrubsolii	0.0002	33
						Manayunkia aestuarina	0.0002	33
						Cyathura carinata	0.0002	33

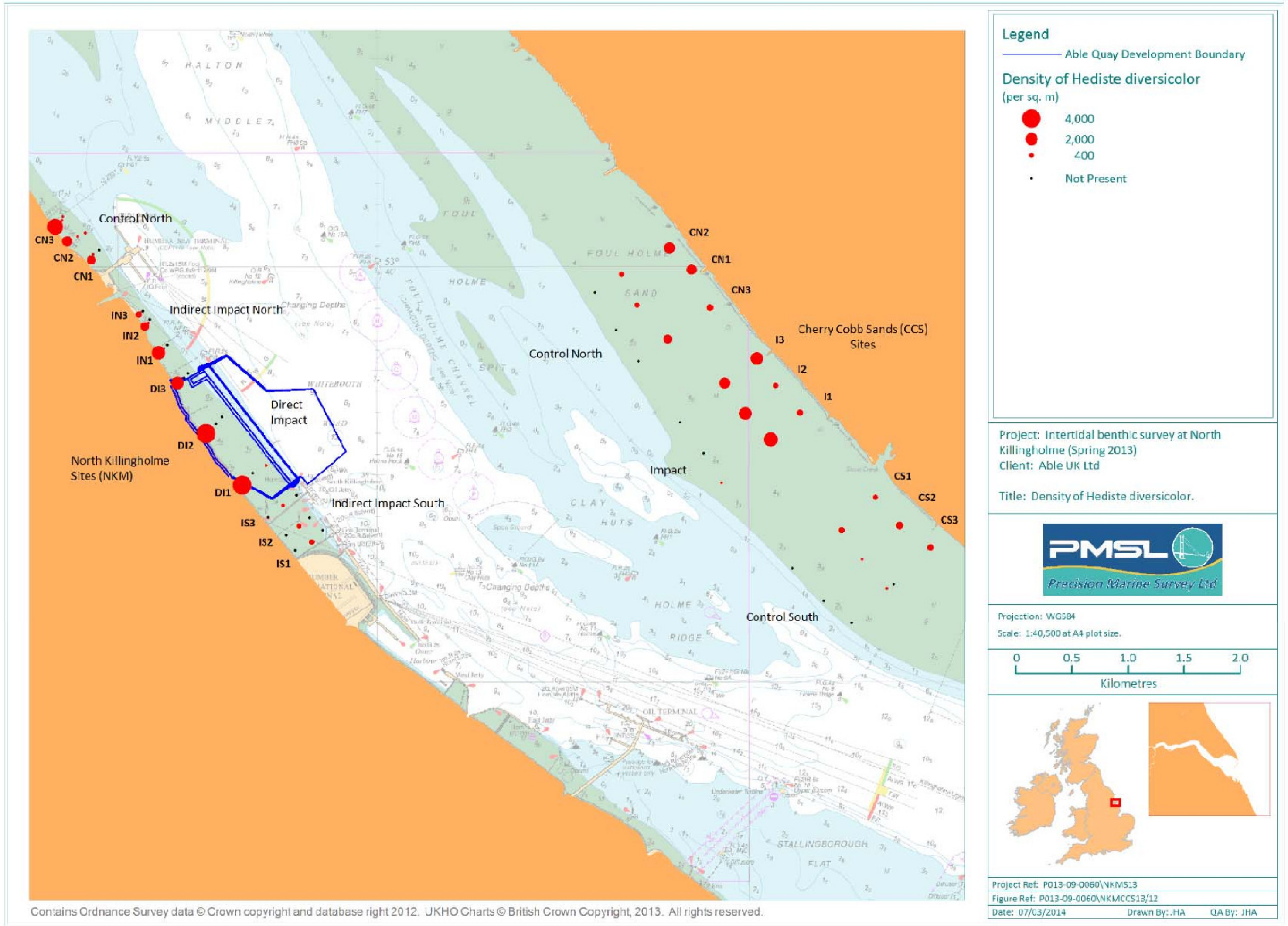

Figure 14. Spatial distribution in numbers of *Hediste diversicolor* (per 1m^2).

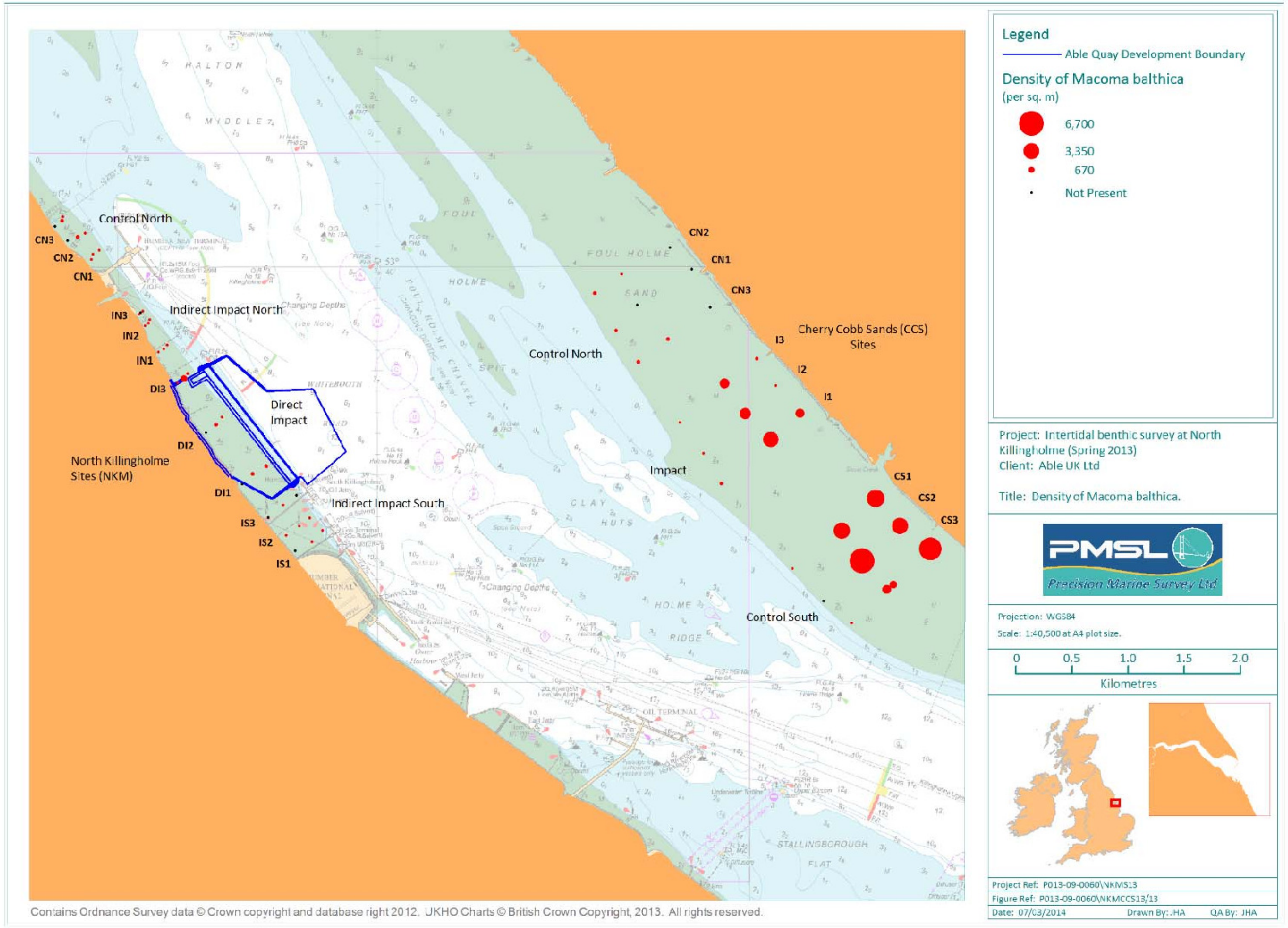

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Figure 15. Spatial distribution in numbers of *Macoma balthica* (per 1m^2).

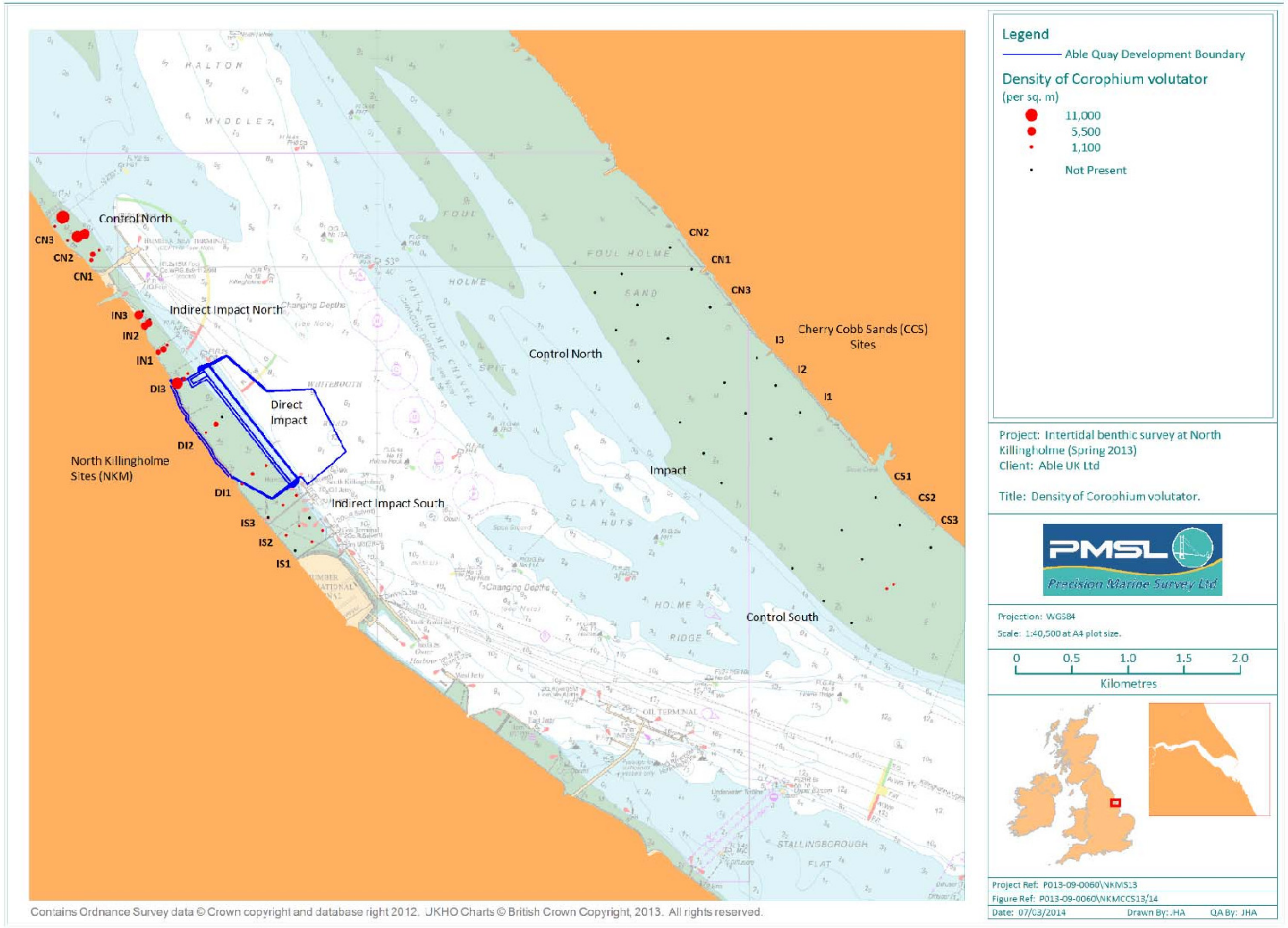

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Figure 16. Spatial distribution in numbers of *Corophium volutator* (per 1m^2).

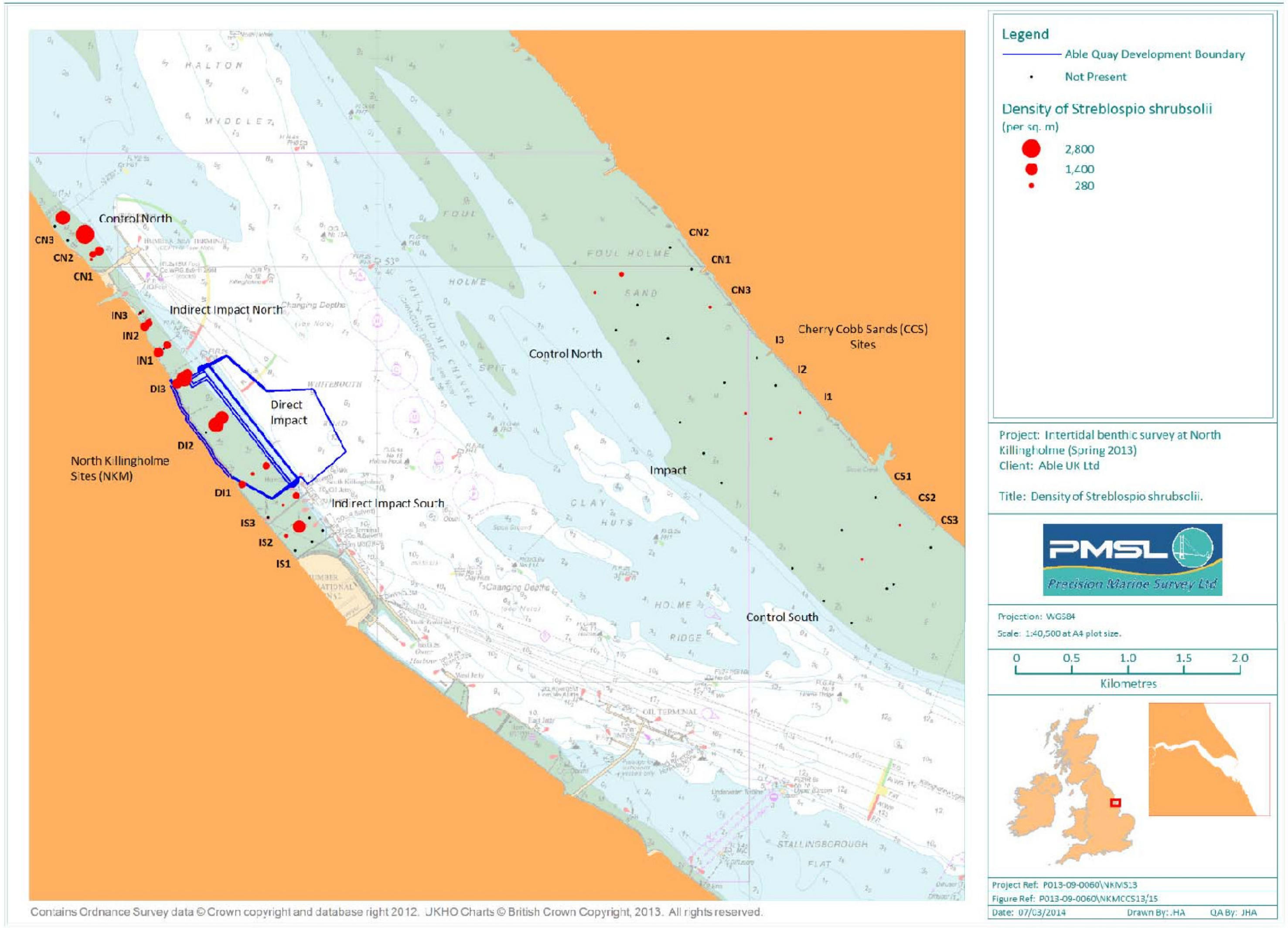

Figure 17. Spatial distribution in numbers of *Streblospio shrubsolii* (per 1m^2).

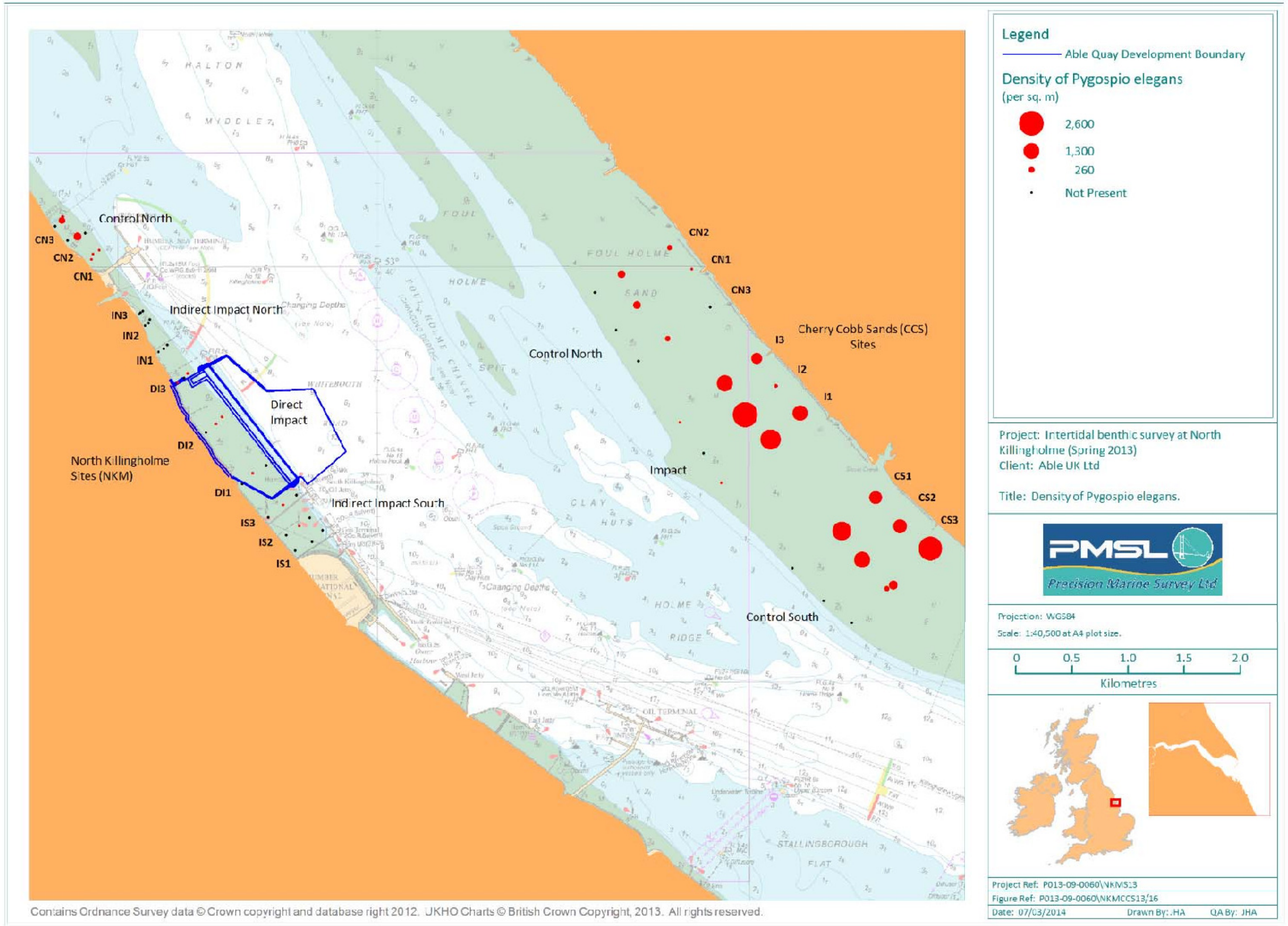

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Figure 18. Spatial distribution in numbers of *Pygospio elegans* (per $1m^2$).

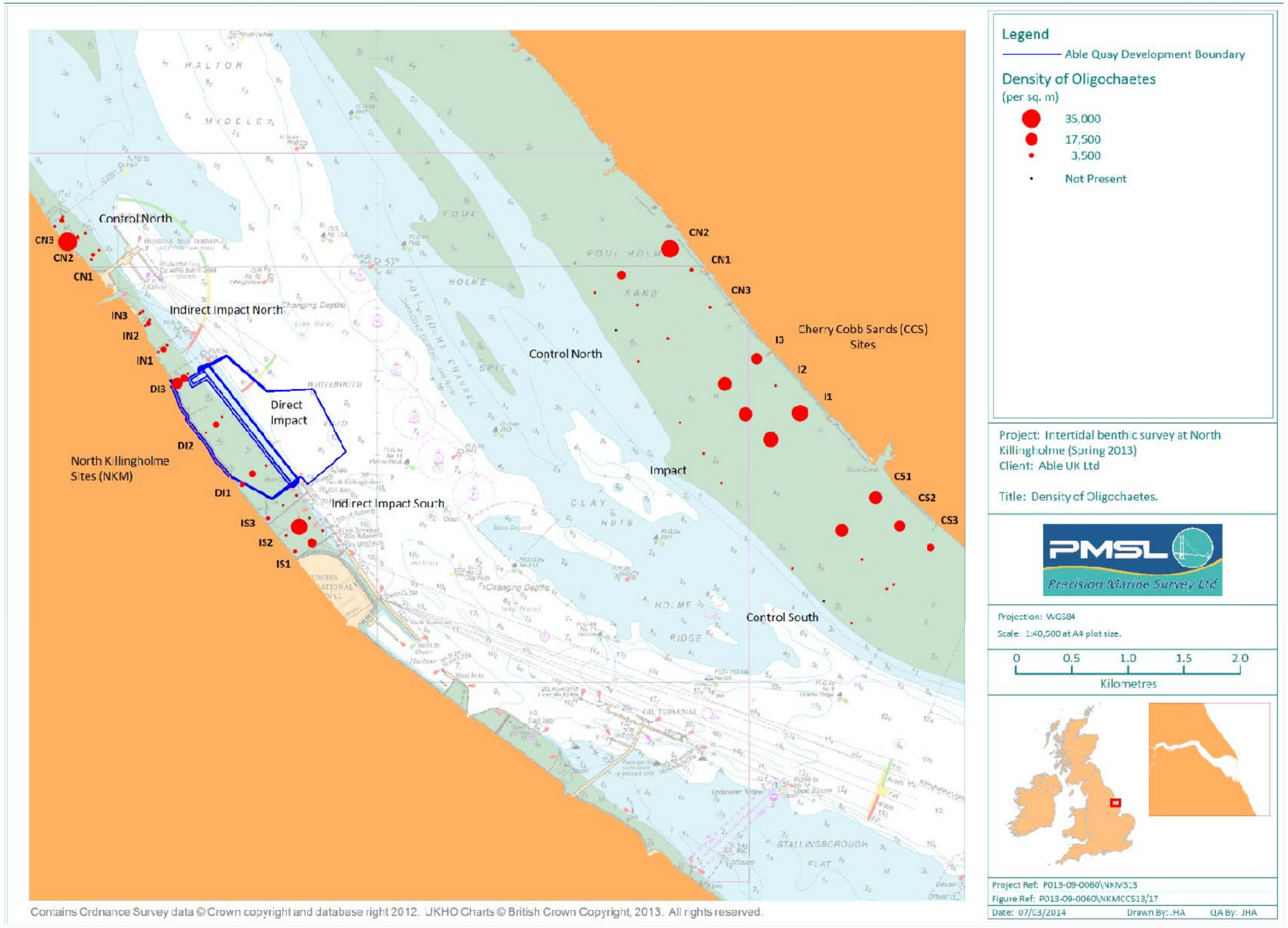

Figure 19. Spatial distribution in numbers of *oligochaete taxa* (per $1m^2$).

3.4 Multivariate Analysis of Community Structure

Multivariate analysis of the abundance data (following square root transformation) was carried out in order to describe the main patterns and assemblages within the area. Classification (cluster analysis) of the data was undertaken using the Bray-Curtis similarity coefficient and grouped average (UPGMA) clustering technique followed by a non-metric MDS (multi-dimensional scaling) ordination both using the PRIMER package (Clarke & Warwick, 2001). Cluster analysis is used to display graphically the similarity between sites based upon their species composition whereby the similarity between sites is calculated (in this case using the Bray-Curtis similarity coefficient) to produce a similarity matrix showing the percent similarity of sites (0% indicating no species in common and 100% indicating an identical community).

These values were then used to plot a dendrogram or tree diagram in which sites are linked at their respective similarity to other sites and consequently it is possible to define groups of sites with similar species composition at a predefined level of similarity. Non metric MDS graphically displays the (rank) similarity between sites as a 2 dimensional plot in which the distances between sites indicates the level of similarity between them. The stress value associated with an MDS plot indicates the how faithful the plot is in representing the similarity between sites with low values (below 0.2) generally indicating a good fit. The station groupings derived from cluster analysis have subsequently been superimposed onto the MDS plots and input into GIS and the dominant species and mean environmental and biological parameters for each group calculated. Site groupings were derived using the similarity profile test (SIMPROF) within the PRIMER package. Characteristic taxa within each group were assessed using the SIMPER routine in PRIMER along with calculations of mean abundance and the % of sites at which the species occurred.

Analysis was undertaken in a number of permutations as follows. Initially analysis was carried out using replicate data for both NKM and CCS. Use of replicate data allows an assessment of variability within a site and also may be used for statistical analysis e.g. using ANOSIM routines in PRIMER. Analysis at a site level (i.e. replicates combined) was also carried out for NKM and CCS and also for the combined dataset for both survey areas simultaneously. Analysis at a site level simplifies assessment of spatial patterns in community structure which integrates small scale variability/noise at the sites and is useful in defining biotopes for the survey area as these are defined at a site level and given that individual replicates were sampled directly in close proximity from identical sediments there is no risk of pooling samples from widely differing habitats. Aside from simplifying interpretation of biotopes this also allowed correlations between species data and sedimentary data using the BEST routine within PRIMER.

Results of multivariate analysis on replicate data for NKM and CCS are provided in Appendices 8 and 9. These indicated a series of sample groups at varying levels of similarity ranging from 10% to over 80% which separate the main communities in the respective survey areas. Aside from a few outlier replicate samples which had no taxa the replicate samples from the same sites tended to fall into the same groups (i.e. are clustered together) although there is a degree of intra-site variability as is usually the case, particularly in dynamic estuarine environments.

In general the results of the replicate analysis defined a similar range of site groups (communities) to those identified using site data (with replicates combined) and the combined analysis of NKM and CCS site data together indicated that the sites from each area were generally separated into different groups. The site groups from the combined dataset generally matched those derived when the data from NKM and CCS were analysed separately so to avoid repetition the results discussed here are those based on the combined NKM and CCS dataset.

The results of cluster analysis on the NKM and CCS data are shown in Figures 20 to 22 which show the dendrogram with symbols to show SIMPROF group (Figure 20), survey area (Figure 21) and shore level (Figure 22). The spatial distribution of cluster groups and derived biotopes are provided in Figures 23 and 24 whilst the results of nMDS (with separate plots to highlight group, survey area and shore level) are provided in Figure 25. A high level of variability between sites is present with similarities between sites varying from under 5% to over 90% and SIMPROF derived 14 site groups. The results of cluster analysis and ordination highlight a degree of separation between survey areas (and particularly between NKM and CCS sites) whilst differences based on shore level were also relatively well defined.

The characteristic taxa at the sites in each group are highlighted in Table 13 which includes contribution to group similarity (from SIMPER analysis) along with mean abundance (per $0.01m^2$ and $1m^2$) and the frequency of occurrence (% of sites) for each species (species which account for no similarity are not included in the table). Also provided are the list of sites in each group and a summary of sedimentary parameters.

Group a includes a single site from the low shore at CCS (CS2L) which contained only a single taxa (*Nephtys hombergii*) in sandy sediments and this sites was separated at less than 5% similarity from the remaining sites. Group b included five upper shore sites from both NKM and CCS which were all characterised by sandy mud and species such as *Tubificoides* agg. (*pseudogaster*) and insect taxa (Collembola sp. and Diptera sp.) with other taxa such as Nematoda, *Hediste diversicolor* and Enchytraeidae oligochaetes occurring in variable numbers. Group c included two mid shore sites from the southernmost control transect at CCS in muddy sand with moderate numbers of *Macoma balthica* along with *Pygospio elegans*, *Nephtys hombergii*, *Corophium volutator* and *Tubificoides benedii*.

Group d includes a series of relatively impoverished low shore sites from both NKM and CCS which includes sandy or muddy sand sites from CCS and sandy mud sites from NKM. These sites are characterised by low numbers of *Macoma balthica* and occasional other taxa such as *Tubificoides benedii*, *Nephtys hombergii*, *Streblospio shrubsolii* and *Hydrobia ulvae*. Group e contains mid shore sites from the northern control area and a mid and upper shore site from the impact area at CCS. These sites were all characterised by sandy mud with high numbers of Nematode worms along with *Hediste diversicolor*, *Manayunkia aestuarina* and *Tubificoides benedii*. Other taxa present include low to moderate numbers of *Pygospio elegans*, *Hydrobia ulvae*, Enchytraeidae, *Macoma balthica* and *Streblospio shrubsolii*.

Groups f and g comprise of individual mid shore sandy mud sites from CCS and NKM respectively which are characterised by *Macoma balthica*, *Pygospio elegans*, *Tubificoides benedii*, Nematoda and *Nephtys hombergii* (group f) or *Tubificoides benedii*, *Hediste* *diversicolor*, *Manayunkia aestuarina* and *Corophium volutator* (group g). Groups h and I contains sites from the mid and upper shore within the CCS impact area (group h) or the southern control area (group i). These sites exhibit very high similarities (>80% similarity) and are all characterised by sandy mud with high numbers of *Tubificoides benedii* along with Nematoda, *Hediste diversicolor*, *Hydrobia ulvae*, *Pygospio elegans* and *Macoma balthica* with a variety of other taxa in lower numbers. Essentially these groups are very similar and both heavily dominated by high densities of *Tubificoides benedii* but differ in rank dominance of taxa with *Hediste diversicolor* more important in group h and *Macoma balthica* more important in group i.

Group j comprises of two mid shore sites from NKM from the direct impact and southern indirect impact area with somewhat similar species composition to groups h and i and dominated by *Tubificoides benedii* along with *Streblospio shrubsolii*, Nematoda, *Hediste diversicolor*, *Macoma balthica* and *Pygospio elegans* but also quite high densities of *Corophium volutator*. Group k comprises of upper or mid shore sites from NKM in mud or sandy mud which are dominated by moderately high abundances of Hediste diversicolor along with *Corophium volutator* and lower numbers of *Tubificoides* oligochaetes.

Group l contains predominantly upper shore sites (and one mid shore site) from the northern control and indirect impact area at NKM in sandy mud with quite high numbers of *Corophium volutator* along with moderate densities of *Hediste diversicolor*, Enchytraeidae, *Tubificoides benedii*, *Streblospio shrubsolii*, Nematoda and *Macoma balthica*. Group m contains a number of midshore and occasional low shore sites from NKM which are also dominated by high numbers of *Corophium volutator* but with moderate densities of *Tubificoides benedii* and *Streblospio shrubsolii* along with lower numbers of taxa such as Nematoda, *Macoma balthica*, *Pygospio elegans* and *Hediste diversicolor* which occur sporadically at certain sites.

Group n contains the remaining low shore sites (and one upper shore site) from NKM which are characterised by moderate numbers of *Streblospio shrubsolii* and *Tubificoides benedii* along with occasional other taxa such as *Corophium volutator*, *Macoma balthica*, Nematoda, *Tubificoides swirencoides*, *Pygospio elegans* and *Nephtys hombergii* which occur in lower densities with varying distribution.

Overall, whilst there is a degree of complexity in terms of benthic community structure and distribution it is evident that many of the observed differences in invertebrate communities are rather subtle as opposed to distinct changes in assemblage. Aside from differences in relation to shore level multivariate analysis also highlighted some differences between survey areas and particularly between NKM and CCS. However, such differences predominantly reflect differences in sediment type and particularly at CCS where there is much greater variation in key sedimentary parameters. The BEST routine in Primer was used to identify correlations between sediment type and shore level (distance from high water) and the patterns in community structure. The results of the BEST routine indicated that all parameters had some correlation to the species data with the parameters median and mean phi grain size having the best correlation (0.473 and 0.464) followed by % sand and mud (0.44) and distance from high water (0.423). Slightly lower correlations were exhibited by other parameters (% LOI: 0.393; sorting: 0.258; kurtosis: 0.255 and skewness: 0.234). The best combination of parameters to correlate with the patterns in species data were mean and median grain size, % mud or sand , % LOI and distance from high water which collectively exhibited a correlation of 0.483.

Whilst more obvious differences in communities could be identified between site groups which had widely differing sediment types (or shore height) the differences between many of the individual cluster groups were often quite subtle and tended to highlight differences in the relative dominance of similar groups of taxa or reflect the distribution of specific taxa which are present in one area but not another. At a broader (survey) level for example the SIMPER routine highlighted *Tubificoides benedii*, *Corophium volutator*, *Streblospio shrubsolii*, Nematoda, *Macoma balthica* and *Hediste diversicolor* as the most characteristic taxa (explaining >90% of similarity) whilst for CCS key taxa are *Macoma balthica*, *Tubificoides benedii*, Nematoda, *Hediste diversicolor*, *Pygospio elegans*, *Hydrobia ulvae* and Enchytraeidae. Key taxa which accounted for differences between the two survey areas included *Tubificoides benedii*, *Corophium volutator* and Nematoda which accounted for over 40% dissimilarity followed by *Hediste diversicolor*, *Macoma balthica*, *Streblospio shrubsolii*, *Tubificoides* agg. (*pseudogaster*), *Pygospio elegans*, Enchytraeidae, *Hydrobia ulvae*, *Manayunkia aestuarina* and *Nephtys hombergii*. These results highlight a degree of overlap between NKM and CCS in terms of broad community composition but also the importance of certain taxa in relation to the observed differences between survey areas - notably *Corophium volutator* which is widespread at NKM but largely absent from CCS.

At a biotope level many of the observed communities appear to be variants of typical estuarine biotopes as classified under the current UK classification (Connor et al. 2004) and a map showing the distribution of main biotopes is provided in Figure 24. Areas of upper shore sandy mud at both NKM and CCS which have greater elevation and often in closer proximity to saltmarsh (e.g. group b) are usually characterised by *Tubificoides* spp. (notably *T. pseudogaster*) along with variable densities of *Hediste diversicolor* or other polychaetes and insect taxa. These appear to be mid estuarine, upper shore variants of biotopes more commonly found in upper estuarine areas namely *LS.LMu.Uest (Polychaete/oligochaete-dominated upper estuarine mud shores) or LS.LMu.UEst.Hed (Hediste diversicolor in littoral mud).* In certain upper shore areas at NKM or CCS these resemble somewhat transitional variants of sub-biotopes such as*, LS.LMu.UEst.Hed.Ol (Hediste diversicolor and oligochaetes in littoral mud)* or *LS.LMu.UEst.Tben (Tubificoides benedii and other oligochaetes in littoral mud)* depending on the level of dominance by oligochaetes or *Hediste diversicolor*.

Poorly defined or impoverished muddy sands or sands on the low shore at CCS (groups a and d) with variable but generally low numbers of *Nephtys hombergii*, *Macoma balthica* and *Tubificoides benedii* are defined as *LS.LSa.MuSa (Polychaete/bivalve-dominated muddy sand shores)* or *LS.LSa (Littoral Sand)* and presumably reflect relatively dynamic environments. Low shore habitats at NKM tend to be much muddier and examples of these low shore sandy muds at sites in group d have a fairly poorly defined infaunal community perhaps indicating sediment instability and are classified as *LS.LSa.MuSa* but are potentially variants of *LS.LMu.MEst.NhomMacStr (Nephtys hombergii, Macoma balthica and Streblospio shrubsolii in littoral sandy mud)*. These habitats tend to be relatively impoverished and characterised by low to moderate numbers of *Streblospio shrubsolii*, and *Tubificoides benedii* and occasional *Macoma balthica*, *Nephtys hombergii* and *Corophium volutator*. Muddy sands on the mid shore were restricted to one area at the southern end of CCS (group c) which was characterised by *Macoma balthica*, *Pygospio elegans* and *Nephtys hombergii* fall under the biotope *LS.LSa.MuSa.MacAre (Macoma balthica and Arenicola marina in littoral muddy sand)*. Variable populations of *Arenicola marina* were evident in this area from observations of surface casts (usually up to 5 to 10 per m^2) but this taxa was not picked up during core sampling due to their patchy distribution.

Groups e to j form a series of closely related groups which are cluster together at around 45% similarity and are predominantly mid shore or less elevated upper shore sandy mud sites at CCS (with occasional sites from NKM). These sites tend to be the most diverse areas with a variety of taxa including varying abundances of taxa such as *Macoma balthica*, *Tubificoides benedii*, *Hediste diversicolor*, *Pygospio elegans* and *Manayunkia aestuarina*. The majority of sites in these groups are variants of *LS.LMu.MEst.HedMac (Hediste diversicolor and Macoma balthica in littoral sandy mud*) although the mid shore habitats from CCS in groups h and i tend to form the more typical examples of this biotope with higher abundances *Macoma balthica* and *Hediste diversicolor* and relatively diverse infaunal assemblages. Certain sites at CCS (group e) and NKM (sites in groups g and j) are somewhat variable and whilst moderate numbers of *Macoma balthica* and *Hediste diversicolor* indicate the biotope *LS.LMu.MEst.HedMac* these communities are less well defined and are considered transitional forms of the biotope.

The remaining sites in groups k to n exhibit a degree of similarity to the sites in groups e to j and are separated from them at around 30% similarity and include both mid and upper shore sites (groups k to m) and lower shore sites (group n) from NKM. At many of the sites in groups k to m a transitional form of *LS.LMu.MEst.HedMac* appears to be present with but with lower numbers of *Macoma balthica* and a relatively high density of *Corophium volutator*, oligochaetes or *Streblospio shrubsolii*. Sites on the upper shore in group k which lack *Macoma balthica* could fall under the biotope *LS.LMu.UEst.Hed (Hediste diversicolor in littoral mud)* whilst other areas on the mid and upper shore at NKM (groups l and m) have a transitional form of *LS.LMu.MEst.HedMac* which also show some resemblance to upper estuarine biotopes such as *LS.LMu.UEst.Hed.Cvol (Hediste diversicolor and Corophium volutator in littoral mud)* or *LS.LMu.UEst.Hed.Str (Hediste diversicolor and Streblospio shrubsolii in littoral sandy mud)*. Sites in group n are loosely associated with groups l and m (at around 40% similarity) but are predominantly low shore sites with poorly defined communities and as described for group d above have been ascribed *LS.LSa.MuSa*. These could be an impoverished variant of *LS.LMu.MEst.NhomMacStr (Nephtys hombergii, Macoma balthica and Streblospio shrubsolii in littoral sandy mud)* or a perhaps a low shore continuation of *LS.LMu.MEst.HedMac* which is subject to sediment instability leading to the development of a reduced faunal assemblage.

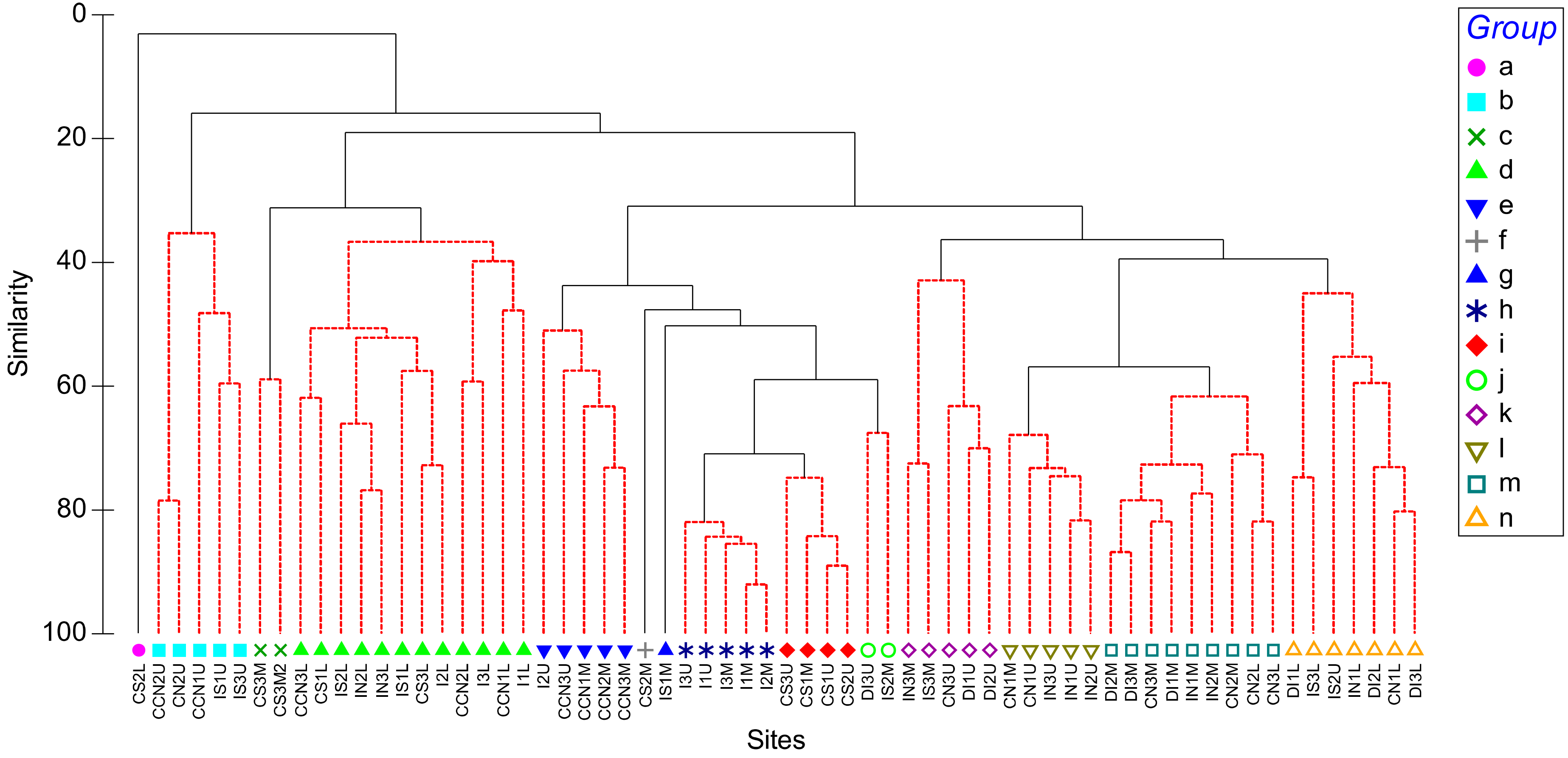

Figure 20. Results of cluster analysis on sites from North Killingholme & Cherry Cobb Sands (samples highlighted by group).

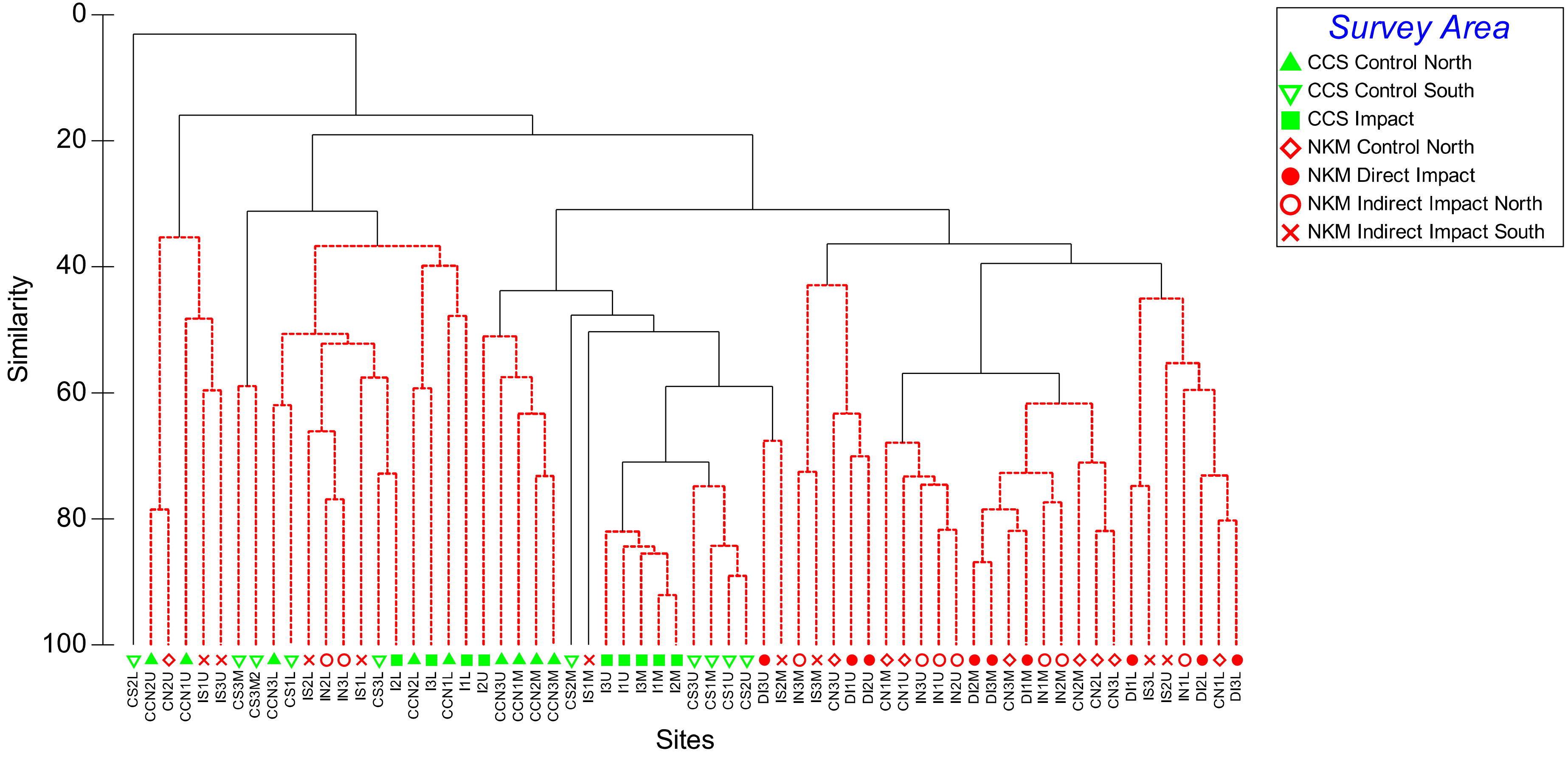

Figure 21. Results of cluster analysis on sites from North Killingholme & Cherry Cobb Sands (samples highlighted by area).

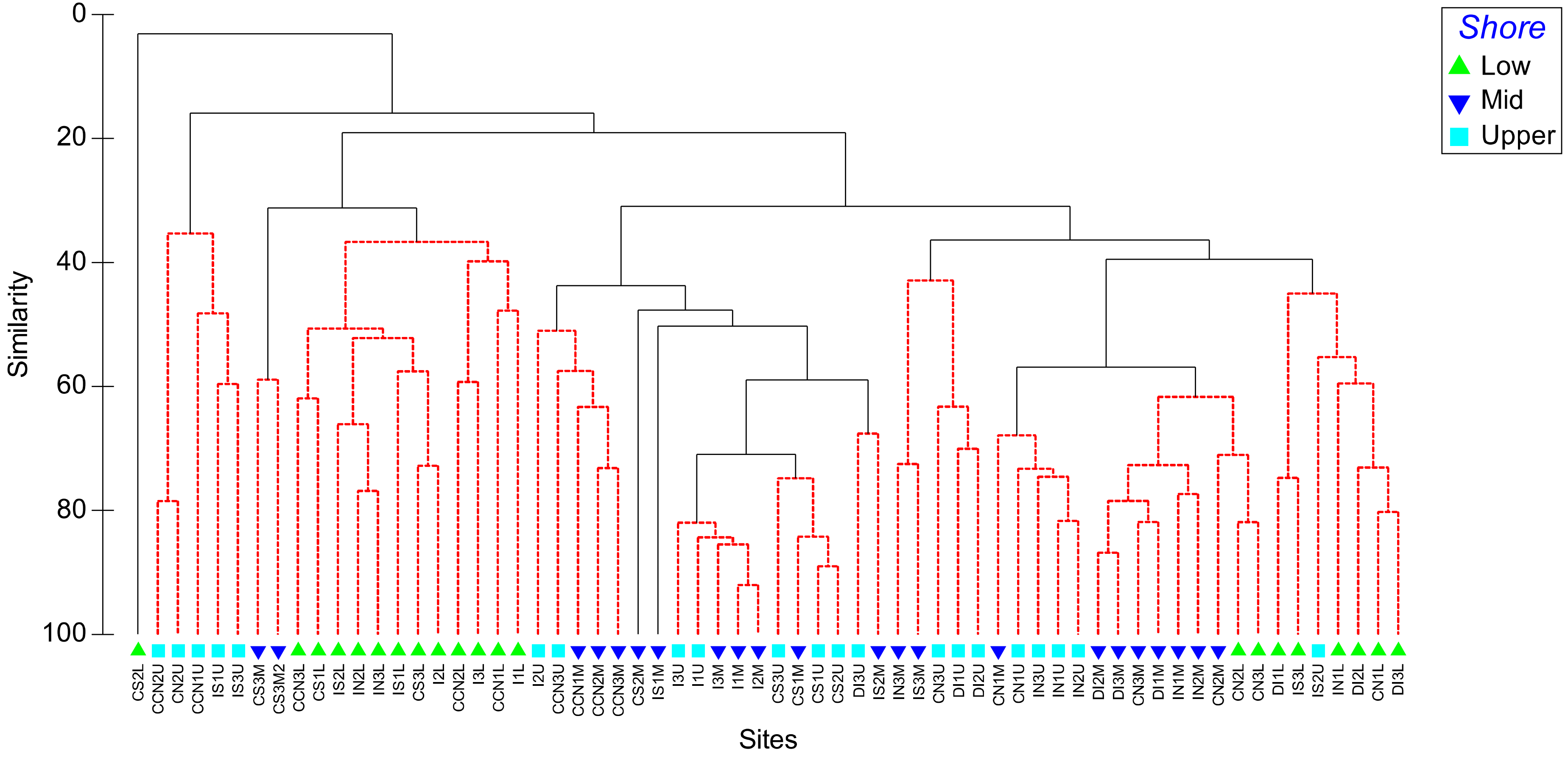

Figure 22. Results of cluster analysis on sites from North Killingholme & Cherry Cobb Sands (samples highlighted by shore).

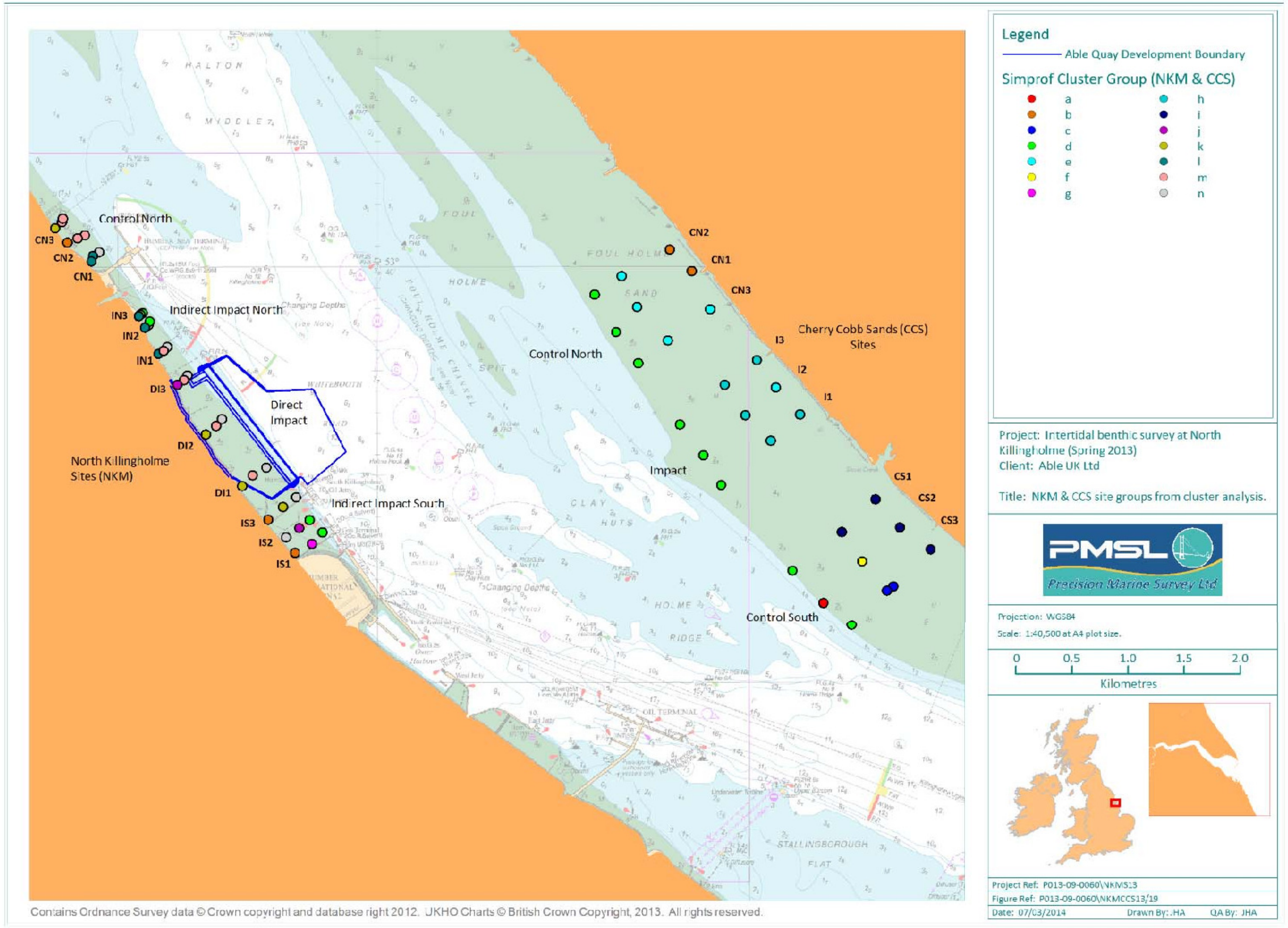

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Figure 23. Spatial distribution of site groups from cluster analysis of North Killingholme & Cherry Cobb Sands data.

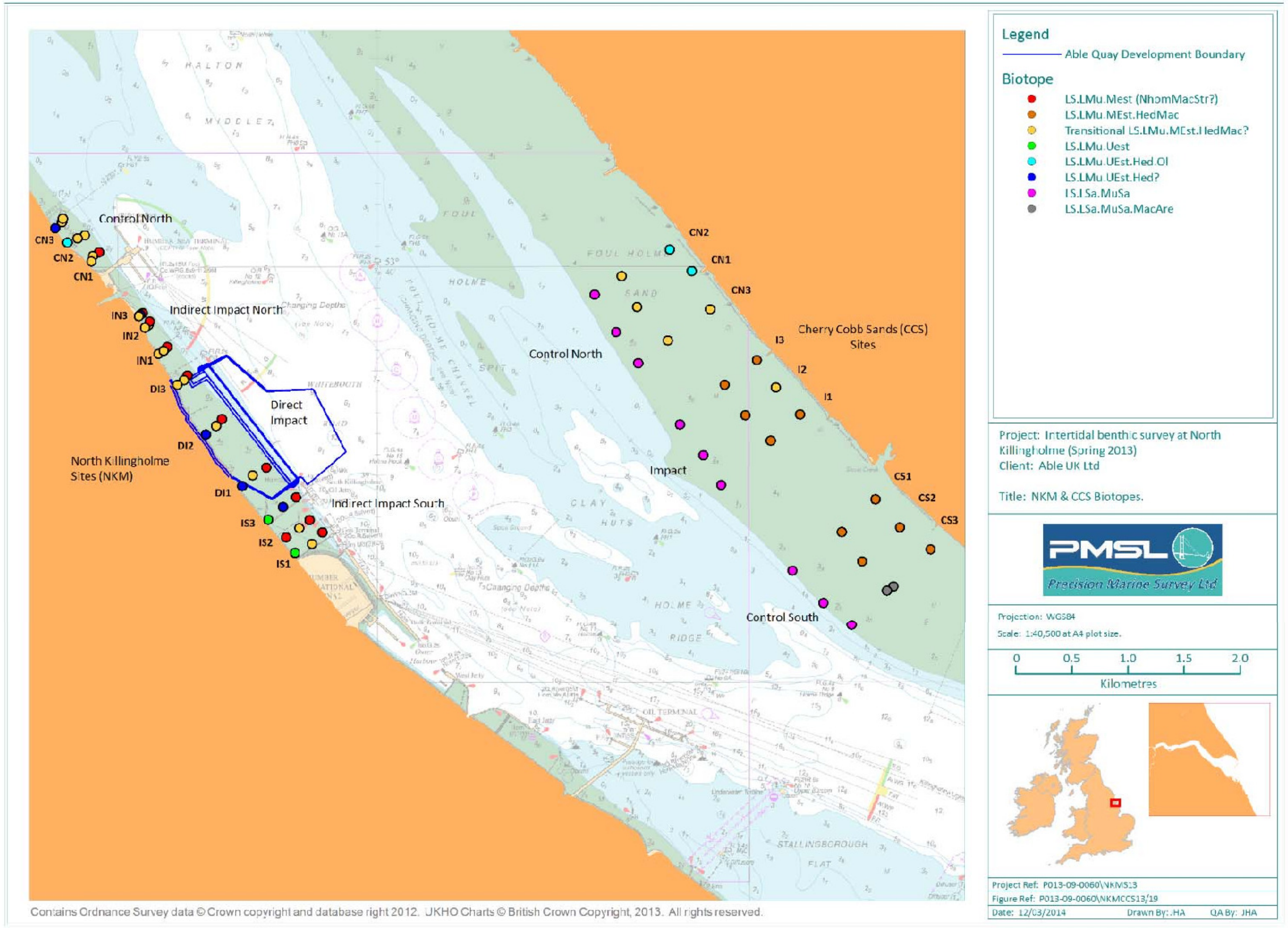

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Figure 24. Distribution of biotopes at North Killingholme and Cherry Cobb Sands.

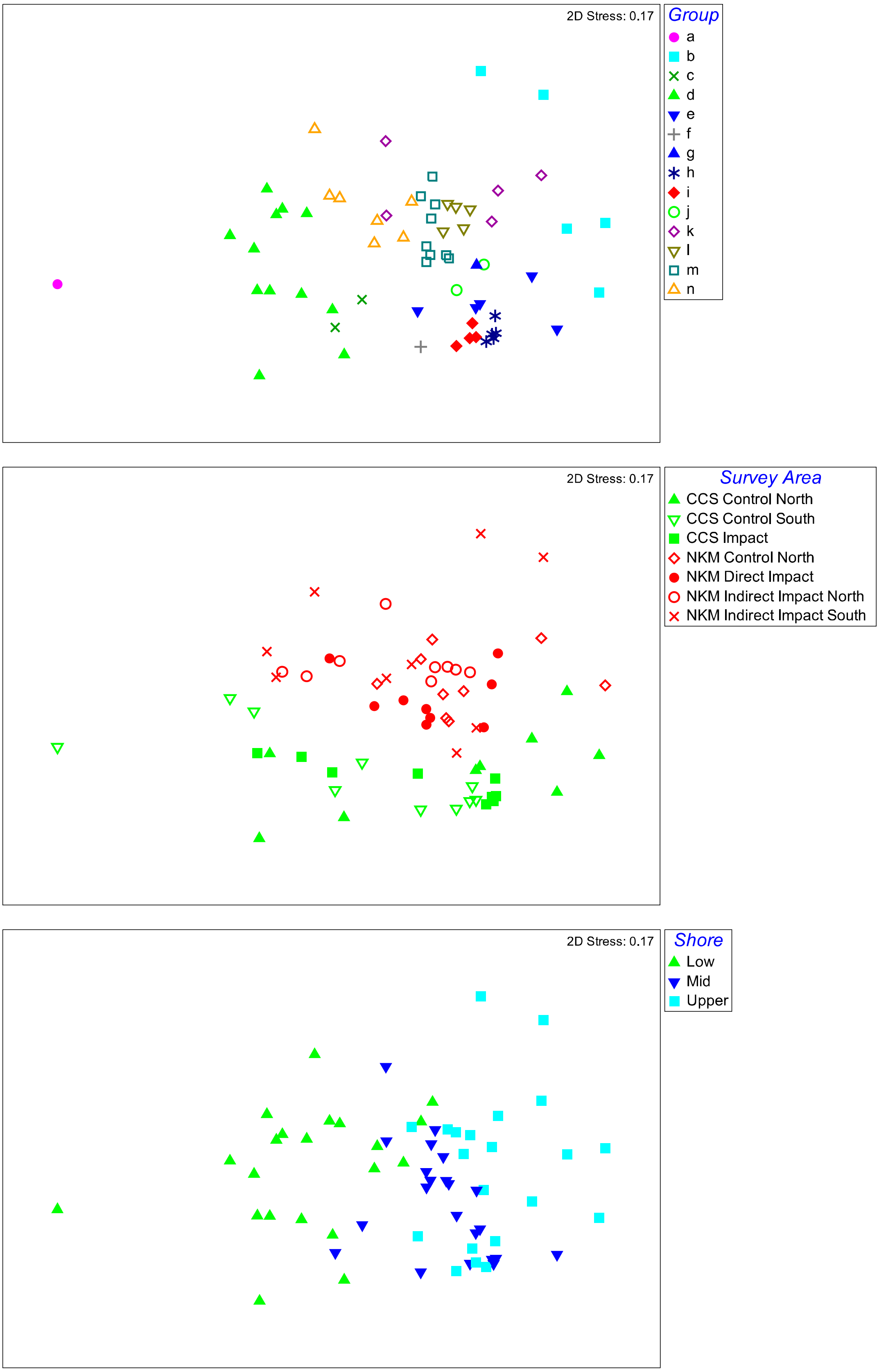

Figure 25. Results of nMDS on site data (North Killingholme & Cherry Cobb Sands) with samples highlighted by group, area and shore level.

Table 13. Characteristic taxa from SIMPER analysis of groups derived from cluster analysis for North Killingholme & Cherry Cobb Sands (site data).

Group a

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CS2L	CCS	Sand	2.473	97.45	2.55	1.41

Species	Abundance (per 0.01m^2)	Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Nephtys hombergii	0.67	67	-	-

Group b (Average similarity: 44.71%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CN1U	CCS	Sandy Mud	5.986	12.57	87.43	8.10
CN2U	CCS	Sandy Mud	5.646	19.98	80.02	9.75
CN2U	NKM	Sandy Mud	5.99	12.35	87.65	10.00
IS1U	NKM	Sandy Mud	6.21	11.71	88.29	11.73
IS3U	NKM	Sandy Mud	6.29	11.20	88.80	9.68

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Tubificoides agg. (pseudogaster)	112.47	11247	100	52.47
Collembola sp.	12.73	1273	100	12.4
Diptera sp.	3.13	313	100	10.2
Nematoda	10.33	1033	80	9.43
Hediste diversicolor	8.53	853	60	7.99
Enchytraeidae	27.47	2747	60	5.36
Tubificoides benedii	0.40	40	40	1.19
Pygospio elegans	0.47	47	40	0.65
Manayunkia aestuarina	0.80	80	40	0.32

Group c (Average similarity: 58.96%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CS3M	CCS	Muddy Sand	3.320	83.63	16.37	2.05
CS3M2	CCS	Muddy Sand	3.321	80.72	19.28	1.57

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Macoma balthica	9.50	950	100	47.13
Pygospio elegans	2.67	267	100	18.14
Nephtys hombergii	1.17	117	100	12.83
Corophium volutator	1.83	183	100	12.83
Tubificoides benedii	0.67	67	100	9.07

Group d (Average similarity: 45.16%)						
Sites	**Area**	**Sediment Type**	**Median Phi**	**% Sand**	**% Mud**	**% LOI**
CN1L	CCS	Muddy Sand	3.708	58.94	41.06	3.69
CN2L	CCS	Muddy Sand	3.710	61.94	38.06	3.46
CN3L	CCS	Muddy Sand	3.344	80.88	19.12	2.26
CS1L	CCS	Sand	2.879	91.34	8.66	1.55
CS3L	CCS	Muddy Sand	2.791	83.36	16.64	2.67
I1L	CCS	Sand	3.122	92.81	7.19	1.72
I2L	CCS	Sand	3.241	90.86	9.14	1.86
I3L	CCS	Muddy Sand	3.533	66.15	33.85	4.14
IN2L	NKM	Sandy Mud	5.57	15.33	84.67	6.89
IN3L	NKM	Sandy Mud	5.19	22.40	77.60	5.85
IS1L	NKM	Sandy Mud	4.05	48.46	51.54	5.36
IS2L	NKM	Sandy Mud	4.47	36.37	63.63	5.77
		Species	**Mean Abundance (per 0.01m^2)**	**Mean Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**
		Macoma balthica	1.17	117	100	54.82
		Tubificoides benedii	0.58	58	83	34.51
		Nephtys hombergii	0.22	22	33	3.71
		Streblospio shrubsolii	0.14	14	25	1.79
		Hydrobia ulvae	0.14	14	25	1.56
		Nematoda	0.22	22	25	1.51
		Mytilidae juv.	0.08	8	17	0.54
		Eteone longa/flava agg.	0.06	6	17	0.46
		Pygospio elegans	0.08	8	17	0.4
		Manayunkia aestuarina	0.06	6	17	0.35
		Enchytraeidae	0.08	8	17	0.35

Group e (Average similarity: 57.69%)						
Sites	**Area**	**Sediment Type**	**Median Phi**	**% Sand**	**% Mud**	**% LOI**
CN1M	CCS	Sandy Mud	5.163	20.37	79.63	6.23
CN2M	CCS	Sandy Mud	5.437	18.57	81.43	7.89
CN3M	CCS	Sandy Mud	5.074	22.08	77.92	7.03
CN3U	CCS	Sandy Mud	5.871	12.24	87.76	9.52
I2U	CCS	Sandy Mud	5.426	15.49	84.51	6.57
		Species	**Mean Abundance (per 0.01m^2)**	**Mean Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**
		Nematoda	36.67	3667	100	39.85
		Hediste diversicolor	5.60	560	100	20.2
		Manayunkia aestuarina	5.67	567	100	11.59
		Tubificoides benedii	20.53	2053	80	8.09
		Pygospio elegans	1.80	180	80	6.44
		Hydrobia ulvae	2.07	207	80	6.42
		Enchytraeidae	3.80	380	80	5.24
		Macoma balthica	0.67	67	60	1.7
		Streblospio shrubsolii	0.67	67	40	0.48

Group f						
Sites	**Area**	**Sediment Type**	**Median Phi**	**% Sand**	**% Mud**	**% LOI**
CS2M	CCS	Sandy Mud	4.437	38.23	61.77	4.50
		Species	**Abundance (per 0.01m^2)**	**Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**
		Macoma balthica	66.33	6633	-	-
		Pygospio elegans	12.33	1233	-	-
		Tubificoides benedii	11.33	1133	-	-
		Nematoda	6.00	600	-	-
		Nephtys hombergii	2.00	200	-	-
		Eteone longa/flava agg.	1.67	167	-	-
		Tharyx sp.	1.67	167	-	-
		Hediste diversicolor	1.33	133	-	-
		Hydrobia ulvae	1.00	100	-	-
		Caulleriella killariensis	0.67	67	-	-
		Streblospio shrubsolii	0.33	33	-	-
		Enchytraeidae	0.33	33	-	-
		Sphaerodoropsis baltica	0.33	33	-	-
		Retusa obtusa	0.33	33	-	-
		Mytilidae juv.	0.33	33	-	-

Group g						
Sites	**Area**	**Sediment Type**	**Median Phi**	**% Sand**	**% Mud**	**% LOI**
IS1M	NKM	Sandy Mud	5.48	17.83	82.17	8.99
		Species	**Abundance (per 0.01m^2)**	**Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**
		Tubificoides benedii	82.33	8233	-	-
		Hediste diversicolor	4.67	467	-	-
		Manayunkia aestuarina	4.00	400	-	-
		Corophium volutator	2.67	267	-	-
		Tubificoides agg. (pseudogaster)	0.67	67	-	-
		Nematoda	0.33	33	-	-
		Macoma balthica	0.33	33	-	-

Group h (Average similarity: 84.45%)						
Sites	**Area**	**Sediment Type**	**Median Phi**	**% Sand**	**% Mud**	**% LOI**
I1M	CCS	Sandy Mud	5.373	19.96	80.04	6.47
I1U	CCS	Sandy Mud	4.837	25.24	74.76	4.95
I2M	CCS	Sandy Mud	5.215	20.32	79.68	6.37
I3M	CCS	Sandy Mud	5.248	19.19	80.81	6.53
I3U	CCS	Sandy Mud	5.485	16.89	83.11	7.14
		Species	**Mean Abundance (per 0.01m^2)**	**Mean Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**
		Tubificoides benedii	203.20	20320	100	38.68
		Nematoda	35.40	3540	100	15.66
		Hediste diversicolor	16.53	1653	100	10.54
		Hydrobia ulvae	18.47	1847	100	10.12
		Pygospio elegans	14.47	1447	100	9.1
		Macoma balthica	13.60	1360	100	7.97
		Enchytraeidae	7.07	707	100	6.42
		Eteone longa/flava agg.	0.20	20	60	0.5
		Streblospio shrubsolii	0.27	27	60	0.48
		Manayunkia aestuarina	0.33	33	40	0.19
		Diptera sp.	0.13	13	40	0.18
		Cyathura carinata	0.13	13	40	0.16

Group i (Average similarity: 80.38%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CS1M	CCS	Sandy Mud	4.786	28.00	72.00	5.06
CS1U	CCS	Sandy Mud	4.540	33.02	66.98	5.00
CS2U	CCS	Sandy Mud	4.551	31.27	68.73	4.84
CS3U	CCS	Sandy Mud	4.309	40.29	59.71	4.53

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Tubificoides benedii	139.75	13975	100	41.93
Macoma balthica	38.50	3850	100	22.17
Pygospio elegans	14.25	1425	100	12.39
Nematoda	9.42	942	100	9.66
Hediste diversicolor	5.92	592	100	8.85
Eteone longa/flava agg.	1.00	100	75	2.09
Hydrobia ulvae	1.08	108	75	1.43
Tubificoides agg. (pseudogaster)	0.75	75	50	0.74
Cyathura carinata	0.17	17	50	0.37
Abra tenuis	0.33	33	50	0.37

Group j (Average similarity: 67.65%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
DI3U	NKM	Sandy Mud	5.60	17.35	82.65	8.47
IS2M	NKM	Sandy Mud	6.26	11.13	88.87	10.00

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Tubificoides benedii	205.83	20583	100	57.65
Streblospio shrubsolii	11.17	1117	100	14.65
Nematoda	9.50	950	100	9.81
Hediste diversicolor	12.00	1200	100	8.6
Macoma balthica	0.83	83	100	3.85
Pygospio elegans	0.50	50	100	2.72
Corophium volutator	48.67	4867	100	2.72

Group k (Average similarity: 52.72%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CN3U	NKM	Mud	6.36	7.74	92.26	9.82
DI1U	NKM	Sandy Mud	5.85	16.97	83.03	10.38
DI2U	NKM	Sandy Mud	5.77	14.70	85.30	8.65
IN3M	NKM	Sandy Mud	5.81	14.49	85.51	7.92
IS3M	NKM	Sandy Mud	5.72	16.66	83.34	8.97

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Hediste diversicolor	22.87	2287	100	42.8
Corophium volutator	3.33	333	100	29.44
Tubificoides benedii	8.93	893	80	22.08
Tubificoides agg. (pseudogaster)	3.27	327	40	3.14
Nematoda	0.80	80	40	1.46
Streblospio shrubsolii	1.20	120	40	1.08

Group l (Average similarity: 72.28%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CN1M	NKM	Sandy Mud	4.82	27.27	72.73	5.01
CN1U	NKM	Sandy Mud	5.27	18.63	81.37	7.16
IN1U	NKM	Sandy Mud	6.07	15.25	84.75	9.94
IN2U	NKM	Sandy Mud	5.93	14.15	85.85	8.37
IN3U	NKM	Sandy Mud	5.82	15.10	84.90	8.89

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Corophium volutator	31.60	3160	100	35.67
Hediste diversicolor	9.93	993	100	16.56
Enchytraeidae	4.27	427	100	12.98
Tubificoides benedii	4.87	487	100	10.47
Streblospio shrubsolii	4.27	427	100	9.88
Nematoda	1.60	160	100	6.43
Macoma balthica	0.40	40	100	4.47
Tubificoides agg. (pseudogaster)	2.47	247	60	2.63
Pygospio elegans	0.20	20	40	0.46
Manayunkia aestuarina	0.13	13	40	0.46

Group m (Average similarity: 68.83%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CN2L	NKM	Sandy Mud	5.35	21.26	78.74	6.21
CN2M	NKM	Sandy Mud	5.15	23.30	76.70	5.24
CN3L	NKM	Sandy Mud	5.95	12.68	87.32	8.18
CN3M	NKM	Sandy Mud	5.48	16.93	83.07	6.21
DI1M	NKM	Sandy Mud	5.55	17.88	82.12	9.09
DI2M	NKM	Sandy Mud	5.30	21.04	78.96	6.77
DI3M	NKM	Sandy Mud	5.27	20.94	79.06	7.01
IN1M	NKM	Sandy Mud	5.38	17.99	82.01	6.94
IN2M	NKM	Sandy Mud	5.97	12.80	87.20	7.56

Species	Mean Abundance (per 0.01m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Corophium volutator	50.00	5000	100	38.49
Tubificoides benedii	33.11	3311	100	28.27
Streblospio shrubsolii	10.26	1026	89	11.44
Nematoda	4.89	489	100	11.24
Macoma balthica	1.93	193	100	7.16
Pygospio elegans	0.70	70	56	1.28
Hediste diversicolor	0.26	26	56	1.1
Tubificoides agg. (pseudogaster)	0.19	19	33	0.41
Enchytraeidae	0.22	22	33	0.32
Tharyx sp.	0.30	30	22	0.16
Diptera sp.	0.22	22	22	0.13

Group n (Average similarity: 54.87%)

Sites	Area	Sediment Type	Median Phi	% Sand	% Mud	% LOI
CN1L	NKM	Sandy Mud	5.71	16.56	83.44	6.35
DI1L	NKM	Sandy Mud	5.82	16.84	83.16	7.11
DI2L	NKM	Sandy Mud	5.62	19.57	80.43	7.46
DI3L	NKM	Sandy Mud	5.56	18.07	81.93	8.05
IN1L	NKM	Sandy Mud	5.25	22.90	77.10	6.65
IS2U	NKM	Sandy Mud	5.74	18.66	81.34	9.74
IS3L	NKM	Sandy Mud	5.88	16.48	83.52	7.73

Species	Mean Abundance (per $0.01m^2$)	Mean Abundance (per $1m^2$)	% of Sites Recorded	% Contribution to similarity
Streblospio shrubsolii	7.05	705	100	42.66
Tubificoides benedii	3.38	338	100	22.52
Corophium volutator	0.62	62	86	9.75
Macoma balthica	0.67	67	86	9.22
Nematoda	3.29	329	57	9.09
Tubificoides swirencoides	1.62	162	43	4.33
Pygospio elegans	0.19	19	43	1.44
Nephtys hombergii	0.14	14	29	0.54
Diptera sp.	0.19	19	29	0.45

4. Subtidal Benthic Survey Results

As outlined in Section 2 the subtidal benthic survey collected 90 samples from thirty sites from four areas (impact area, secondary impact, control north and control south). Details on sample positions, depth and sediment type are provided in Appendix 10 with the distribution of sample sites shown in Figure 26.

4.1 Sedimentary Parameters

The results of Particle Size Analysis is provided in Appendix 11 and a summary of key sedimentary parameters and average water depths are provided in Table 14 with maps showing the distribution of sediment types, sediment composition and median phi grain size shown in Figures 27 to 29. The sediments collected during survey were similar within each site and the data provided here are based on particle size analysis from a single representative sample per site (sediment sub-samples from the remaining samples have been stored for future analysis if required). Sample sites within the survey areas ranged from 1.5m CD to 10m CD with upstream areas generally exhibiting slightly shallower depths. Sediments ranged from sands or muddy sands to sandy gravel and sandy mud.

Gravel content ranged from 0% at the majority of sites to 84% at site CS 5 and the southern (downstream) control sites tended to have the highest gravel content. Sand and mud content varied considerably throughout the area with some spatial variability between areas. The northern control site included cleaner sand, muddy sand or sandy mud with no sites having a gravel component whilst mud content ranged from 3.5% to 81%. Conversely the southern control area included sandy gravels, gravel and gravelly muddy sand with gravel content ranging from 0% to 84% and mud content ranging from 0.07% to 68%. The two impact areas tended to exhibit muddier sediments with mud or sandy mud and a varying gravel content (gravelly muddy sand or gravelly sandy mud). Gravel content in the impact areas ranged from 0% to 8% at the direct impact area and 0% to 12% at the secondary impact area whilst mud content in these areas ranged from 42% to 90% at the direct impact area and 2.3% to 76% at the secondary impact area. Aside from the sandier sites in the northern control area the majority of sites exhibited poorly or very poorly sediments which ranged from very fine skewed to coarse skewed and % LOI varied from 1% to 11%.

4.2 Biological Parameters

A range of biological parameters were calculated for the samples as undertaken for the intertidal invertebrate survey. A summary of the biological parameters at each site is provided in Table 15 which gives average values per 0.1m^2 for each site whilst the values of biological parameters from the individual replicates are provided in Appendix 12. Replicate samples have also been combined to provide summaries of overall ABC structure per site (in Appendix 13). The spatial variation in average values of key biological parameters per site (0.1m^2) is highlighted in Figures 30 to 33. Numbers of taxa were generally low with mean numbers per site ranging from one to ten taxa per 0.1m^2 and a high proportion of individual samples had less than five taxa with no clear difference between areas.

The number of individuals at the sites were also relatively low with many sites having fewer than 20 individuals. A few sites had higher numbers of animals including sites CS 7 (mean value of 125 individuals per $0.1m^2$) and DI 3 (mean value of 134 individuals per $0.1m^2$). Just under half the sites mean abundances of under 10 per $0.1m^2$ and whilst there were no major differences between survey areas the lowest number of species and numbers of individuals tended to occur in slightly deeper water in the main channels, particularly downstream of the development area in the secondary impact or southern control areas which presumably reflects increased tidal stress. AFDW biomass tended to be low in comparison to intertidal communities and whilst evenness values were generally moderate to high (>0.75) other diversity metrics tended to exhibit moderately low values.

ABC plots generally exhibited curves with biomass curves above abundance plots (and positive w values) although sites which had few taxa could not provide particularly meaningful curves. Calculation of average ABC w statistics based on replicate data indicated that some sites e.g. sites SI 8, SI 5, SI 1, DI 6, DI 3, CS 1 and CS 2 had low average w values at or below zero. ABC curves derived for the sites as a whole (replicates combined) as provided in Appendix 12 showed negative w values at sites CS 1, CS 3, DI 3 and SI 5 whilst sites CN 2, CN 3, DI 2, DI 6, DI 7, SI 1 and SI 7 had w values just above zero. Of the sites with low w statistics listed above sites CS 1 and SI 5 exhibited ABC plots with abundance curves above the biomass curves whilst the remainder exhibited intersecting curves. Such results are likely to be representative of the relatively dynamic conditions related to tidal stress or sediment disturbance and salinity fluctuations within the estuary rather than indicative of significant anthropogenic impacts.

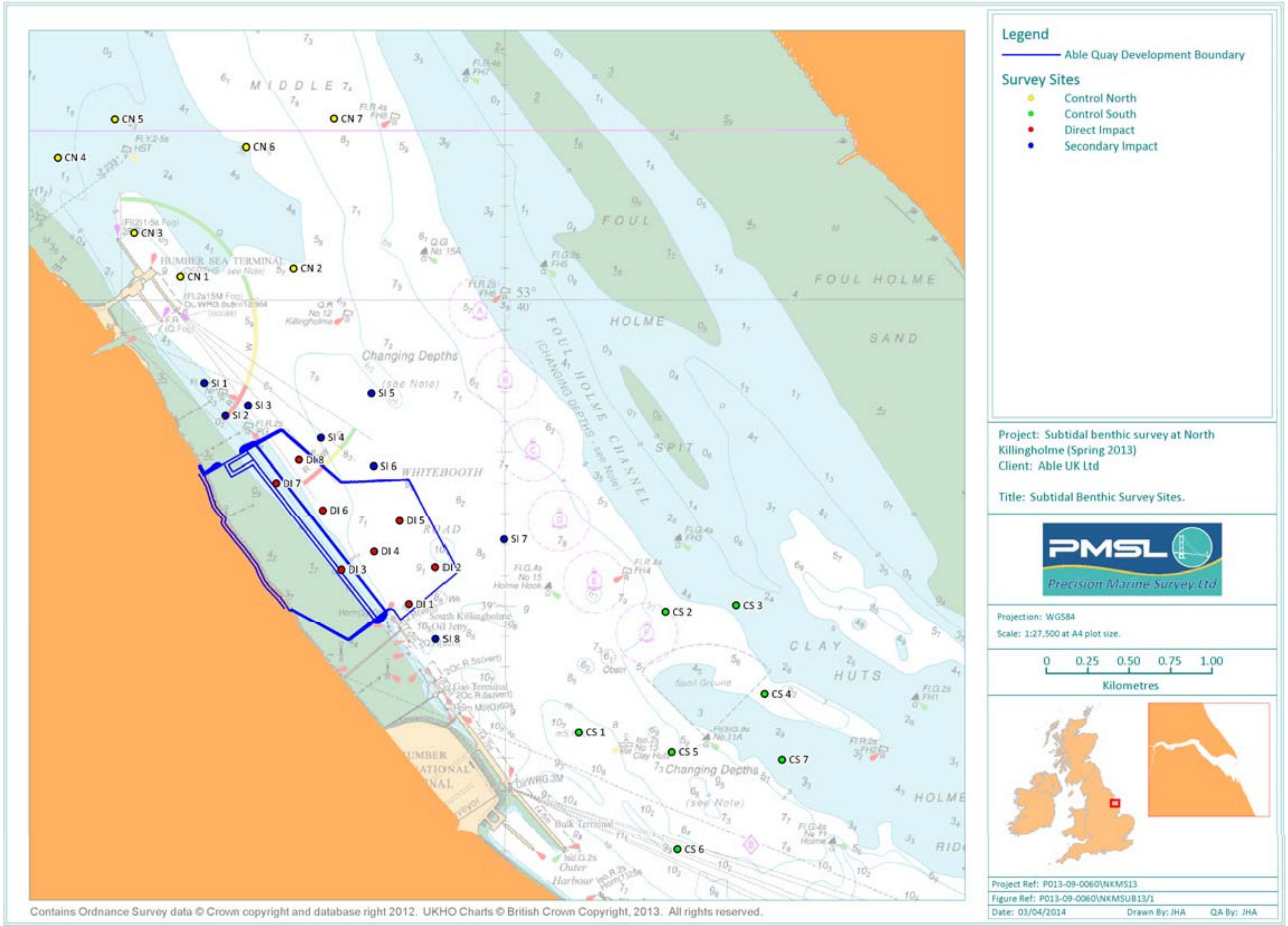

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Figure 26. Location of subtidal benthic survey sites.

Table 14. Summary of sedimentary parameters and water depth from the subtidal benthic survey.

AREA	SAMPLE	TEXTURAL GROUP	MEDIAN PHI GRAIN SIZE	MEAN PHI GRAIN SIZE	SORTING		SKEWNESS		% GRAVEL	% SAND	% MUD	% LOI	DEPTH (m CD)
Control North	CN 1	Muddy Sand	3.02	3.71	2.26	Very Poorly Sorted	0.42	Very Fine Skewed	0.00	67.04	32.96	3.30	7.3
	CN 2	Sand	2.97	3.00	0.94	Moderately Sorted	0.31	Very Fine Skewed	0.00	92.38	7.62	3.60	5.0
	CN 3	Muddy Sand	3.64	4.28	2.14	Very Poorly Sorted	0.36	Very Fine Skewed	0.00	58.61	41.39	4.04	8.5
	CN 4	Sandy Mud	5.81	5.74	1.81	Poorly Sorted	-0.07	Symmetrical	0.00	18.85	81.15	6.05	1.7
	CN 5	Sandy Mud	5.72	5.48	2.08	Very Poorly Sorted	-0.16	Coarse Skewed	0.00	26.94	73.06	5.58	2.6
	CN 6	Sand	2.89	2.89	0.55	Moderately Well Sorted	0.06	Symmetrical	0.00	96.51	3.49	1.17	4.5
	CN 7	Sandy Mud	5.95	5.85	1.77	Poorly Sorted	-0.09	Symmetrical	0.00	17.32	82.68	8.38	7.0
Control South	CS 1	Sandy Gravel	-0.93	-1.06	1.11	Poorly Sorted	-0.06	Symmetrical	47.01	52.92	0.07	1.49	10.0
	CS 2	Sandy Gravel	0.14	-0.18	1.99	Poorly Sorted	-0.13	Coarse Skewed	34.57	61.52	3.91	3.75	6.6
	CS 3	Slightly Gravelly Muddy Sand	2.19	3.33	2.45	Very Poorly Sorted	0.60	Very Fine Skewed	0.76	68.73	30.51	3.07	5.1
	CS 4	Slightly Gravelly Muddy Sand	1.68	2.58	2.04	Very Poorly Sorted	0.68	Very Fine Skewed	2.20	78.39	19.42	1.36	6.7
	CS 5	Gravel	-2.60	-2.42	1.21	Poorly Sorted	0.25	Fine Skewed	84.25	15.43	0.32	4.04	7.7
	CS 6	Gravelly Muddy Sand	0.67	0.31	2.38	Very Poorly Sorted	-0.03	Symmetrical	20.64	65.41	13.95	9.28	10.4
	CS 7	Sandy Mud	5.37	5.07	2.38	Very Poorly Sorted	-0.20	Coarse Skewed	0.00	31.68	68.32	7.08	4.0
Direct Impact	DI 1	Sandy Mud	5.64	5.44	2.11	Very Poorly Sorted	-0.16	Coarse Skewed	0.00	27.35	72.65	5.51	9.2
	DI 2	Gravelly Muddy Sand	3.60	4.08	2.65	Very Poorly Sorted	0.11	Fine Skewed	8.12	49.50	42.37	10.16	8.8
	DI 3	Mud	6.43	6.29	1.63	Poorly Sorted	-0.15	Coarse Skewed	0.00	9.94	90.06	8.02	2.5
	DI 4	Gravelly Mud	4.23	4.14	2.92	Very Poorly Sorted	-0.11	Coarse Skewed	5.25	42.38	52.37	4.26	7.8
	DI 5	Slightly Gravelly Sandy Mud	5.38	5.31	2.10	Very Poorly Sorted	-0.03	Symmetrical	1.08	36.69	62.24	6.61	8.4
	DI 6	Sandy Mud	5.49	5.55	1.72	Poorly Sorted	0.03	Symmetrical	0.00	20.75	79.25	7.40	6.4
	DI 7	Sandy Mud	5.83	5.78	1.76	Poorly Sorted	-0.05	Symmetrical	0.00	18.25	81.75	7.05	2.5
	DI 8	Sandy Mud	4.21	4.57	2.04	Very Poorly Sorted	0.24	Fine Skewed	0.00	45.07	54.93	3.75	6.0
Secondary Impact	SI 1	Sandy Mud	5.46	5.44	2.02	Very Poorly Sorted	-0.03	Symmetrical	0.00	28.27	71.73	7.38	3.7
	SI 2	Sandy Mud	5.66	5.59	1.93	Poorly Sorted	-0.05	Symmetrical	0.00	24.26	75.74	6.41	2.9
	SI 3	Sandy Mud	5.73	5.64	1.90	Poorly Sorted	-0.08	Symmetrical	0.00	23.15	76.85	7.56	5.8
	SI 4	Slightly Gravelly Sandy Mud	4.90	4.44	2.96	Very Poorly Sorted	-0.24	Coarse Skewed	4.40	37.71	57.89	11.31	7.3
	SI 5	Slightly Gravelly Sand	2.73	2.72	0.66	Moderately Well Sorted	-0.02	Symmetrical	0.16	97.51	2.33	3.07	6.7
	SI 6	Sandy Mud	4.62	4.99	1.99	Poorly Sorted	0.25	Fine Skewed	0.00	41.93	58.07	4.79	7.8
	SI 7	Sandy Mud	4.01	4.59	2.05	Very Poorly Sorted	0.38	Very Fine Skewed	0.00	49.84	50.16	3.77	7.6
	SI 8	Gravelly Muddy Sand	-0.03	0.34	1.93	Poorly Sorted	0.53	Very Fine Skewed	12.40	76.18	11.43	1.87	9.8

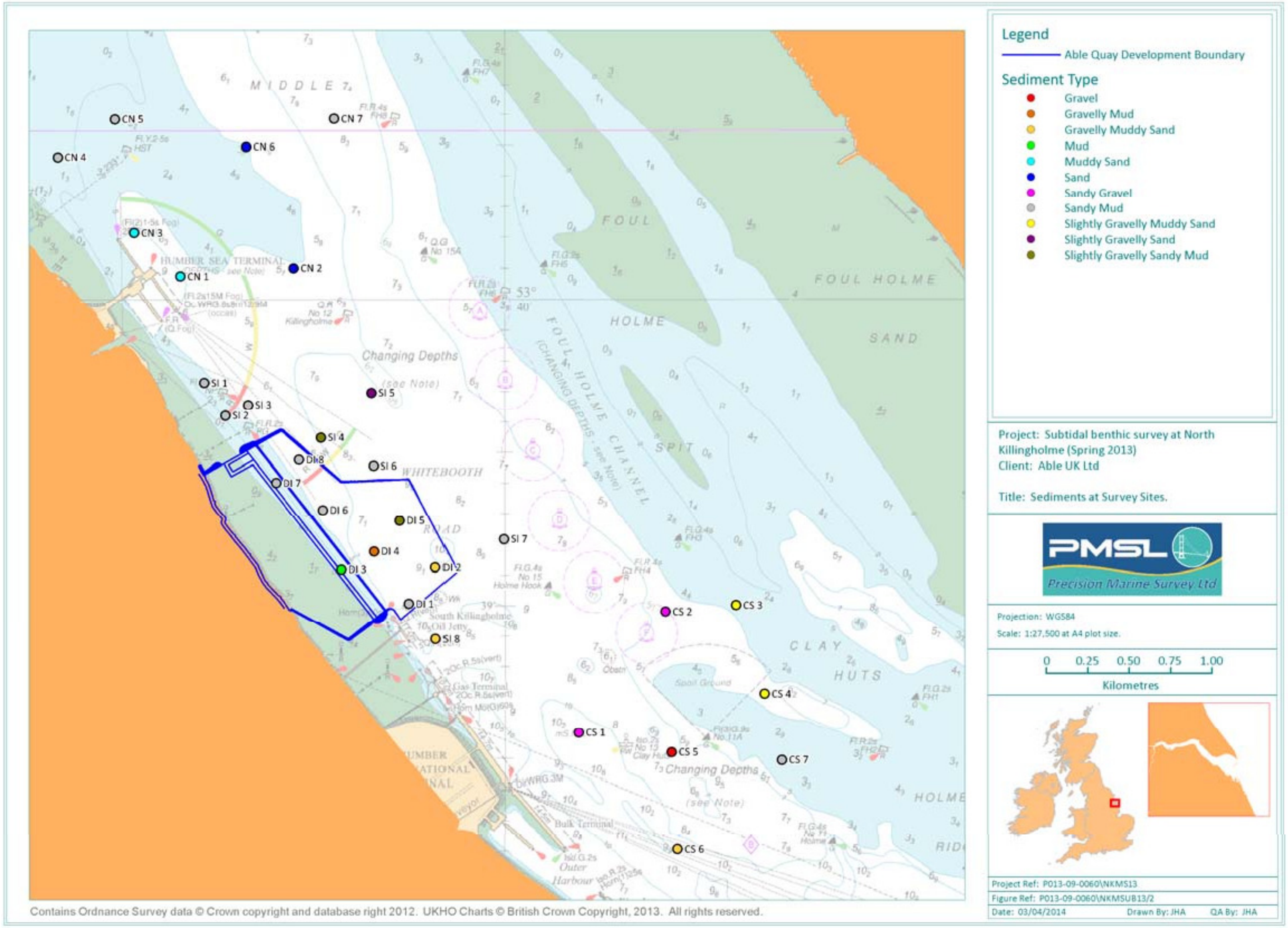

Figure 27. Sediment type at the subtidal benthic survey sites.

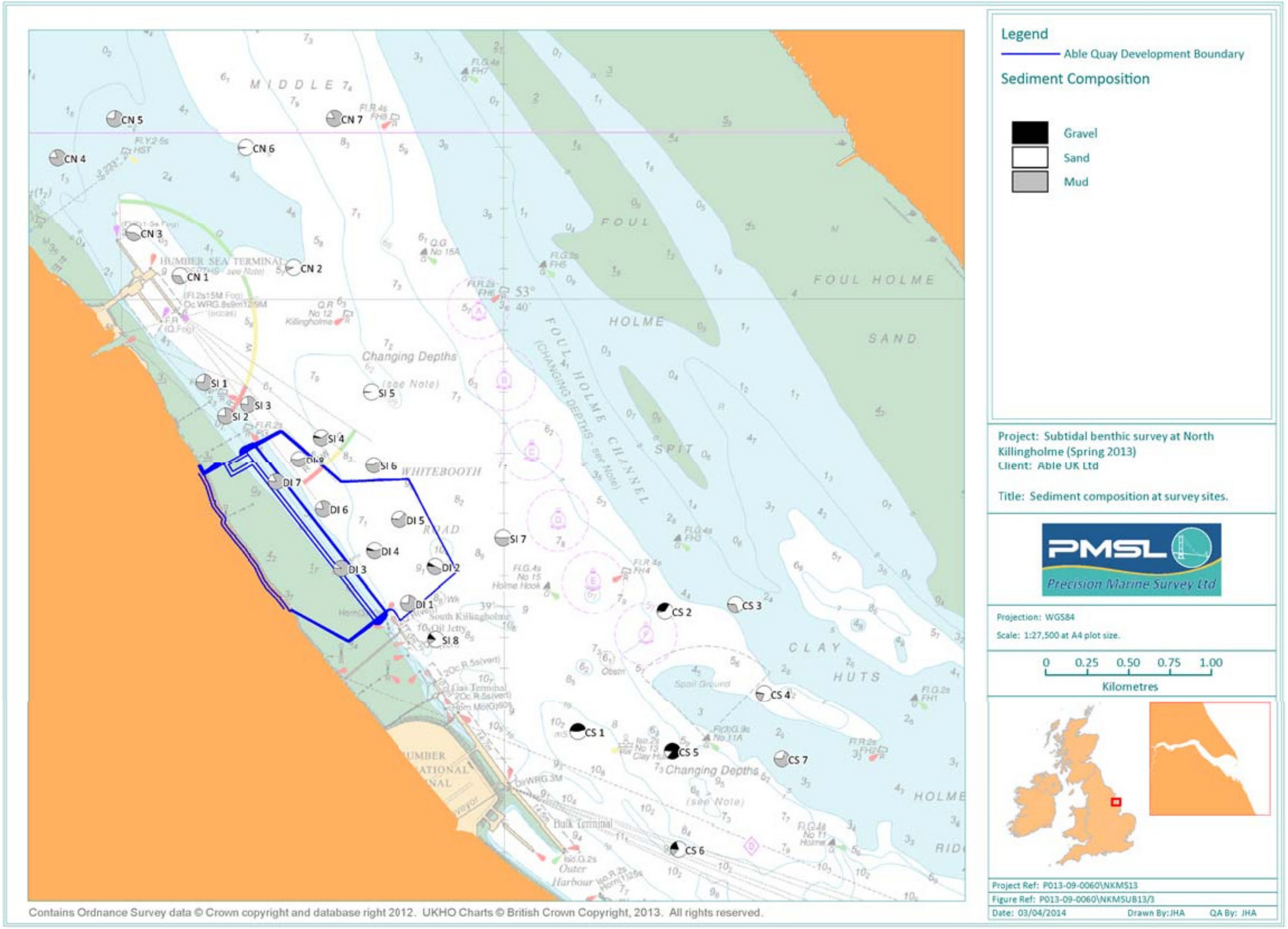

Figure 28. Sediment composition at the subtidal benthic survey sites.

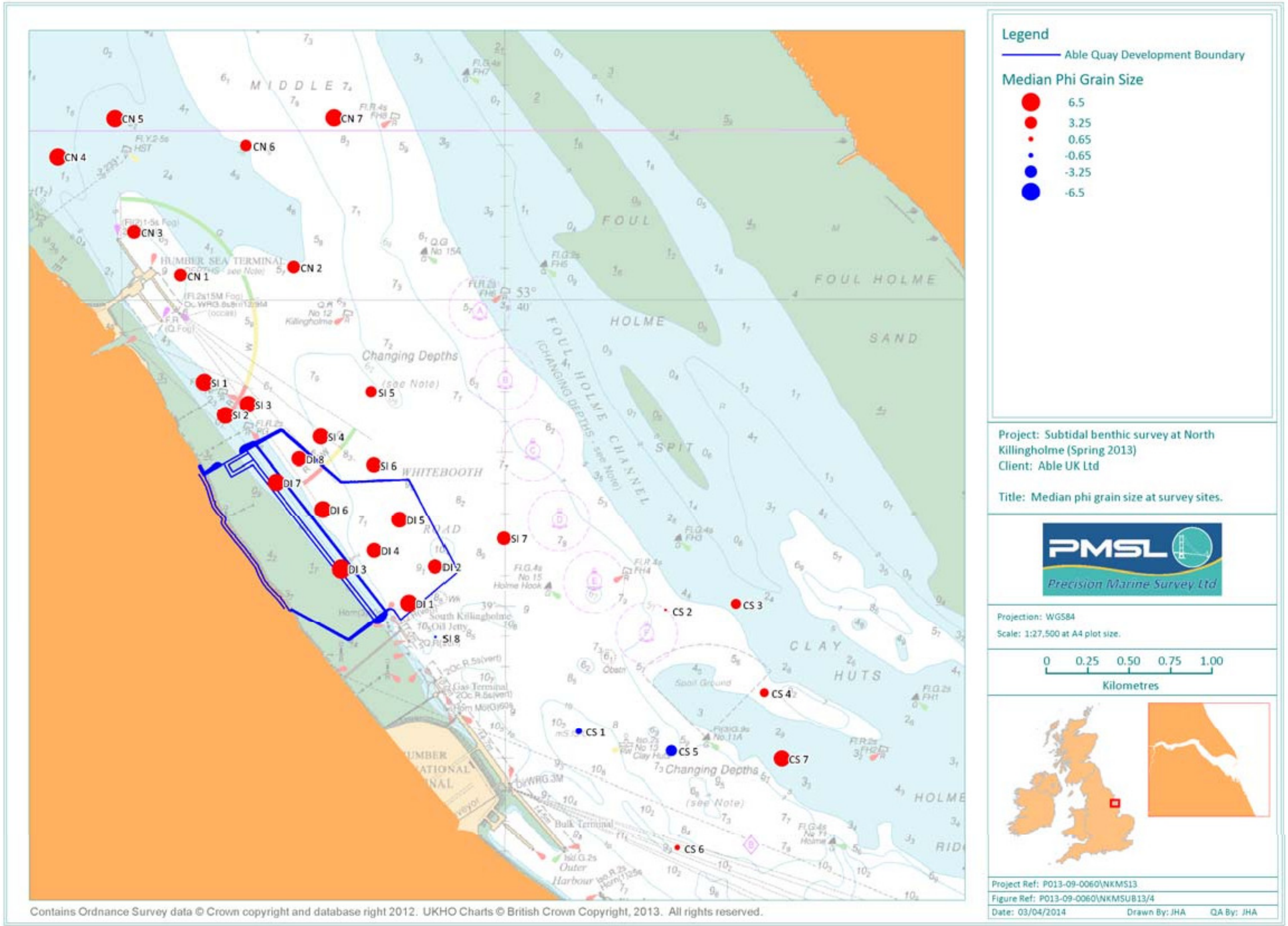

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Figure 29. Median phi grain size at the subtidal benthic survey sites.

Table 15. Mean biological parameters at the subtidal benthic survey sites.

Area	Site	Mean Numbers of Taxa	Mean Numbers of Individuals		Mean Biomass (AFDW g)		Mean Margalef's d	Mean Pielou's J	Mean Shannon's H'	Mean AFDW ABC w stat
			per 0.1 m^2	per 1 m^2	per 0.1 m^2	per 1 m^2				
Control North	CN 1	3.33	6.67	67	0.0052	0.0515	1.06	0.76	1.15	0.36
	CN 2	5.33	22.33	223	0.0046	0.0461	1.35	0.83	1.85	0.18
	CN 3	2.67	47.00	470	0.0066	0.0662	0.52	0.48	0.58	0.22
	CN 4	9.67	55.00	550	0.0076	0.0756	2.14	0.78	2.50	0.23
	CN 5	5.00	17.67	177	0.0123	0.1227	1.18	0.66	1.42	0.28
	CN 6	5.00	15.67	157	0.0012	0.0122	1.48	0.93	2.16	0.16
	CN 7	2.67	2.67	27	0.0006	0.0055	1.39	0.97	1.17	0.24
Control South	CS 1	1.00	2.00	20	0.0000	0.0002	0.46	0.92	0.31	-0.06
	CS 2	1.67	1.67	17	0.0003	0.0032	0.00	-	0.00	0.00
	CS 3	4.00	11.00	110	0.0019	0.0191	1.05	0.86	1.17	0.50
	CS 4	2.33	5.67	57	0.0024	0.0244	1.05	0.95	1.14	0.28
	CS 5	2.00	2.33	23	0.0829	0.8292	1.08	1.00	0.67	0.50
	CS 6	3.00	9.67	97	0.0076	0.0757	1.06	0.95	1.27	0.44
	CS 7	8.33	125.33	1253	0.0080	0.0799	1.45	0.65	1.90	0.18
Direct Impact	DI 1	5.67	8.00	80	0.0050	0.0496	2.28	0.96	2.30	0.66
	DI 2	3.67	5.67	57	0.0004	0.0036	0.60	0.68	0.68	0.26
	DI 3	8.00	134.00	1340	0.0139	0.1387	1.44	0.59	1.75	-0.04
	DI 4	1.00	3.00	30	0.0002	0.0017	0.36	1.00	0.33	0.28
	DI 5	3.33	5.33	53	0.0012	0.0124	1.34	0.92	1.41	0.41
	DI 6	8.00	28.67	287	0.0093	0.0934	1.84	0.56	1.64	-0.07
	DI 7	3.67	21.67	217	0.0083	0.0827	0.90	0.73	1.34	0.30
	DI 8	5.67	17.00	170	0.0281	0.2809	1.63	0.85	2.04	0.28
Secondary Impact	SI 1	7.33	70.33	703	0.0266	0.2659	1.44	0.55	1.55	0.08
	SI 2	4.33	5.33	53	0.0143	0.1428	2.01	0.98	1.88	0.79
	SI 3	7.67	14.67	147	0.0122	0.1222	2.34	0.93	2.50	0.66
	SI 4	1.33	1.33	13	0.0097	0.0968	1.44	1.00	0.67	0.77
	SI 5	2.00	2.00	20	0.0000	0.0002	0.72	0.81	0.27	-0.15
	SI 6	2.67	4.33	43	0.0008	0.0078	0.62	0.84	0.75	0.21
	SI 7	2.33	24.33	243	0.0160	0.1597	0.41	0.63	0.77	0.14
	SI 8	1.67	2.00	20	0.0001	0.0014	0.46	0.92	0.31	-0.05

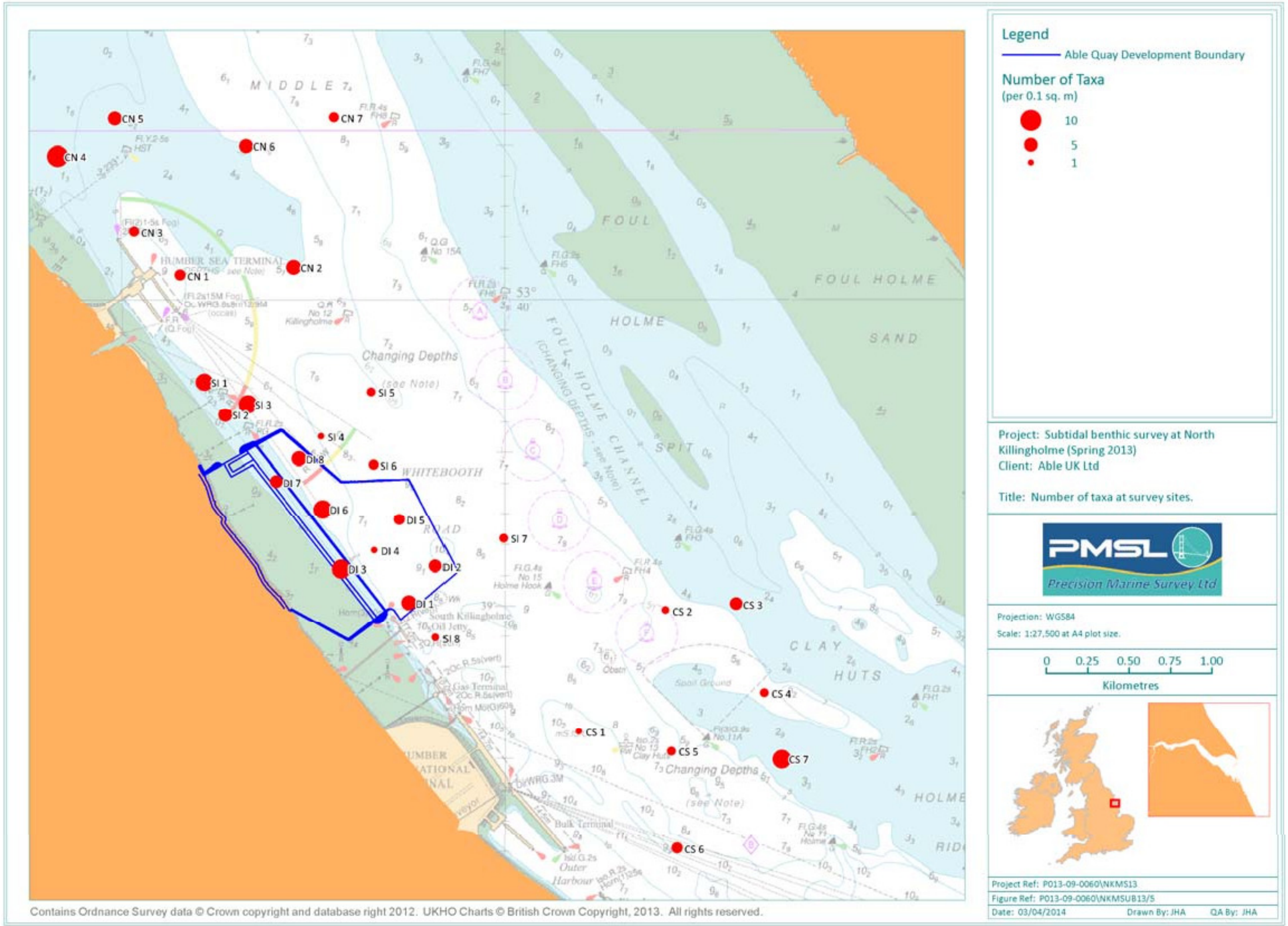

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Figure 30. Mean number of taxa per $0.1m^2$ at the subtidal benthic survey sites.

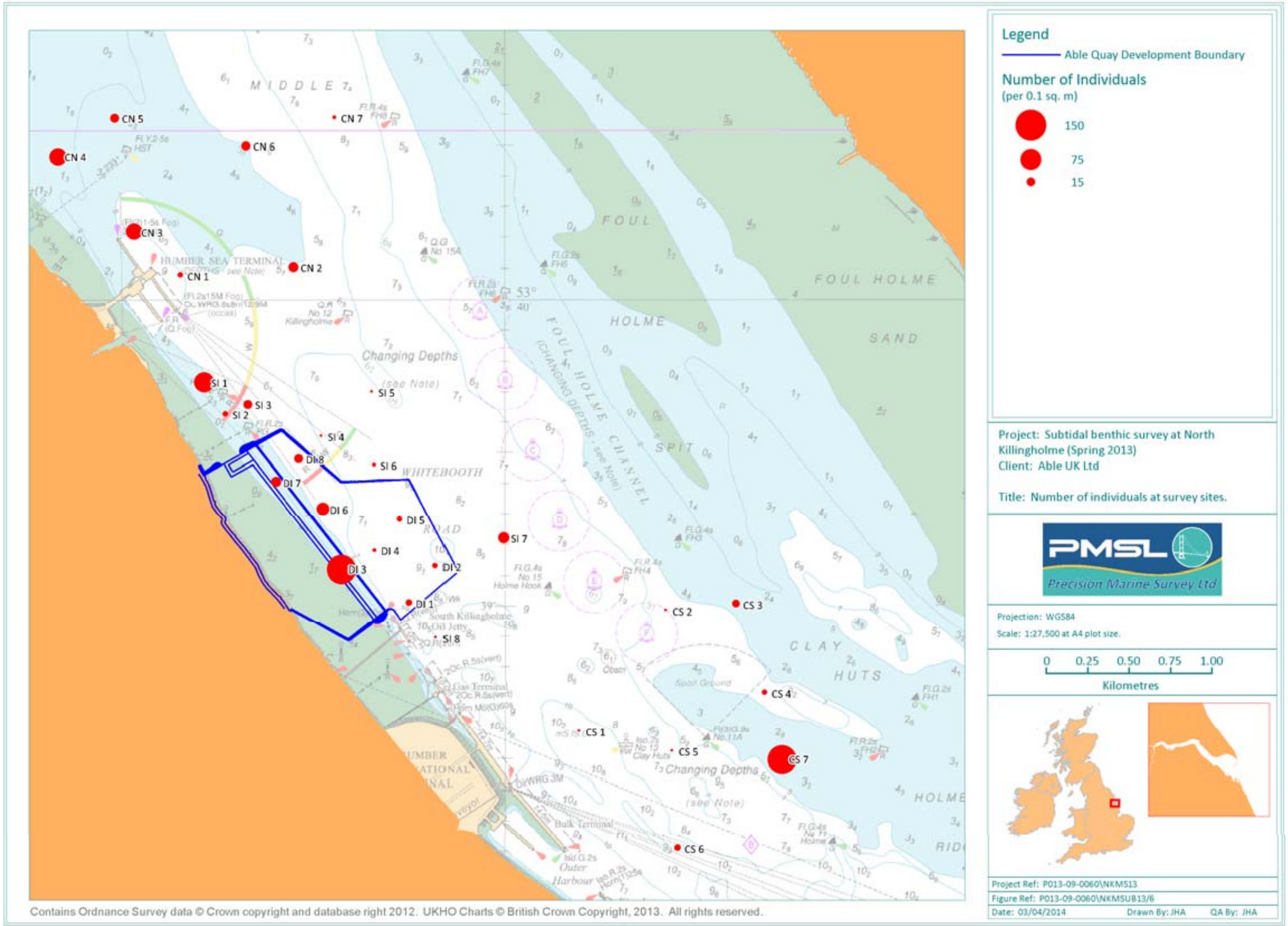

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Figure 31. Mean number of individuals per 0.1m^2 at the subtidal benthic survey sites.

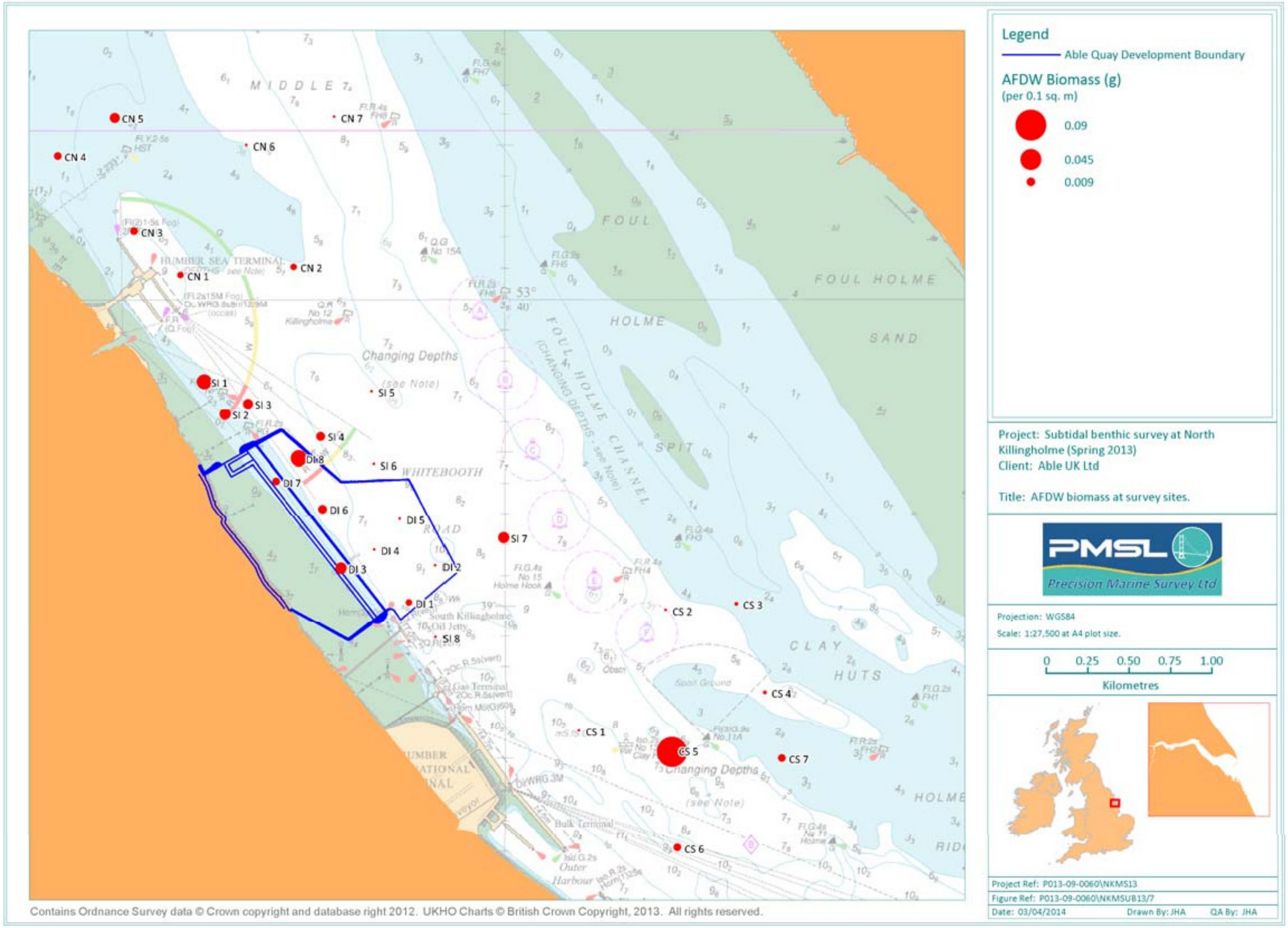

Figure 32. Mean AFDW biomass per 0.1m^2 at the subtidal benthic survey sites.

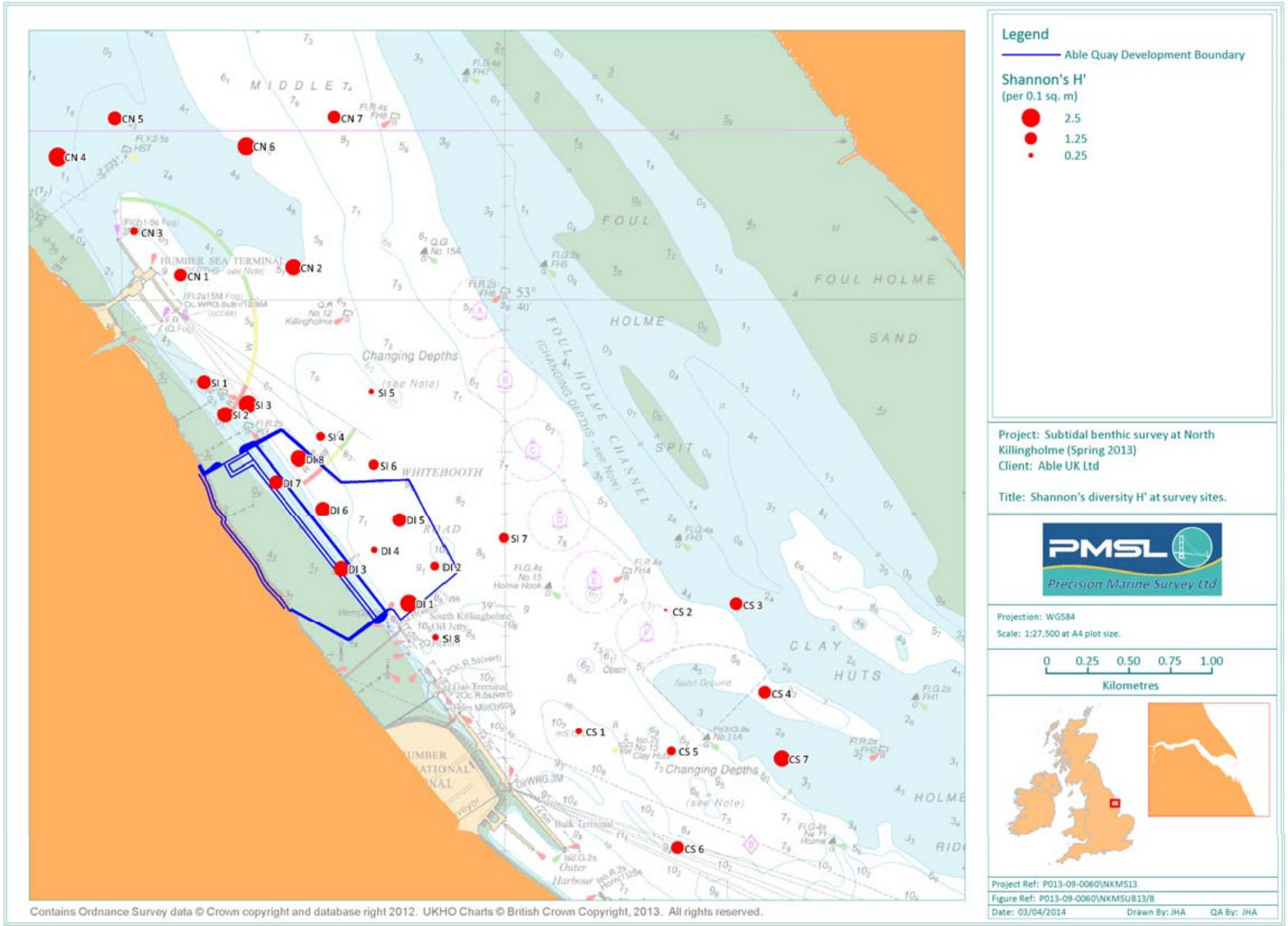

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Figure 33. Mean Shannon's diversity H' per $0.1 m^2$ at the subtidal benthic survey sites.

4.3 Species Composition

In total 47 taxa were recorded during the subtidal survey although many of these were in low densities or only recorded occasionally. A summary of species collected during the survey are provided in Tables 16 and 17 which highlight the species collected in each survey area ranked by abundance and biomass respectively and the full species matrix from the survey are provided in Appendices 14 and 15. Sites in the northern control area were characterised by *Gammarus salinus* which was recorded at 76% of the samples along with a variety of other taxa recorded in lower numbers and frequency including Copepoda, *Streblospio shrubsolii*, *Arenicola marina*, *Capitella* sp., *Neomysis integer*, Nematoda, *Macoma balthica* and *Tubificoides benedii*. *Macoma balthica* and *Gammarus salinus* had the highest contribution in terms of biomass in this area. The southern control area included a more variable range of species with *Polydora cornuta* numerically dominant but only present in 14% of samples. Other taxa recorded in low densities included species such as Nematoda, *Corophium volutator*, *Neomysis integer*, *Arenicola marina*, Ostracoda, *Pygospio elegans*, *Eurydice pulchra*, Nemertea, *Capitella* sp., Copepoda and *Gammarus salinus.*

In terms of biomass *Crangon crangon* along with *Polydora cornuta*, *Gammarus salinus* and *Neomysis integer* had the highest values at the southern control area although *Crangon crangon* was only present at 5% of samples. The direct impact and secondary impact areas had highest numbers of *Streblospio shrubsolii* which were recorded at 54% and 33% of the samples respectively. The direct impact area also included moderate densities of *Tubificoides swirencoides*, *Corophium volutator*, *Macoma balthica*, *Capitella* sp. and *Tubificoides benedii* whilst the secondary impact area was also characterised by low numbers of *Capitella* sp., *Arenicola marina*, Nematoda, *Tubificoides benedii*, *Macoma balthica* and *Tubificoides swirencoides*. In these areas *Macoma balthica* contributed the highest biomass along with other taxa such as *Crangon crangon*, *Arenicola marina* and *Nephtys hombergii*. A range of other taxa were also occasionally recorded across the survey area in low numbers along with occasional encrusting or colonial taxa such as hydroids and bryozoa usually present as small colonies on pieces of shell or larger stones.

Table 16. Summary of dominant taxa by abundance at the subtidal benthic survey areas.

Control North					Control South				
Taxa	**Mean Abundance**		**Cumulative % contribution**	**% of Samples**	**Taxa**	**Mean Abundance**		**Cumulative % contribution**	**% of Samples**
	per 0.1 m^2	**per 1 m^2**				**per 0.1 m^2**	**per 1 m^2**		
Gammarus salinus	10.24	102	42.24	76	Polydora cornuta	10.57	106	46.93	14
Copepoda	4.67	47	61.49	76	Nematoda	2.86	29	59.62	29
Streblospio shrubsolii	2.48	25	71.71	24	Corophium volutator	2.19	22	69.34	19
Arenicola marina	2.00	20	79.96	67	Neomysis integer	1.24	12	74.84	24
Capitella sp.	1.90	19	87.82	62	Arenicola marina	1.14	11	79.92	14
Neomysis integer	0.86	9	91.36	43	Ostracoda	0.95	10	84.14	5
Nematoda	0.57	6	93.71	14	Pygospio elegans	0.71	7	87.32	14
Macoma balthica	0.29	3	94.89	24	Eurydice pulchra	0.57	6	89.85	29
Tubificoides benedii	0.24	2	95.87	14	Nemertea	0.52	5	92.18	14
Pygospio elegans	0.19	2	96.66	10	Capitella sp.	0.38	4	93.87	14
Eteone longa/flava agg.	0.14	1	97.25	14	Copepoda	0.29	3	95.14	19
Tubificoides swirencoides	0.14	1	97.84	10	Gammarus salinus	0.29	3	96.41	19
Gammarus sp.	0.14	1	98.43	10	Platyhelminthes	0.14	1	97.04	10
Mysidacea indet	0.14	1	99.02	5	Eteone longa/flava agg.	0.10	1	97.46	10
Nephtys hombergii	0.05	0.5	99.21	5	Cyathura carinata	0.10	1	97.89	5
Scoloplos armiger	0.05	0.5	99.41	5	Mytilidae juv.	0.10	1	98.31	5
Ostracoda	0.05	0.5	99.61	5	Autolytinae sp.	0.05	0.5	98.52	5
Mesopodopsis slabberi	0.05	0.5	99.80	5	Aonides paucibranchiata	0.05	0.5	98.73	5
Corophium volutator	0.05	0.5	100.00	5	Streblospio shrubsolii	0.05	0.5	98.94	5
Entoprocta	P	P		5	Enchytraeidae	0.05	0.5	99.15	5
Conopeum reticulum	P	P		5	Mysidacea indet	0.05	0.5	99.37	5
					Schistomysis kervillei	0.05	0.5	99.58	5
					Gammarus sp.	0.05	0.5	99.79	5
					Crangon crangon	0.05	0.5	100.00	5
					Hartlaubella gelatinosa	P	P		10
					Orbiniidae sp.	P	P		10
					Conopeum reticulum	P	P		10
					Sertularia	P	P		5
					Phyllodocidae sp.	P	P		5

Direct Impact					**Secondary Impact**				
Taxa	**Mean Abundance**		**Cumulative % contribution**	**% of Samples**	**Taxa**	**Mean Abundance**		**Cumulative % contribution**	**% of Samples**
	per 0.1 m^2	**per 1 m^2**				**per 0.1 m^2**	**per 1 m^2**		
Streblospio shrubsolii	10.71	107	38.36	54	Streblospio shrubsolii	6.67	67	42.73	33
Tubificoides swirencoides	7.08	71	63.73	29	Capitella sp.	2.88	29	61.15	46
Corophium volutator	2.50	25	72.69	33	Arenicola marina	1.39	14	70.07	42
Macoma balthica	1.33	13	77.46	42	Nematoda	1.13	11	77.28	38
Capitella sp.	1.13	11	81.49	46	Tubificoides benedii	0.96	10	83.42	25
Tubificoides benedii	1.08	11	85.37	38	Macoma balthica	0.83	8	88.76	46
Tharyx sp.	0.63	6	87.61	21	Tubificoides swirencoides	0.71	7	93.30	13
Nematoda	0.58	6	89.70	21	Tharyx sp.	0.21	2	94.64	17
Mesopodopsis slabberi	0.58	6	91.79	13	Nephtys hombergii	0.21	2	95.97	13
Scoloplos armiger	0.42	4	93.28	21	Scoloplos armiger	0.17	2	97.04	17
Schistomysis kervillei	0.33	3	94.48	21	Mytilidae juv.	0.13	1	97.84	13
Arenicola marina	0.33	3	95.67	17	Schistomysis kervillei	0.09	1	98.40	13
Nephtys hombergii	0.25	3	96.57	17	Pygospio elegans	0.04	0.4	98.66	4
Pygospio elegans	0.21	2	97.31	13	Gammarus sp.	0.04	0.4	98.93	4
Mytilidae juv.	0.17	2	97.91	13	Gammarus salinus	0.04	0.4	99.20	4
Neomysis integer	0.13	1	98.36	13	Corophium sp. juv.	0.04	0.4	99.47	4
Aricidea sp.	0.08	1	98.66	8	Corophium volutator	0.04	0.4	99.73	4
Polydora cornuta	0.08	1	98.96	8	Crangon crangon	0.04	0.4	100.00	4
Nephtyidae juv.	0.04	0.4	99.10	4	Sertularia	P	P		8
Tubificoides (pseudogaster) agg.	0.04	0.4	99.25	4	Conopeum reticulum	P	P		8
Pycnogonida indet	0.04	0.4	99.40	4	Neomysis integer	P	P		4
Copepoda	0.04	0.4	99.55	4	Electra crustulenta	P	P		4
Gammarus sp.	0.04	0.4	99.70	4	Bicellariella ciliata	P	P		4
Gammarus salinus	0.04	0.4	99.85	4					
Crangon crangon	0.04	0.4	100.00	4					
Electra monostachys	P	P		8					
Amphiblestrum auritum	P	P		8					
Sertularia	P	P		4					
Conopeum reticulum	P	P		4					
Flustra foliacea	P	P		4					
Bicellariella ciliata	P	P		4					

Table 17. Summary of dominant taxa by biomass at the subtidal benthic survey sites.

Control North					Control South				
Taxa	**Mean AFDW Biomass (g)**		**Cumulative % contribution**	**% of Samples**	**Taxa**	**Mean AFDW Biomass (g)**		**Cumulative % contribution**	**% of Samples**
	per 0.1 m^2	**per 1 m^2**				**per 0.1 m^2**	**per 1 m^2**		
Macoma balthica	0.002241	0.022411	41.29	24	Crangon crangon	0.011842	0.118420	80.35	5
Gammarus salinus	0.001362	0.013618	66.38	76	Polydora cornuta	0.000731	0.007313	85.31	14
Arenicola marina	0.000767	0.007672	80.51	67	Gammarus salinus	0.000631	0.006314	89.60	19
Neomysis integer	0.000483	0.004835	89.42	43	Neomysis integer	0.000552	0.005521	93.34	24
Streblospio shrubsolii	0.000144	0.001440	92.07	24	Corophium volutator	0.000340	0.003398	95.65	19
Capitella sp.	0.000112	0.001120	94.14	62	Schistomysis kervillei	0.000258	0.002576	97.40	5
Nephtys hombergii	0.000070	0.000700	95.43	5	Eurydice pulchra	0.000192	0.001920	98.70	29
Scoloplos armiger	0.000070	0.000699	96.71	5	Orbiniidae sp.	0.000047	0.000472	99.02	10
Mesopodopsis slabberi	0.000066	0.000664	97.94	5	Arenicola marina	0.000031	0.000313	99.23	14
Corophium volutator	0.000043	0.000434	98.74	5	Capitella sp.	0.000027	0.000274	99.42	14
Mysidacea indet	0.000021	0.000214	99.13	5	Nemertea	0.000021	0.000210	99.56	14
Copepoda	0.000017	0.000165	99.44	76	Eteone longa/flava agg.	0.000015	0.000149	99.66	10
Gammarus sp.	0.000010	0.000101	99.62	10	Phyllodocidae sp.	0.000014	0.000145	99.76	5
Eteone longa/flava agg.	0.000010	0.000097	99.80	14	Pygospio elegans	0.000011	0.000111	99.84	14
Tubificoides benedii	0.000006	0.000059	99.91	14	Ostracoda	0.000006	0.000061	99.88	5
Nematoda	0.000003	0.000026	99.96	14	Nematoda	0.000005	0.000053	99.91	29
Pygospio elegans	0.000001	0.000011	99.98	10	Copepoda	0.000003	0.000031	99.94	19
Tubificoides swirencoides	0.000001	0.000008	99.99	10	Platyhelminthes	0.000002	0.000024	99.95	10
Ostracoda	0.000000	0.000004	100.00	5	Gammarus sp.	0.000002	0.000022	99.97	5
Entoprocta	P	P		5	Mysidacea indet	0.000001	0.000015	99.98	5
Conopeum reticulum	P	P		5	Autolytinae sp.	0.000001	0.000008	99.98	5
					Aonides paucibranchiata	0.000001	0.000008	99.99	5
					Streblospio shrubsolii	0.000001	0.000008	99.99	5
					Cyathura carinata	0.000001	0.000007	100.00	5
					Enchytraeidae	0.000000	0.000003	100.00	5
					Mytilidae juv.	0.000000	0.000002	100.00	5
					Hartlaubella gelatinosa	P	P		10
					Conopeum reticulum	P	P		10
					Sertularia	P	P		5

Direct Impact					Secondary Impact				
Taxa	Mean AFDW Biomass (g)		Cumulative % contribution	% of Samples	Taxa	Mean AFDW Biomass (g)		Cumulative % contribution	% of Samples
	per 0.1 m^2	per 1 m^2				per 0.1 m^2	per 1 m^2		
Macoma balthica	0.003290	0.032898	39.71	42	Macoma balthica	0.004020	0.040199	40.36	46
Crangon crangon	0.002156	0.021561	65.73	4	Arenicola marina	0.001673	0.016731	57.16	42
Nephtys hombergii	0.000690	0.006898	74.06	17	Nephtys hombergii	0.001659	0.016589	73.82	13
Streblospio shrubsolii	0.000675	0.006753	82.21	54	Crangon crangon	0.001537	0.015375	89.25	4
Corophium volutator	0.000674	0.006740	90.34	33	Capitella sp.	0.000436	0.004360	93.63	46
Scoloplos armiger	0.000186	0.001862	92.59	21	Streblospio shrubsolii	0.000395	0.003947	97.59	33
Capitella sp.	0.000131	0.001307	94.17	46	Scoloplos armiger	0.000113	0.001129	98.73	17
Arenicola marina	0.000129	0.001290	95.72	17	Tharyx sp.	0.000073	0.000727	99.46	17
Schistomysis kervillei	0.000087	0.000865	96.77	21	Tubificoides benedii	0.000031	0.000310	99.77	25
Tharyx sp.	0.000084	0.000840	97.78	21	Tubificoides swirencoides	0.000010	0.000101	99.87	13
Tubificoides swirencoides	0.000056	0.000562	98.46	29	Nematoda	0.000007	0.000069	99.94	38
Gammarus salinus	0.000034	0.000341	98.87	4	Schistomysis kervillei	0.000002	0.000019	99.96	13
Mesopodopsis slabberi	0.000032	0.000323	99.26	13	Corophium sp. juv.	0.000001	0.000007	99.96	4
Tubificoides benedii	0.000029	0.000287	99.61	38	Corophium volutator	0.000001	0.000007	99.97	4
Neomysis integer	0.000016	0.000155	99.80	13	Neomysis integer	0.000001	0.000006	99.98	4
Pygospio elegans	0.000007	0.000074	99.89	13	Gammarus sp.	0.000001	0.000006	99.98	4
Nematoda	0.000004	0.000038	99.93	21	Gammarus salinus	0.000001	0.000006	99.99	4
Polydora cornuta	0.000001	0.000014	99.95	8	Mytilidae juv.	0.000001	0.000006	100.00	13
Aricidea sp.	0.000001	0.000008	99.96	8	Pygospio elegans	0.000000	0.000005	100.00	4
Nephtyidae juv.	0.000001	0.000007	99.97	4	Sertularia	P	P		8
Copepoda	0.000001	0.000007	99.98	4	Conopeum reticulum	P	P		8
Gammarus sp.	0.000001	0.000006	99.98	4	Electra crustulenta	P	P		4
Mytilidae juv.	0.000001	0.000006	99.99	13	Bicellariella ciliata	P	P		4
Pycnogonida indet	0.000001	0.000006	100.00	4					
bificoides (pseudogaster) a	0.000000	0.000002	100.00	4					
Electra monostachys	P	P		8					
Amphiblestrum auritum	P	P		8					
Sertularia	P	P		4					
Conopeum reticulum	P	P		4					
Flustra foliacea	P	P		4					
Bicellariella ciliata	P	P		4					

4.4 Multivariate Analysis of Community Structure

Multivariate analysis of the abundance data (following square root transformation) was carried out as described for the intertidal invertebrate surveys in order to describe the main patterns and assemblages within the area. Classification (cluster analysis) of the data was undertaken using the Bray-Curtis similarity coefficient and grouped average (UPGMA) clustering technique followed by a non-metric MDS (multi-dimensional scaling) ordination both using the PRIMER package (Clarke & Warwick, 2001). Analysis was undertaken in a number of permutations as follows. Initially analysis was carried out using replicate data for both NKM and CCS. Use of replicate data allows an assessment of variability within a site and also may be used for subsequent statistical analysis e.g. using ANOSIM routines in PRIMER. Analysis at a site level (i.e. replicates combined) was also carried out as this simplifies assessment of spatial patterns in community structure which integrates small scale variability/noise within each site and particularly where numbers of taxa and individuals were very low. Analysis at the site level was is useful in defining biotopes for the survey area and also used to summarise communities in relation to sedimentary parameters.

Results of multivariate analysis on replicate data for are provided in Appendix 16. These indicated a series of 16 sample groups at varying levels of similarly ranging from 0% to 90%. A high level of variability was evident between samples which in part reflects the very low numbers of animals collected at many areas including a number of samples (outlier groups a to e) which contained no taxa. Aside from the outlier replicate samples with no taxa the replicate samples from the same sites tended to fall into the same broad groups (i.e. are clustered together) although there is a degree of intra-site variability as is usually the case, particularly in dynamic estuarine environments. In general the results of the replicate analysis defined a similar range of sample groups (communities) to those identified using site data (replicates combined) with the main groups of samples including those characterised by *Capitella* sp., *Gammarus salinus*, *Arenicola marina*, Copepoda and *Neomysis integer* (group h), *Polydora cornuta* dominated communities (samples from site CS 7 in group i) and a series of groups characterised by *Streblospio shrubsolii* and other taxa such as *Corophium volutator*, *Macoma balthica*, *Capitella* sp. and *Tubificoides* spp. primarily in the direct impact and secondary impact areas (groups j to o). A group of impoverished samples primarily from the southern control area was also identified characterised by *Eurydice pulchra*, Nematoda and *Neomysis integer* (group p).

The site groups from the combined (site) dataset broadly correlated to those derived from replicate data but provided a less complex summary of the main communities which were less influenced by outliers. The results of cluster analysis and nMDS on site data are shown in Figures 34 and 35 which show the dendrogram and nMDS plots with different symbols to highlight SIMPROF group and survey area. The spatial distribution of cluster groups and derived biotopes are provided in Figures 36 and 37. The characteristic taxa at the sites in each group are highlighted in Table 18 which includes contribution to group similarity (from SIMPER analysis) along with mean abundance (per 0.01m^2 and 1m^2) and the frequency of occurrence (% of sites) for each species (species which account for no similarity in the larger groups are not included in the table). Also provided are the list of sites in each group and a summary of sedimentary parameters.

Similarity between sites ranged from <10% to around 80% similarity and 6 groups of sites were identified from the SIMPROF test. Group a included a single site (DI 2) separated from the remaining sites at around 5% similarity which was characterised by gravelly muddy sand and low numbers of *Mesopodopsis slabberi* and occasional Nephtyidae juv., Copepoda and *Schistomysis kervillei*. Group b included two sites from the southern control area (CS1 and CS 5) in coarse gravel and sandy gravel which were very impoverished and characterised primarily by Nematoda with occasional other incidental taxa likely to have been introduced from adjacent muddy habitats. Group c included a single site from the southern control area (CS 7) separated at around 10% similarity which was characterised by boulder clay and sandy mud with moderately high numbers of *Polydora cornuta* along with low numbers of other taxa such as Nematoda, *Corophium volutator*, *Arenicola marina*, *Pygospio elegans* and Nemertea sp.

The majority of the remaining sites from the control areas (CN 2, 3, 5, 6 and 7 and CS 2, 3, 4 and 6) where characterised by variable sediments including sand, muddy sand, sandy mud, and gravel and gravelly muddy sand. Sites in this group were clustered together at around 35% similarity and included a variable range of taxa but were primarily characterised by *Gammarus salinus*, Copepoda and *Neomysis integer* along with a variety of other taxa in low densities such as *Capitella* sp., *Eurydice pulchra*, *Arenicola marina* and Nematoda. Group e includes a series of sites in mud or sandy mud primarily from the direct impact and secondary impact area which were separated at 42% similarity characterised by *Streblospio shrubsolii*, *Macoma balthica*, *Tubificoides benedii*, *Tubificoides swirencoides*, Nematoda, *Capitella* sp., *Corophium volutator* and *Tharyx* sp. Group f incorporated the remaining sites from the direct impact and secondary impact area (and one northern control site) in sandy mud, muddy sand or slightly gravelly muddy sand. These sites were impoverished and characterised by occasional *Capitella* sp. and/or *Arenicola marina* along with sporadic individuals of other taxa such as *Macoma balthica*, Mytilidae juv., Nematoda, *Scoloplos armiger*, *Schistomysis kervillei*, *Corophium* sp. juv., *Eteone longa/flava* and *Gammarus* spp. The results of BEST analysis showed the largest correlation between environmental parameters and community structure was for gravel content (0.415) followed by median and mean grain size (0.357 and 0.339) and mud content, % LOI and sand content (0.245, 0.202 and 0.125 respectively). Sorting, water depth and skewness had the lowest correlations (0.099, 0.079 and 0.039 respectively). No combination of parameters improved upon the correlation by gravel content alone.

In terms of biotopes (Figure 37) the survey sites appear to cover a range of rather impoverished and often transitional forms of variable salinity biotopes which are typically recorded in the middle Humber. These *include SS.SMx.SMxVS - Sublittoral mixed sediment in variable salinity (estuaries) and SS.SCS.SCSVS - Sublittoral coarse sediment in variable salinity (estuaries)* in groups a and b or other impoverished sites with gravelly sediments. Site DI 2 in group a also resembles a muddy variant of *SS.SSa.SSaVS.MoSaVS - Infralittoral mobile sand in variable salinity (estuaries)* due to the presence of *Mesopodopsis slabberi*. Site CS 7 in group c falls under the biotope *SS.SMu.SMuVS.PolCvol - Polydora ciliata and Corophium volutator in variable salinity infralittoral firm mud or clay* whilst sites in group d are generally variants of *SS.SSa.SSaVS* biotopes with elements of *SS.SSa.SSaVS.MoSaVS and SS.SSa.SSaVS.NintGam (Neomysis integer and Gammarus spp. in fluctuating low salinity infralittoral mobile sand)* and the extent of the latter biotope is known to vary from upper estuary to mid estuary in the Humber on a temporal basis (Allen *et al.* 2003) and may also occur on exposed clay/mud habitats. Groups e and f are somewhat transitional and often rather impoverished forms of *SS.SMu.SMuVS - Sublittoral mud in variable salinity (estuaries)* and at inshore sites may be transitional with adjacent low shore biotopes recorded during the intertidal invertebrate survey. Certain sites in groups e and f with somewhat higher numbers of *Capitella* could also be transitional or low density variants of the biotope *SS.SMu.SMuVS.CapTubi - Capitella capitata and Tubificoides spp. in reduced salinity infralittoral muddy sediment* or *SS.SSa.IMuSa.ArelSa - Arenicola marina in infralittoral fine sand or muddy sand*.

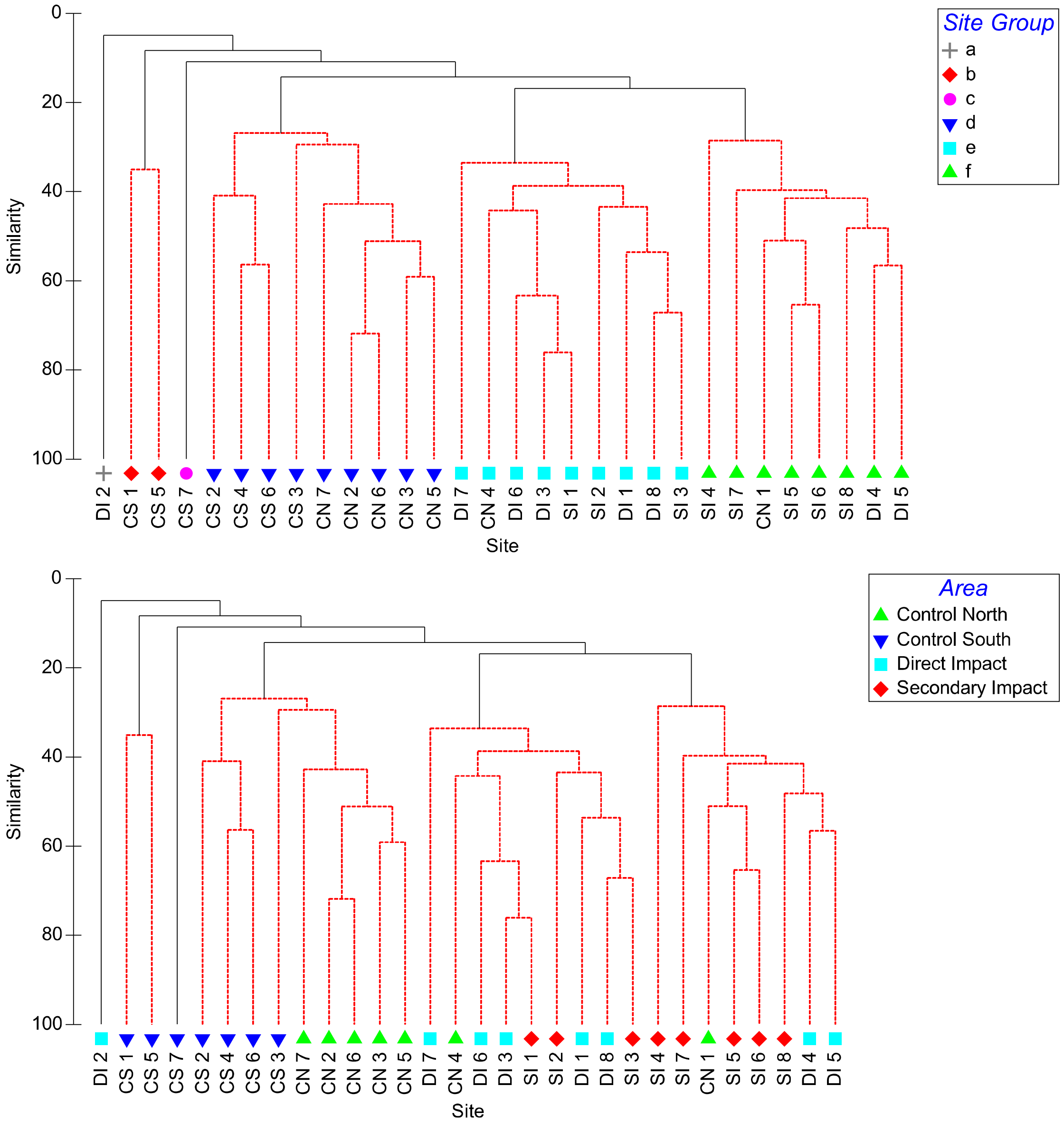
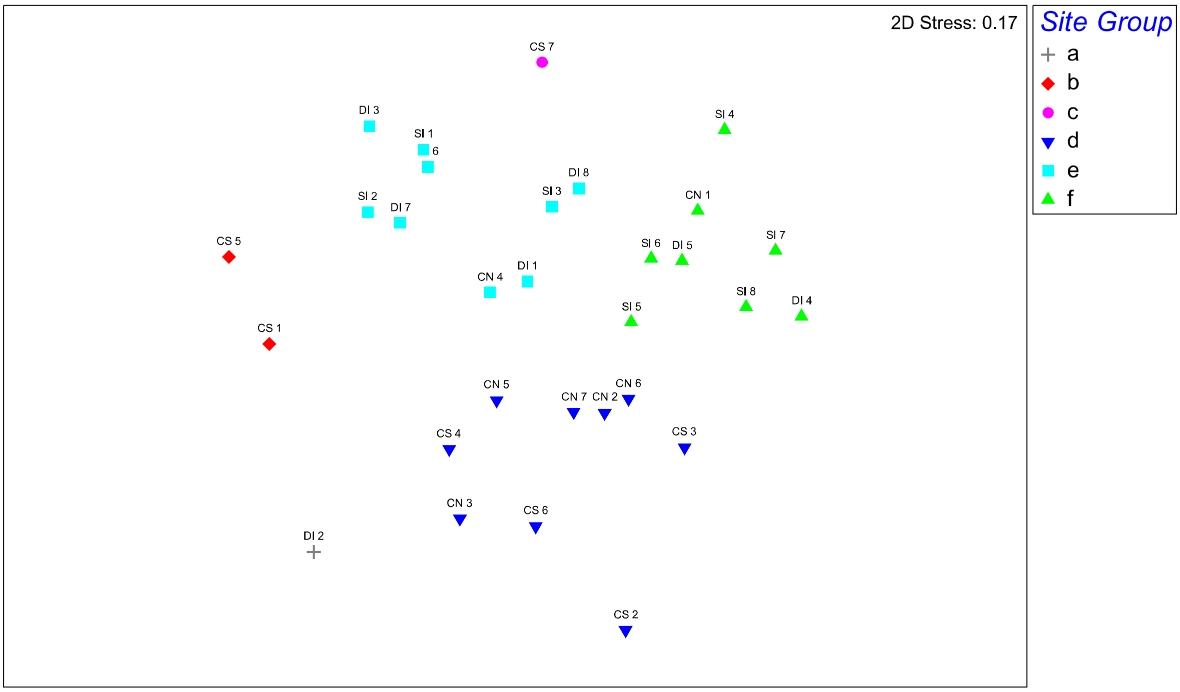


Figure 34. Results of cluster analysis on site data from the subtidal benthic survey with sites highlighted by group (top) and area (bottom).



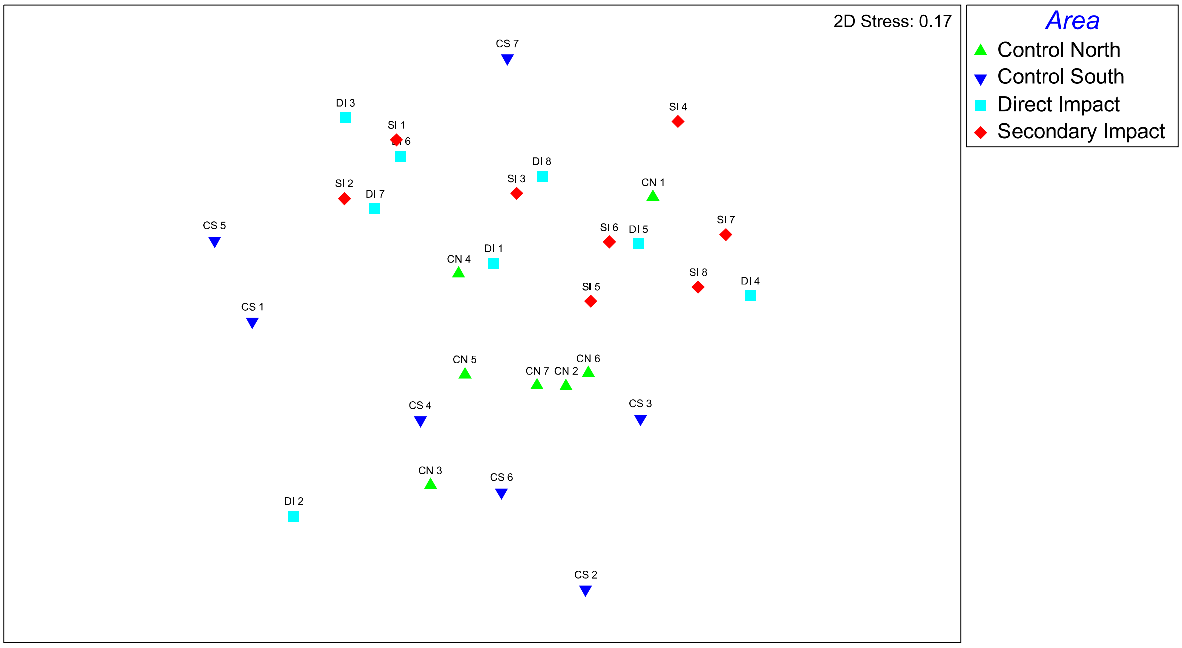


Figure 35. Results of nMDS on site data from the subtidal benthic survey with sites highlighted by group (top) and area (bottom).

Table 18. Characteristic taxa from SIMPER analysis of groups derived from cluster analysis on the subtidal benthic site data.

Group a						
Sites	**Sediment Type**	**Median Phi**	**% Gravel**	**% Sand**	**% Mud**	**Depth (m CD)**
DI 2	Gravelly Muddy Sand	3.60	8.12	49.50	42.37	8.8
	Species	**Abundance (per 0.1m^2)**	**Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**	
	Mesopodopsis slabberi	4.67	47	-	-	
	Nephtyidae juv.	0.33	3	-	-	
	Copepoda	0.33	3	-	-	
	Schistomysis kervillei	0.33	3	-	-	

Group b (Average similarity: 35.07%)						
Sites	**Sediment Type**	**Median Phi**	**% Gravel**	**% Sand**	**% Mud**	**Depth (m CD)**
CS 1	Sandy Gravel	-0.93	47.01	52.92	0.07	10.0
CS 5	Gravel	-2.60	84.25	15.43	0.32	7.7
	Species	**Mean Abundance (per 0.1m^2)**	**Mean Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**	
	Nematoda	1.00	10	100	100	
	Platyhelminthes	0.33	3	50	0	
	Aonides paucibranchiata	0.17	2	50	0	
	Corophium volutator	0.17	2	50	0	
	Crangon crangon	0.17	2	50	0	
	Enchytraeidae	0.17	2	50	0	
	Streblospio shrubsolii	0.17	2	50	0	

Group c						
Sites	**Sediment Type**	**Median Phi**	**% Gravel**	**% Sand**	**% Mud**	**Depth (m CD)**
CS 7	Sandy Mud	5.37	0.00	31.68	68.32	4.0
	Species	**Abundance (per 0.1m^2)**	**Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**	
	Polydora cornuta	74.00	740	-	-	
	Nematoda	17.00	170	-	-	
	Corophium volutator	15.00	150	-	-	
	Arenicola marina	8.00	80	-	-	
	Pygospio elegans	5.00	50	-	-	
	Nemertea	3.67	37	-	-	
	Cyathura carinata	0.67	7	-	-	
	Mytilidae juv.	0.67	7	-	-	
	Eteone longa/flava agg.	0.33	3	-	-	
	Autolytinae sp.	0.33	3	-	-	
	Mysidacea indet	0.33	3	-	-	
	Gammarus salinus	0.33	3	-	-	

Group d (Average similarity: 35.45%)

Sites	Sediment Type	Median Phi	% Gravel	% Sand	% Mud	Depth (m CD)
CN 2	Sand	2.97	0.00	92.38	7.62	5.0
CN 3	Muddy Sand	3.64	0.00	58.61	41.39	8.5
CN 5	Sandy Mud	5.72	0.00	26.94	73.06	2.6
CN 6	Sand	2.89	0.00	96.51	3.49	4.5
CN 7	Sandy Mud	5.95	0.00	17.32	82.68	7.0
CS 2	Sandy Gravel	0.14	34.57	61.52	3.91	6.6
CS 3	Slightly Gravelly Muddy Sand	2.19	0.76	68.73	30.51	5.1
CS 4	Slightly Gravelly Muddy Sand	1.68	2.20	78.39	19.42	6.7
CS 6	Gravelly Muddy Sand	0.67	20.64	65.41	13.95	10.4

Species	Mean Abundance (per 0.1m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Gammarus salinus	7.89	79	89	31.86
Copepoda	1.81	18	89	25.97
Neomysis integer	1.37	14	89	21.8
Capitella sp.	1.37	14	56	8.89
Eurydice pulchra	0.44	4	44	7.61
Arenicola marina	0.37	4	33	1.74
Nematoda	0.15	1	22	0.61
Eteone longa/flava agg.	0.07	1	22	0.57
Gammarus sp.	0.11	1	22	0.51
Streblospio shrubsolii	0.07	1	22	0.44

Group e (Average similarity: 42.46%)

Sites	Sediment Type	Median Phi	% Gravel	% Sand	% Mud	Depth (m CD)
CN 4	Sandy Mud	5.81	0.00	18.85	81.15	1.7
DI 1	Sandy Mud	5.64	0.00	27.35	72.65	9.2
DI 3	Mud	6.43	0.00	9.94	90.06	2.5
DI 6	Sandy Mud	5.49	0.00	20.75	79.25	6.4
DI 7	Sandy Mud	5.83	0.00	18.25	81.75	2.5
DI 8	Sandy Mud	4.21	0.00	45.07	54.93	6.0
SI 1	Sandy Mud	5.46	0.00	28.27	71.73	3.7
SI 2	Sandy Mud	5.66	0.00	24.26	75.74	2.9
SI 3	Sandy Mud	5.73	0.00	23.15	76.85	5.8

Species	Mean Abundance (per 0.1m^2)	Mean Abundance (per 1m^2)	% of Sites Recorded	% Contribution to similarity
Streblospio shrubsolii	17.30	173	100	31.78
Macoma balthica	1.85	19	100	15.83
Tubificoides benedii	1.96	20	89	12.76
Tubificoides swirencoides	7.04	70	78	8.2
Nematoda	1.85	19	78	8.12
Capitella sp.	0.93	9	67	5.88
Corophium volutator	2.30	23	56	4.11
Tharyx sp.	0.74	7	56	2.91
Arenicola marina	0.74	7	33	1.65
Scoloplos armiger	0.44	4	33	1.65
Nephtys hombergii	0.41	4	44	1.61
Pygospio elegans	0.37	4	44	1.61
Schistomysis kervillei	0.26	3	44	1.49
Neomysis integer	0.37	4	33	0.99
Crangon crangon	0.07	1	22	0.43
Mytilidae juv.	0.11	1	22	0.34
Gammarus sp.	0.07	1	22	0.23
Gammarus salinus	0.30	3	22	0.23
Aricidea sp.	0.07	1	22	0.17

Group f (Average similarity: 40.44%)						
Sites	**Sediment Type**	**Median Phi**	**% Gravel**	**% Sand**	**% Mud**	**Depth (m CD)**
CN 1	Muddy Sand	3.02	0.00	67.04	32.96	7.3
DI 4	Gravelly Mud	4.23	5.25	42.38	52.37	7.8
DI 5	Slightly Gravelly Sandy Mud	5.38	1.08	36.69	62.24	8.4
SI 4	Slightly Gravelly Sandy Mud	4.90	4.40	37.71	57.89	7.3
SI 5	Slightly Gravelly Sand	2.73	0.16	97.51	2.33	6.7
SI 6	Sandy Mud	4.62	0.00	41.93	58.07	7.8
SI 7	Sandy Mud	4.01	0.00	49.84	50.16	7.6
SI 8	Gravelly Muddy Sand	-0.03	12.40	76.18	11.43	9.8
	Species	**Mean Abundance (per 0.1m^2)**	**Mean Abundance (per 1m^2)**	**% of Sites Recorded**	**% Contribution to similarity**	
	Capitella sp.	3.42	34	88	47.42	
	Arenicola marina	1.83	18	88	37.34	
	Macoma balthica	0.21	2	50	7.75	
	Mytilidae juv.	0.17	2	38	4.94	
	Nematoda	0.08	1	25	1.55	
	Scoloplos armiger	0.08	1	25	1.01	

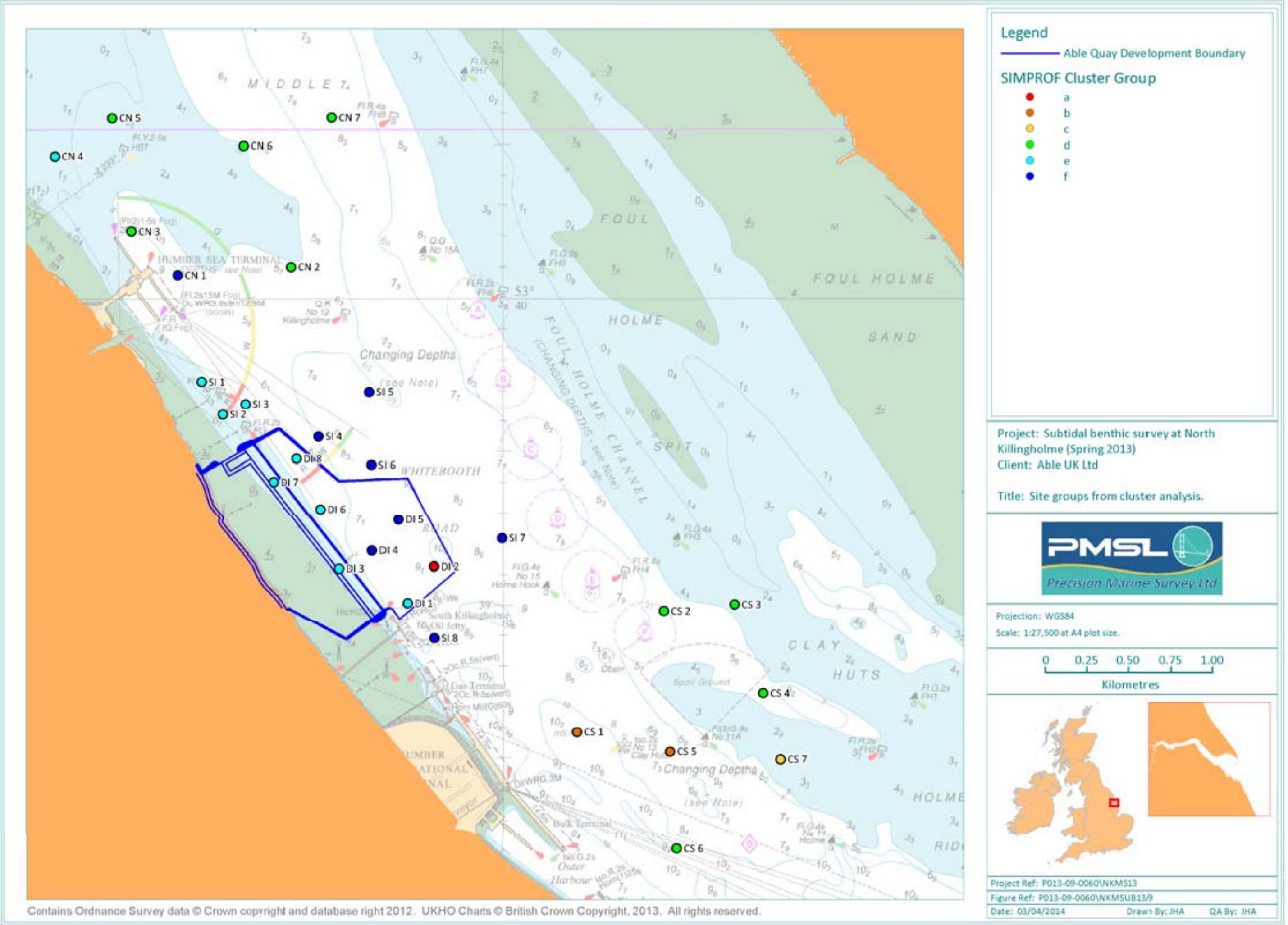


Figure 36. Spatial distribution of SIMPROF groups derived from cluster analysis on subtidal benthic data.

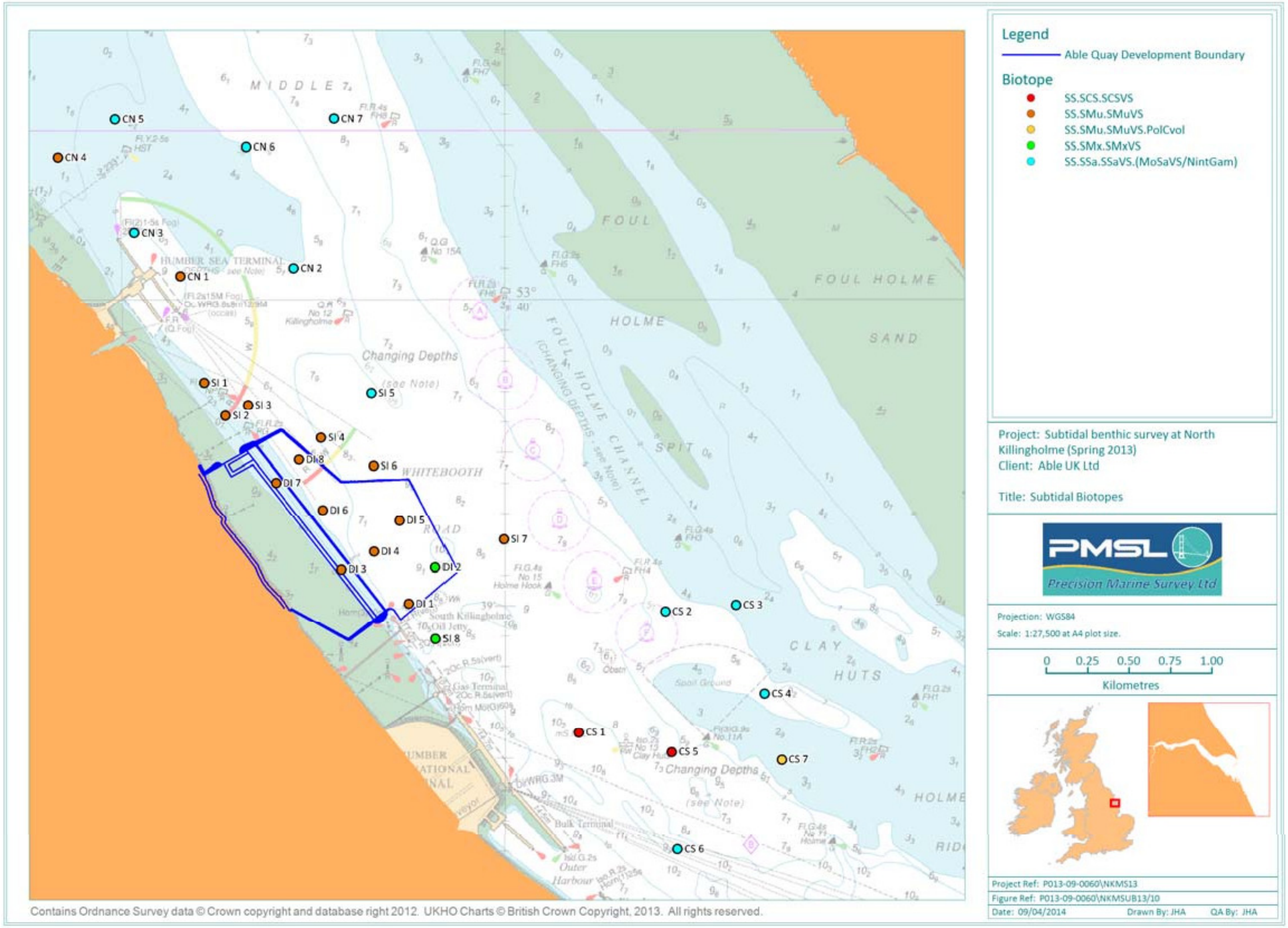


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Figure 37. Spatial distribution of biotopes at subtidal benthic survey sites.

5. Intertidal Fish Survey Results

Beam trawl and seine netting surveys were carried out in June 2013 within and immediately adjacent to the development area and also at control sites further upstream. The location of sampling stations are given in Figure 38 and for the beam trawl survey four stations were positioned within the likely impact area with a further 4 stations positioned upstream to act as controls. Similarly, four seine netting stations were located within the impact zone and four controls stations located upstream.

5.1 Beam Trawl Survey

Two replicate beam trawls were undertaken at each sampling station to derive 8 beam trawl samples within the impact area (stations BT1 – BT4) and 8 samples in the control area further upstream (stations BT5 – BT8) A total of 11 species of fish were captured during the survey along with 13 species of invertebrates which were primarily crustacea (Table 19).

Table 19. Beam trawl species richness and abundance matrix

Scientific Name	BT 1		BT 2		BT 3		BT 4		BT 5		BT 6		BT 7		BT 8	
Replicate	A	B	A	B	A	B	A	B	A	B	A	B	A	B	A	B
Mysidacea sp. Indet	0	0	24	0	0	0	0	0	0	0	0	1	0	0	0	0
Leptomysis gracilis	0	0	0	0	0	0	10	0	1	0	7	0	0	0	0	0
Neomysis integer	131	59	365	225	121	101	277	94	33	0	302	2	86	176	124	217
Praunus flexuosus	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0
Gammarellus homari	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
Gammarus sp. Indet	0	0	0	2	0	0	0	3	0	0	1	0	3	3	8	7
Gammarus zaddachi	4	2	0	1	0	1	1	8	3	0	12	0	21	23	18	27
Corophium volutator	3	2	6	4	0	0	3	1	14	39	5	16	0	0	1	0
Eurydice pulchra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Crangon allmanni	0	0	6	0	0	0	0	0	0	0	1	0	0	0	1	0
Crangon crangon	61	61	180	156	126	48	107	156	112	9	110	18	126	130	124	107
Carcinus maenas	0	2	1		2	1	0	0	0	1	0	0	1	0	0	0
Macoma balthica	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Sprattus sprattus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Syngnathus rostellatus	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
Agonus cataphractus	0	0	0	0	0	0	0	1	2	0	0	0	0	0	1	1
Liparis liparis	0	0	0	0	0	0	0	0	1	0	4	0	2	3	0	2
Liparis montagui	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
Pomatoschistus microps	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Pomatoschistus minutus	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0
Pleuronectidae sp. Indet	2	0	5	0	2	0	0	5	4	0	2	0	0	1	1	1
Platichthys flesus	8	6	3	3	2	1	16	4	8	3	5	7	1	0	1	1
Pleuronectes platessa	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
Solea solea	2	4	16	6	22	7	18	31	10	17	7	7	1	1	0	2
Fucus spiralis	0	0	P	0	0	0	0	P	P	0	0	P	0	0	0	0
No. of species	7	7	10	9	7	6	8	10	13	5	15	7	8	9	13	9
Abundance	211	136	606	399	276	159	433	303	192	69	460	51	241	339	283	365

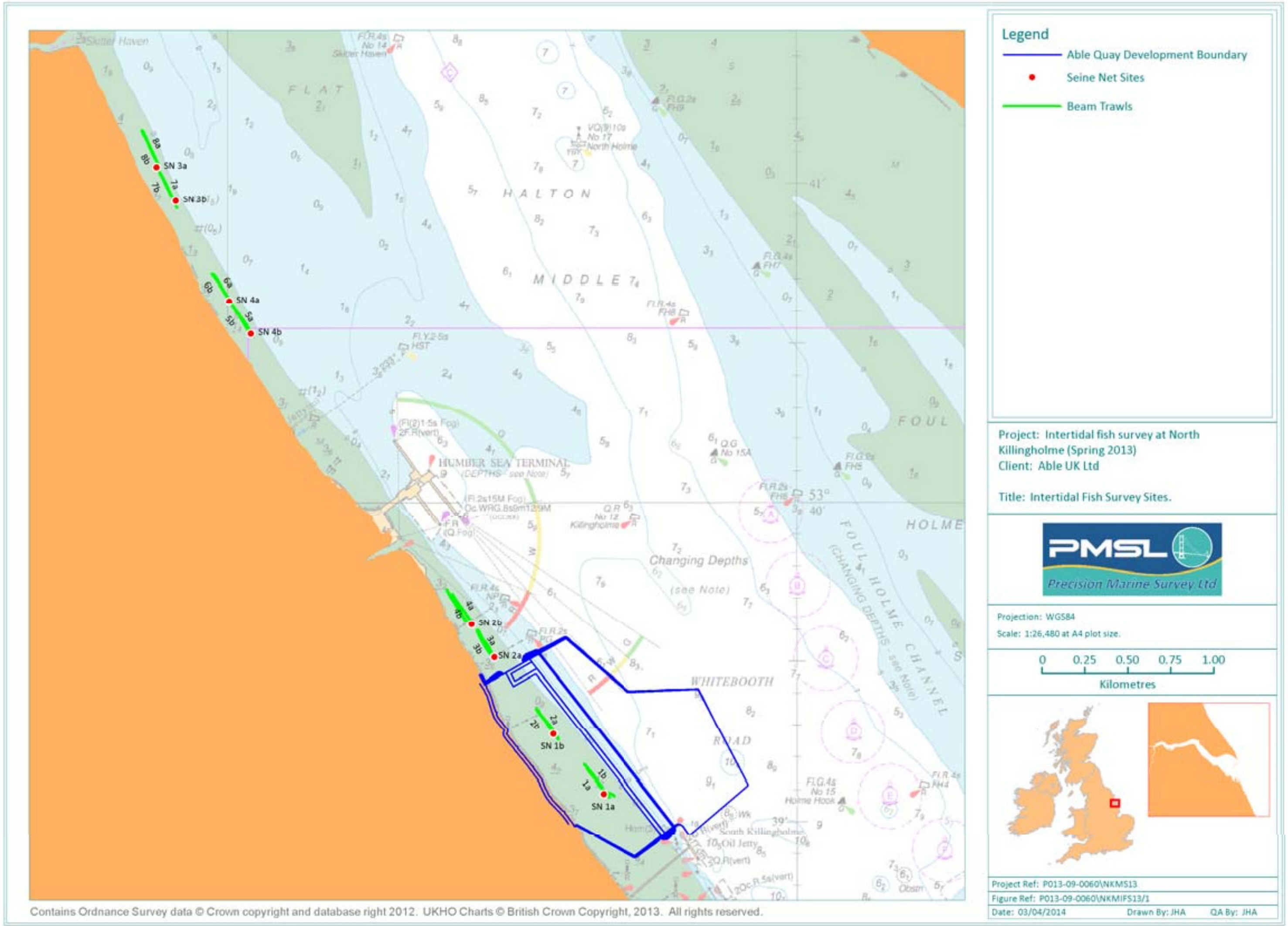

Figure 38. Location of intertidal fish survey samples.

The beam trawl stations within the development and impact zone (BT1 – BT4) exhibited low species richness ranging from two to four species of fish per trawl (Figure 39), with beam trawl station BT4b recording the highest number of species (four taxa in total). Sampling at the control stations (BT5 – BT8) recorded a higher species diversity, with species richness ranging from two to eight species. The largest number of fish species were recorded from trawl BT6a (eight taxa recorded).

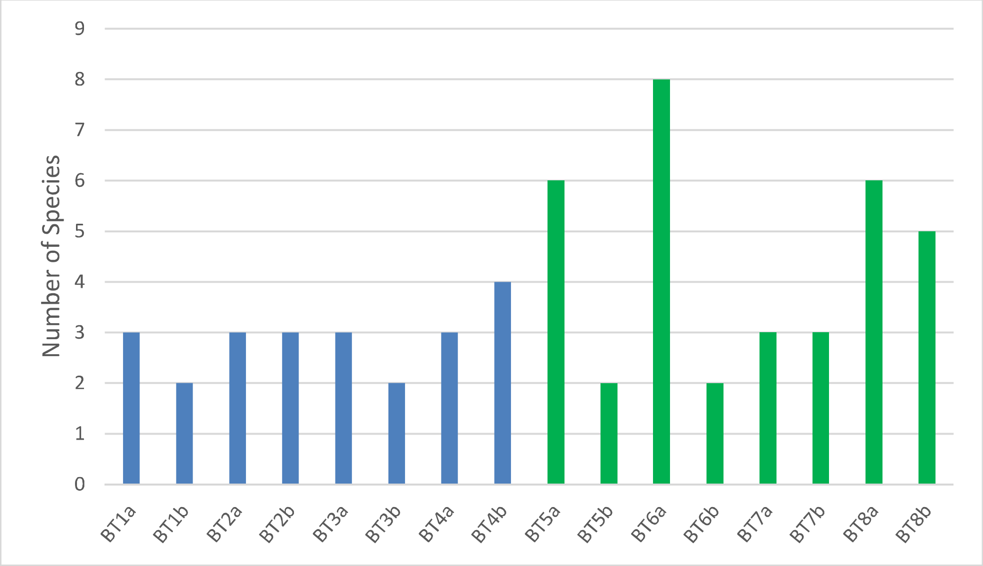

Figure 39. Fish species richness for beam trawls.

In respect to abundance (number of individuals) the beam trawl stations within the development and impact area produced the greater number of fish (ranging from 8 – 41 individuals) with slightly lower numbers recorded at the control sites (Figure 40) where numbers captured per beam trawl sample range from 4 to 27.

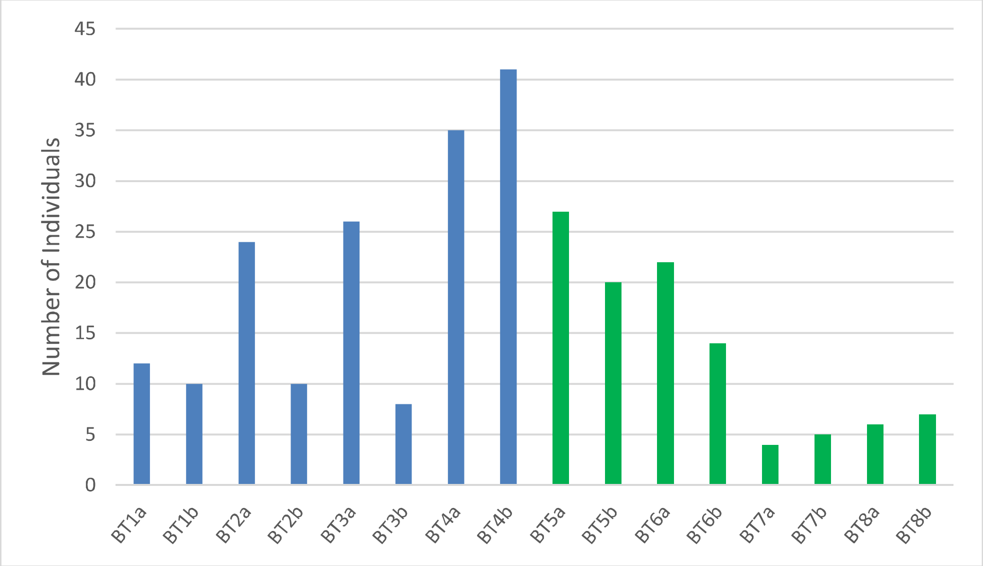

Figure 40. Fish abundance for beam trawls.

Within macro-tidal estuaries such as the Humber, fish species may often be designated into an ecological guild, which describes its functioning within the water body in relation to its life stage, reproductive status and nutritional requirements. The species of fish recorded during the beam trawl survey are frequently described as being assigned to a particular ecological guild and in this respect these fish covered three ecological guilds, marine adventitious (MA), marine juvenile migrants (MJ) and estuarine residents (ER). Five species of fish were described as estuarine residents (Dover sole, flounder, common and sand gobies and Nilsson's pipefish), there were 3 species of marine juvenile (sprat, Pleuronectidae juveniles and plaice), with 3 marine adventitious species (Pogge, common sea snail and Montagu's sea snail).

Figure 41 illustrates the percentage occurrence of individual ecological guilds within the fish assemblage, and which shows that throughout the study area estuarine residents are the dominant guild. With the exception of sampling station BT4b, estuarine residents and to a lesser extent marine juvenile migrants are representative of the guilds recorded within the developmental impact zone although at BT4b a single marine adventitious species was recorded. At the control sampling stations, marine adventitious species are increasingly more representative, although estuarine residents still dominate the assemblage.

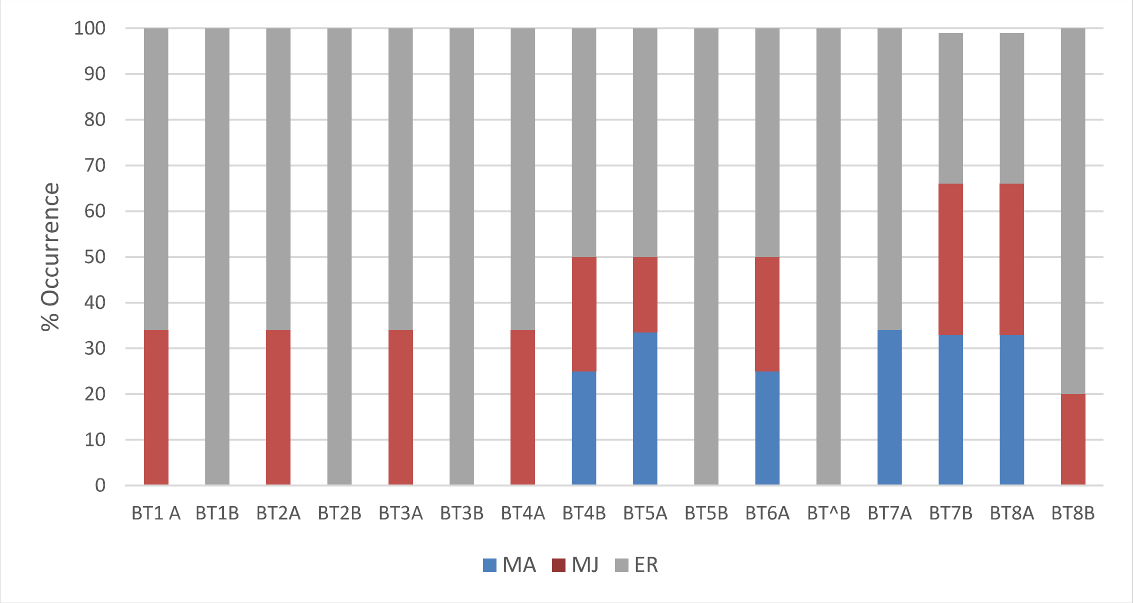

Figure 41. Distribution of fish species within ecological guilds for individual beam trawl stations

Data collated for fish abundance and analysed by ecological guild shows that estuarine residents were more abundant than species in the other guilds (Figure 42), particularly in the development area where estuarine residents represented 92% of the total fish abundance, compared to the control stations were estuarine residents accounted for 60% of the fish abundance. Marine juvenile migrants represented 7% of the fish abundance in the development/impact area compared to 12% at the control stations, whilst marine adventitious species accounted for less than 1% in the development zone and 28% at the control stations.

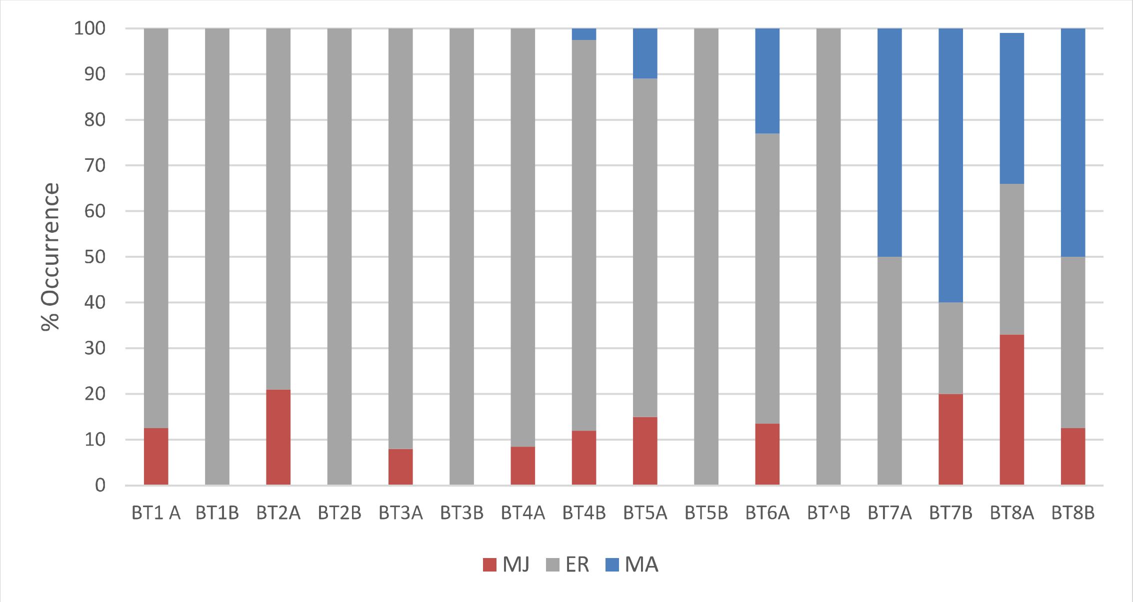

Figure 42. Distribution of fish abundance within ecological guilds for individual beam trawl stations.

5.1.1 Invertebrates

In addition to fish, an evaluation of invertebrates caught during the beam trawl study was also carried out and in total 13 invertebrate species were recorded from the 16 trawl samples. The number of invertebrate species recorded from trawls in the development/impact area varied between 4 to 6 species, whilst the abundance ranged between 126 to 582 (Figure 43).

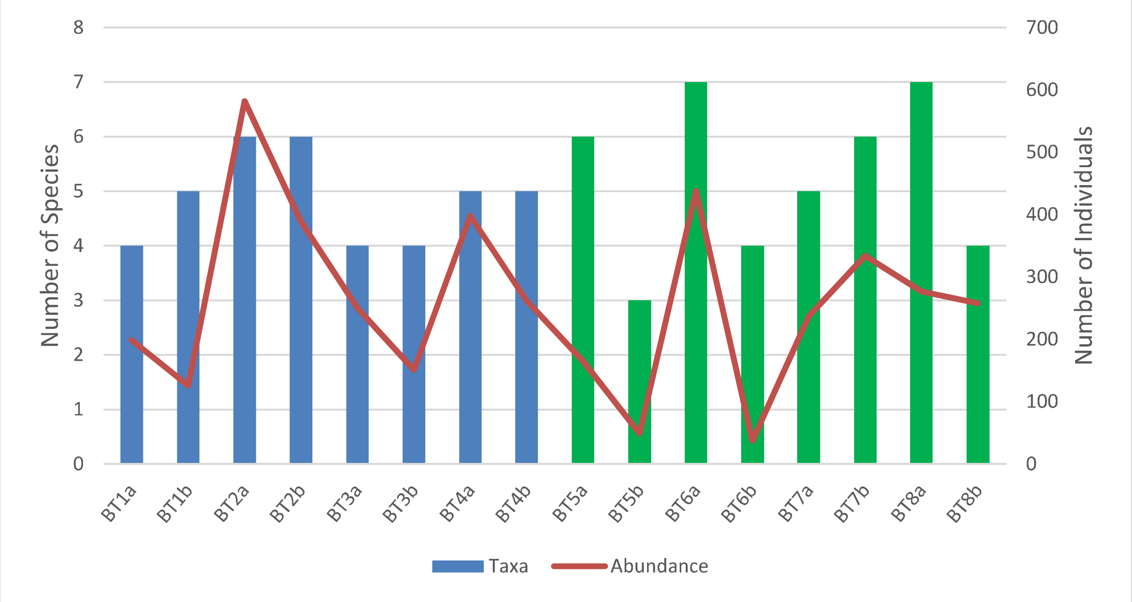

Figure 43. Total invertebrate species richness and abundance for beam trawls.

The control stations were slightly more diverse with 3 to 7 species recorded, although the abundance of invertebrates at individual stations was lower than that recorded within the development area and ranged between 37 and 438 (Figure 43).