Able UK Ltd

Intertidal benthic invertebrate survey at North Killingholme (Spring 2013).

Survey Report and Interim Results from the Autumn Killingholme Survey and the Spring Cherry Cobb Sands Survey

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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 and the compensation site at Cherry Cobb Sands. The current report summarises the results of the spring intertidal benthic survey at North Killingholme undertaken in May 2013 and also provides a brief summary of data processed to date from the autumn 2013 NKM intertidal survey and the spring CCS intertidal benthic survey.

2. Methods

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 (where possible in close proximity to sample sites utilised for the 2010 characterisation survey) 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. 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 is provided below and the positions of the samples provided in Figure 1.

Survey areas		area code	Transect	Number of replicate benthic		
				Upper	Mid	Lower
Impact	Under direct footprint of quay development	**DI**	DI.1	3	3	3
			DI.2	3	3	3
			DI.3	3	3	3
	Under the area of indirect impact north of the quay development	**IIN**	IIN.1	3	3	3
			IIN.2	3	3	3
			IIN.3	3	3	3
	Under the area of indirect impact south of the quay development	**IIS**	IIS.1	3	3	3
			IIS.2	3	3	3
			IIS.3	3	3	3
Control	Control area north of NKM	**CN**	CN.1	3	3	3
			CN.2	3	3	3
			CN.3	3	3	3

12 transects

3 locations x transect = 36 locations

3 repl x location = 108 samples = n

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.
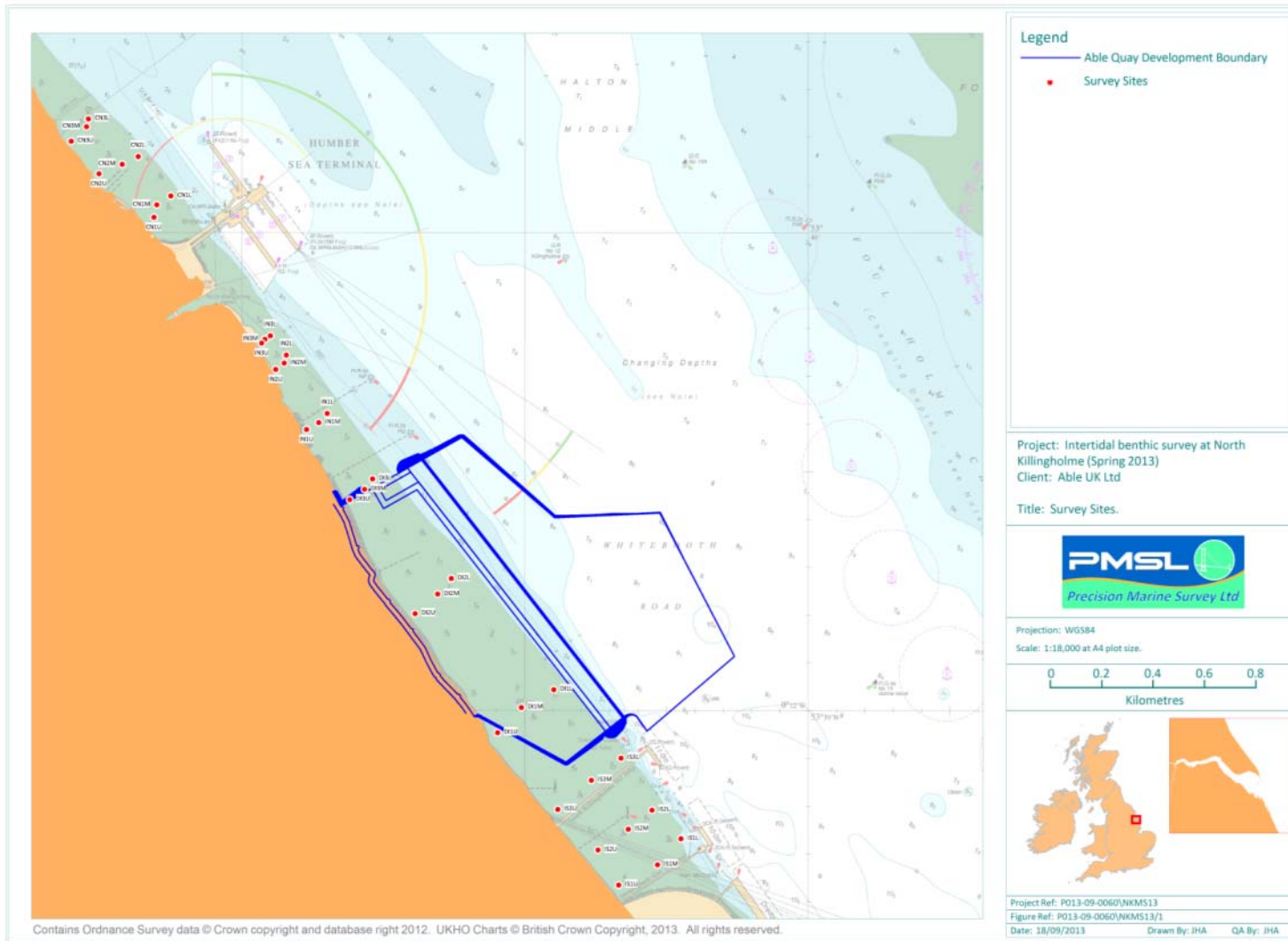
Figure 1.   Location of survey sites.

2.1   Laboratory Analysis

All laboratory methodologies were based on best practice and followed tried and tested method statements widely acknowledged within the industry (Rees et al, 1990, Barnett 1993, Turner 1999, Cooper & Rees 2002, Boyd et al, 2002, Prior et al, 2004 & Proudfoot et al, 2003). 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.

2.2   Sorting

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.

2.3   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.

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).

2.4   Biomass

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. Preliminary results presented here include wet weight biomass data although the final report will include Ash Free Dry Weight Biomass data (using, for example, Rumohr et al., 1987; Ricciardi and Bourget, 1998; and Eleftheriou and Basford, 1989) for comparison with targets. Following analysis each specimen was returned to its sample pot and stored in 70% IMS (Industrial Methylated Spirits).

2.5   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.

Total organic carbon was determined by a loss on ignition methodology. 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 600ºC for four hours. Once the sample has cooled the sample is then re-weighed and the difference between the two weights expressed as the percentage loss on ignition.

Particle size analysis is currently being completed and full results of this analysis will be included in the final report.

3.   Results

3.1   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 wet weight) at each site/replicate (B). Note – wet weight only is provided in this preliminary report – the final report will include AFDW biomass.

•   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 station. 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 Table 1 which gives average values per $0.01m^2$ whilst the values of biological parameters from the individual replicates are provided in Table 2. Replicate samples have also been pooled (i.e. per $0.03m^2$) to provide total values of the biological parameters based on the full species list which integrates any small scale variability in species composition at each site as shown in Table 3 and in addition the numbers of individuals (abundance) and biomass are also expressed per square metre. The pooled data were also used to derive values for the w statistic from ABC curves. A series of summary graphs/tables showing average values for each zone/shore level have also been derived from the pooled data (Figure 2) and the spatial variation in these parameters is highlighted in Figures 3 to 9.

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 values ranging from 0.005g to 1.7g per core. Total abundances and biomass based on pooled replicates when scaled up to values per metre square range from 167 to 38800 animals per m^2 and 0.05g to 174g 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 0.01m2 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 ABC plots shown in Appendix 1 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 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 for example were observed. No particular spatial pattern was evident in terms of ABC curves and resultant w statistics with examples of high and low values of w in all four survey areas although the direct impact (development) area generally included fewer low values.

Table 1.   Mean values of biological parameters for each site (0.01m^2).

Area	Shore	Site	Mean Numbers of Taxa	Mean Numbers of Individuals	Mean Biomass (g)	Mean Margalef's d	Mean Pielou's J	Mean Shannon's H'
Control North	Low	CN1L	4.00	14.67	0.0053	1.18	0.87	1.71
	Mid	CN1M	7.00	56.00	0.1105	1.43	0.70	1.85
	Upper	CN1U	7.33	37.67	0.5074	1.76	0.78	2.22
	Low	CN2L	5.00	107.33	0.1191	0.86	0.52	1.19
	Mid	CN2M	7.00	131.33	0.3008	1.23	0.46	1.27
	Upper	CN2U	5.33	388.00	1.3916	0.74	0.30	0.72
	Low	CN3L	5.67	129.00	0.1803	0.97	0.43	1.07
	Mid	CN3M	7.33	98.00	0.1237	1.39	0.66	1.91
	Upper	CN3U	3.67	47.67	0.3484	0.70	0.63	1.19
Direct Impact	Low	DI1L	3.33	13.00	0.1413	1.00	0.79	1.25
	Mid	DI1M	6.67	69.67	0.3312	1.18	0.52	1.35
	Upper	DI1U	6.67	81.00	1.7358	1.29	0.71	1.92
	Low	DI2L	4.67	26.67	0.0459	1.11	0.75	1.64
	Mid	DI2M	6.00	101.67	0.2949	0.95	0.78	1.87
	Upper	DI2U	2.67	56.67	0.5516	0.41	0.69	0.96
	Low	DI3L	4.33	29.67	0.0072	0.96	0.84	1.59
	Mid	DI3M	5.67	113.33	0.5089	0.99	0.66	1.66
	Upper	DI3U	7.00	294.33	0.7106	1.06	0.61	1.72
Indirect Impact North	Low	IN1L	3.33	9.67	0.0927	1.35	0.89	1.53
	Mid	IN1M	4.00	81.67	0.1585	0.61	0.64	1.18
	Upper	IN1U	7.00	72.00	0.4656	1.40	0.81	2.29
	Low	IN2L	1.67	1.67	0.0317	0.72	0.81	0.27
	Mid	IN2M	6.33	88.00	0.1842	1.19	0.59	1.52
	Upper	IN2U	6.00	66.67	0.2535	1.20	0.70	1.80
	Low	IN3L	2.00	2.33	0.0721	1.86	0.96	0.64
	Mid	IN3M	1.67	6.33	0.0343	0.69	0.91	0.76
	Upper	IN3U	5.33	67.00	0.1892	0.97	0.45	1.04
Indirect Impact South	Low	IS1L	1.00	1.00	0.0836	1.44	1.00	0.33
	Mid	IS1M	4.00	95.00	0.2362	0.65	0.35	0.68
	Upper	IS1U	2.67	22.00	0.0300	0.57	0.63	0.82
	Low	IS2L	1.33	2.33	0.0005	0.36	0.81	0.27
	Mid	IS2M	5.33	283.67	0.4536	0.77	0.21	0.51
	Upper	IS2U	3.67	18.33	0.0755	1.04	0.81	1.46
	Low	IS3L	3.00	12.33	0.0123	1.13	0.78	1.23
	Mid	IS3M	3.67	12.33	0.1388	1.10	0.75	1.39
	Upper	IS3U	3.33	63.00	0.0273	0.93	0.75	1.07

Table 2.   Values of biological parameters for each sample (0.01m^2).

Area	Shore	Sample	Quantitative Taxa	Qualitative Taxa	Numbers of Individuals	Biomass (g)	Margalef's d	Pielou's J	Shannon's H
	Low	CN1L A	4	4	12	0.0046	1.21	0.94	1.89
	Low	CN1L B	3	3	21	0.0082	0.66	0.87	1.38
	Low	CN1L C	5	5	11	0.003	1.67	0.80	1.87
	Mid	CN1M A	5	5	53	0.1222	1.01	0.74	1.73
	Mid	CN1M B	9	10	85	0.1373	1.80	0.59	1.88
	Mid	CN1M C	6	6	30	0.0721	1.47	0.75	1.93
	Upper	CN1U A	8	8	30	0.2125	2.06	0.72	2.17
	Upper	CN1U B	7	7	40	0.6878	1.63	0.85	2.39
	Upper	CN1U C	7	7	43	0.6218	1.60	0.75	2.11
	Low	CN2L A	5	5	80	0.0886	0.91	0.59	1.37
	Low	CN2L B	6	6	112	0.139	1.06	0.47	1.21
	Low	CN2L C	4	4	130	0.1298	0.62	0.49	0.99
	Mid	CN2M A	5	5	116	0.192	0.84	0.47	1.09
Control North	Mid	CN2M B	9	9	132	0.3383	1.64	0.40	1.26
	Mid	CN2M C	7	7	146	0.372	1.20	0.52	1.45
	Upper	CN2U A	5	5	552	1.0233	0.63	0.32	0.74
	Upper	CN2U B	5	5	295	1.6589	0.70	0.31	0.72
	Upper	CN2U C	6	6	317	1.4926	0.87	0.27	0.70
	Low	CN3L A	4	4	141	0.2106	0.61	0.42	0.84
	Low	CN3L B	6	6	137	0.1749	1.02	0.43	1.11
	Low	CN3L C	7	7	109	0.1555	1.28	0.45	1.26
	Mid	CN3M A	8	8	86	0.1224	1.57	0.71	2.14
	Mid	CN3M B	7	7	120	0.14	1.25	0.70	1.96
	Mid	CN3M C	7	7	88	0.1086	1.34	0.58	1.63
	Upper	CN3U A	4	4	67	0.4289	0.71	0.86	1.73
	Upper	CN3U B	4	4	37	0.4188	0.83	0.44	0.88
	Upper	CN3U C	3	3	39	0.1976	0.55	0.60	0.96
	Low	DI1L A	3	3	11	0.1884	0.83	0.78	1.24
	Low	DI1L B	5	5	25	0.1104	1.24	0.68	1.58
	Low	DI1L C	2	2	3	0.1252	0.91	0.92	0.92
	Mid	DI1M A	6	7	74	0.5286	1.16	0.61	1.59
	Mid	DI1M B	6	6	69	0.2539	1.18	0.48	1.23
	Mid	DI1M C	6	7	66	0.2112	1.19	0.47	1.22
	Upper	DI1U A	8	8	96	1.8106	1.53	0.71	2.14
	Upper	DI1U B	6	6	76	1.658	1.15	0.64	1.67
	Upper	DI1U C	6	6	71	1.7389	1.17	0.76	1.96
	Low	DI2L A	4	4	27	0.0424	0.91	0.73	1.45
	Low	DI2L B	4	4	23	0.0061	0.96	0.83	1.67
	Low	DI2L C	6	6	30	0.0893	1.47	0.69	1.79
	Mid	DI2M A	5	6	66	0.3292	0.95	0.83	1.92
Direct Impact	Mid	DI2M B	6	6	116	0.2325	1.05	0.71	1.83
	Mid	DI2M C	5	6	123	0.323	0.83	0.81	1.87
	Upper	DI2U A	2	2	54	0.7409	0.25	0.65	0.65
	Upper	DI2U B	3	3	53	0.447	0.50	0.55	0.87
	Upper	DI2U C	3	3	63	0.4668	0.48	0.86	1.36
	Low	DI3L A	3	3	21	0.006	0.66	0.92	1.46
	Low	DI3L B	3	3	27	0.0094	0.61	0.98	1.56
	Low	DI3L C	7	7	41	0.0063	1.62	0.62	1.75
	Mid	DI3M A	6	6	126	0.4557	1.03	0.67	1.72
	Mid	DI3M B	5	5	101	0.8778	0.87	0.69	1.60
	Mid	DI3M C	6	6	113	0.1932	1.06	0.64	1.65
	Upper	DI3U A	7	7	274	0.6427	1.07	0.60	1.68
	Upper	DI3U B	7	7	337	0.8236	1.03	0.59	1.65
	Upper	DI3U C	7	7	272	0.6656	1.07	0.65	1.84

Area	Shore	Sample	Quantitative Taxa	Qualitative Taxa	Numbers of Individuals	Biomass (g)	Margalef's d	Pielou's J	Shannon's H
	Low	IN1L A	3	3	19	0.1539	0.68	0.74	1.17
	Low	IN1L B	3	3	3	0.0856	1.82	1.00	1.58
	Low	IN1L C	4	4	7	0.0386	1.54	0.92	1.84
	Mid	IN1M A	4	4	76	0.1294	0.69	0.55	1.10
	Mid	IN1M B	4	4	72	0.1623	0.70	0.62	1.24
	Mid	IN1M C	3	4	97	0.1838	0.44	0.76	1.20
	Upper	IN1U A	7	7	72	0.4319	1.40	0.74	2.08
	Upper	IN1U B	7	7	74	0.5359	1.39	0.82	2.32
	Upper	IN1U C	7	7	70	0.429	1.41	0.88	2.47
	Low	IN2L A	2	2	4	0.0944	0.72	0.81	0.81
	Low	IN2L B	0	2	0	0.0005	-	-	0.00
	Low	IN2L C	1	1	1	0.0001	-	-	0.00
	Mid	IN2M A	7	7	81	0.1648	1.37	0.62	1.75
Indirect Impact North	Mid	IN2M B	4	4	84	0.1205	0.68	0.59	1.19
	Mid	IN2M C	8	8	99	0.2673	1.52	0.54	1.63
	Upper	IN2U A	6	6	55	0.2897	1.25	0.80	2.07
	Upper	IN2U B	5	5	83	0.1997	0.91	0.57	1.33
	Upper	IN2U C	7	7	62	0.2711	1.45	0.72	2.01
	Low	IN3L A	1	1	1	0.0001	-	-	0.00
	Low	IN3L B	4	4	5	0.216	1.86	0.96	1.92
	Low	IN3L C	1	1	1	0.0001	-	-	0.00
	Mid	IN3M A	0	0	0	0	-	-	0.00
	Mid	IN3M B	3	3	8	0.0908	0.96	0.82	1.30
	Mid	IN3M C	2	2	11	0.0121	0.42	0.99	0.99
	Upper	IN3U A	5	5	95	0.2607	0.88	0.29	0.67
	Upper	IN3U B	5	5	49	0.1598	1.03	0.53	1.23
	Upper	IN3U C	5	6	57	0.1471	0.99	0.53	1.23
	Low	IS1L A	0	0	0	0	-	-	0.00
	Low	IS1L B	1	1	1	0.2488	-	-	0.00
	Low	IS1L C	2	2	2	0.0021	1.44	1.00	1.00
	Mid	IS1M A	4	4	70	0.1689	0.71	0.41	0.82
	Mid	IS1M B	2	2	65	0.1722	0.24	0.27	0.27
	Mid	IS1M C	6	6	150	0.3675	1.00	0.36	0.94
	Upper	IS1U A	2	2	7	0.0058	0.51	0.86	0.86
	Upper	IS1U B	3	3	26	0.0398	0.61	0.47	0.74
	Upper	IS1U C	3	3	33	0.0445	0.57	0.55	0.87
	Low	IS2L A	1	1	1	0.0001	-	-	0.00
	Low	IS2L B	2	2	4	0.0002	0.72	0.81	0.81
	Low	IS2L C	1	1	2	0.0012	0.00		0.00
	Mid	IS2M A	6	6	233	0.399	0.92	0.22	0.57
Indirect Impact South	Mid	IS2M B	6	6	353	0.4846	0.85	0.20	0.53
	Mid	IS2M C	4	4	265	0.4771	0.54	0.21	0.42
	Upper	IS2U A	2	2	5	0.0038	0.62	0.72	0.72
	Upper	IS2U B	5	5	42	0.2128	1.07	0.82	1.91
	Upper	IS2U C	4	4	8	0.0098	1.44	0.88	1.75
	Low	IS3L A	3	3	3	0.0003	1.82	1.00	1.58
	Low	IS3L B	3	3	26	0.0352	0.61	0.67	1.06
	Low	IS3L C	3	3	8	0.0013	0.96	0.67	1.06
	Mid	IS3M A	3	3	12	0.1341	0.80	0.81	1.28
	Mid	IS3M B	4	4	8	0.2455	1.44	0.88	1.75
	Mid	IS3M C	4	4	17	0.0369	1.06	0.57	1.14
	Upper	IS3U A	4	4	173	0.0719	0.58	0.50	1.00
	Upper	IS3U B	2	3	2	0.0032	1.44	1.00	1.00
	Upper	IS3U C	3	3	14	0.0068	0.76	0.76	1.20

Project ref: P013-09-0060\NKMS13

Table 3.   Total values of biological parameters for each site (replicates pooled).

Area	Shore	Site	No. of Taxa	Numbers of Individuals (0.03m²)	Numbers of Individuals per m²	Biomass (g per 0.03m²)	Biomass (g per m²)	Margalef's d	Pielou's J	Shannon's H	ABC w statistic
Control North	Low	CN1L	6	44	1467	0.0158	0.53	1.32	0.71	1.85	0.09
	Mid	CN1M	12	168	5600	0.3316	11.05	1.95	0.61	2.12	0.06
	Upper	CN1U	10	113	3767	1.5221	50.74	1.90	0.74	2.44	0.28
	Low	CN2L	8	322	10733	0.3574	11.91	1.21	0.40	1.20	0.06
	Mid	CN2M	9	394	13133	0.9023	30.08	1.34	0.42	1.34	-0.01
	Upper	CN2U	8	1164	38800	4.1748	139.16	0.99	0.49	1.46	0.05
	Low	CN3L	8	387	12900	0.541	18.03	1.17	0.36	1.08	0.04
	Mid	CN3M	9	294	9800	0.371	12.37	1.41	0.63	1.98	0.07
	Upper	CN3U	4	143	4767	1.0453	34.84	0.60	0.70	1.41	0.34
Direct Impact	Low	DI1L	6	39	1300	0.424	14.13	1.36	0.72	1.87	0.25
	Mid	DI1M	9	209	6967	0.9937	33.12	1.12	0.53	1.50	-0.01
	Upper	DI1U	9	243	8100	5.2075	173.58	1.46	0.64	2.02	0.25
	Low	DI2L	8	80	2667	0.1378	4.59	1.60	0.65	1.94	0.10
	Mid	DI2M	7	305	10167	0.8847	29.49	0.87	0.74	1.91	0.14
	Upper	DI2U	3	170	5667	1.6547	55.16	0.39	0.67	1.06	0.27
	Low	DI3L	7	89	2967	0.0217	0.72	1.34	0.65	1.83	0.12
	Mid	DI3M	6	340	11333	1.5267	50.89	0.86	0.67	1.73	0.20
	Upper	DI3U	10	883	29433	2.1319	71.06	1.33	0.53	1.75	0.02
Indirect Impact North	Low	IN1L	5	29	967	0.2781	9.27	1.19	0.71	1.66	0.34
	Mid	IN1M	6	245	8167	0.4755	15.85	0.73	0.53	1.23	-0.05
	Upper	IN1U	8	216	7200	1.3968	46.56	1.30	0.78	2.35	0.37
	Low	IN2L	4	5	167	0.095	3.17	1.24	0.86	1.37	0.55
	Mid	IN2M	9	264	8800	0.5526	18.42	1.43	0.51	1.61	-0.01
	Upper	IN2U	8	200	6667	0.7605	25.35	1.32	0.64	1.91	0.08
	Low	IN3L	4	7	233	0.2162	7.21	1.54	0.92	1.84	0.66
	Mid	IN3M	3	19	633	0.1029	3.43	0.68	0.98	1.56	0.66
	Upper	IN3U	7	201	6700	0.5676	18.92	1.13	0.38	1.08	-0.08
Indirect Impact South	Low	IS1L	3	3	100	0.2509	8.36	1.82	1.00	1.58	0.99
	Mid	IS1M	7	285	9500	0.7086	23.62	1.06	0.30	0.84	-0.08
	Upper	IS1U	5	66	2200	0.0901	3.00	0.95	0.56	1.29	-0.12
	Low	IS2L	2	7	233	0.0015	0.05	0.51	0.59	0.59	0.15
	Mid	IS2M	7	851	28367	1.3607	45.36	0.89	0.18	0.52	-0.12
	Upper	IS2U	8	55	1833	0.2264	7.55	1.75	0.83	2.49	0.29
	Low	IS3L	5	37	1233	0.0368	1.23	1.11	0.70	1.63	0.25
	Mid	IS3M	6	37	1233	0.4165	13.88	1.38	0.77	1.98	0.20
	Upper	IS3U	5	189	6300	0.0819	2.73	0.76	0.48	1.10	0.12

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
Low	7.33	7.00	4.33	3.33
Mid	10.00	7.33	6.00	6.67
Upper	7.33	7.33	7.67	6.00

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
Low	251.00	69.33	13.67	15.67
Mid	285.33	284.67	176.00	391.00
Upper	473.33	432.00	205.67	103.33

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
Low	0.30	0.19	0.20	0.10
Mid	0.53	1.14	0.38	0.83
Upper	2.25	3.00	0.91	0.13

Figure 2. **Average values (with standard error) of biological parameters (per 0.03m^2) for each survey area.**

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
■ Low	1.24	1.43	1.32	1.15
■ Mid	1.57	0.95	0.95	1.11
■ Upper	1.17	1.06	1.25	1.15

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
■ Low	0.49	0.67	0.83	0.76
■ Mid	0.55	0.65	0.67	0.42
■ Upper	0.64	0.61	0.60	0.62

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
■ Low	1.38	1.88	1.62	1.27
■ Mid	1.81	1.71	1.47	1.11
■ Upper	1.77	1.61	1.78	1.63

Figure 2 (cont.). Average values (with standard error) of biological parameters (per 0.03m^2) for each survey area.

	Control North	Direct Impact	Indirect Impact North	Indirect Impact South
■ Low	0.06	0.16	0.52	0.46
■ Mid	0.04	0.11	0.20	0.00
■ Upper	0.22	0.18	0.12	0.10

Figure 2 (cont.). Average values (with standard error) of biological parameters (per 0.03m^2) for each survey area.
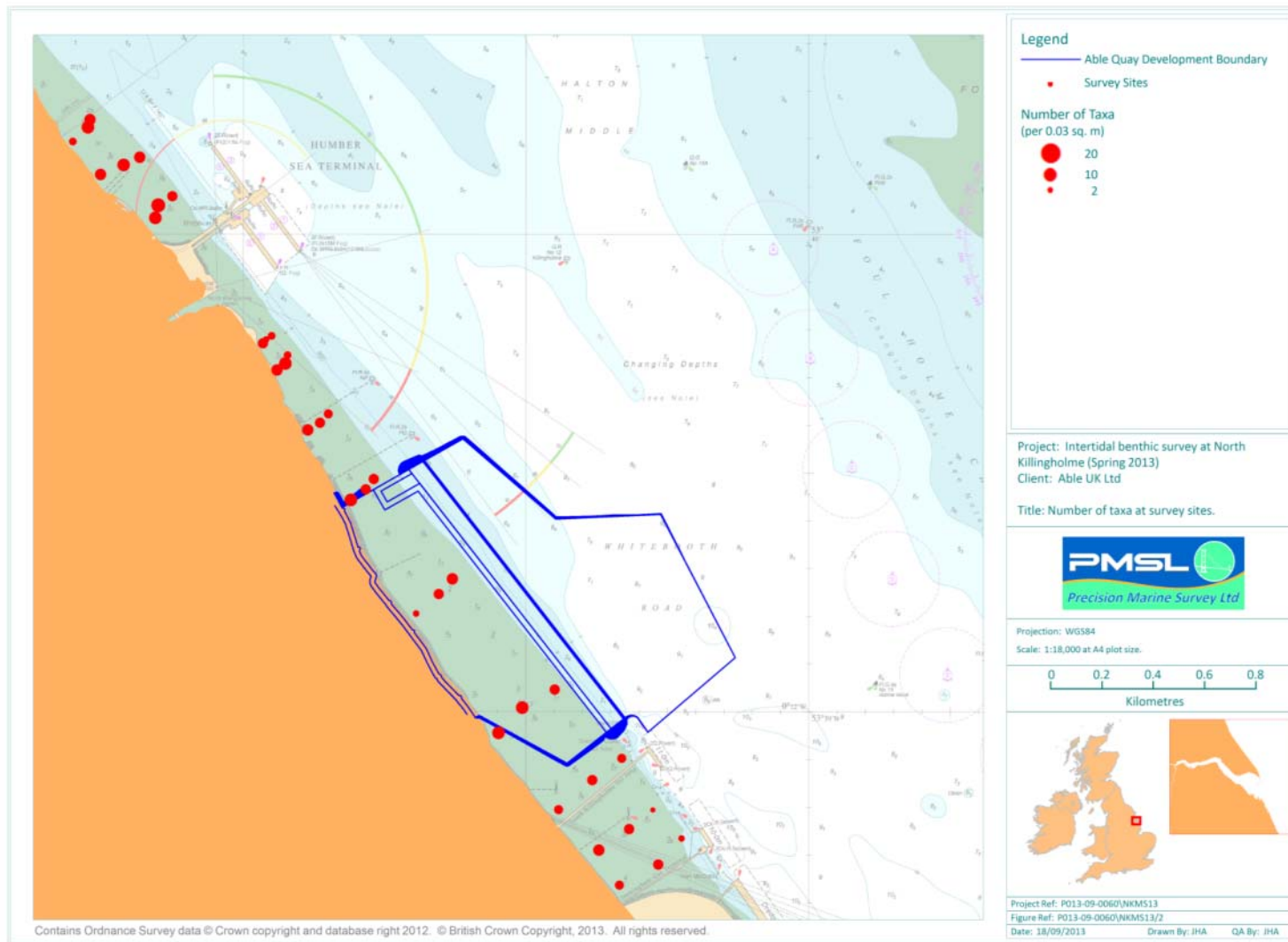
Figure 3.   Number of taxa per 0.03m² at the survey sites.
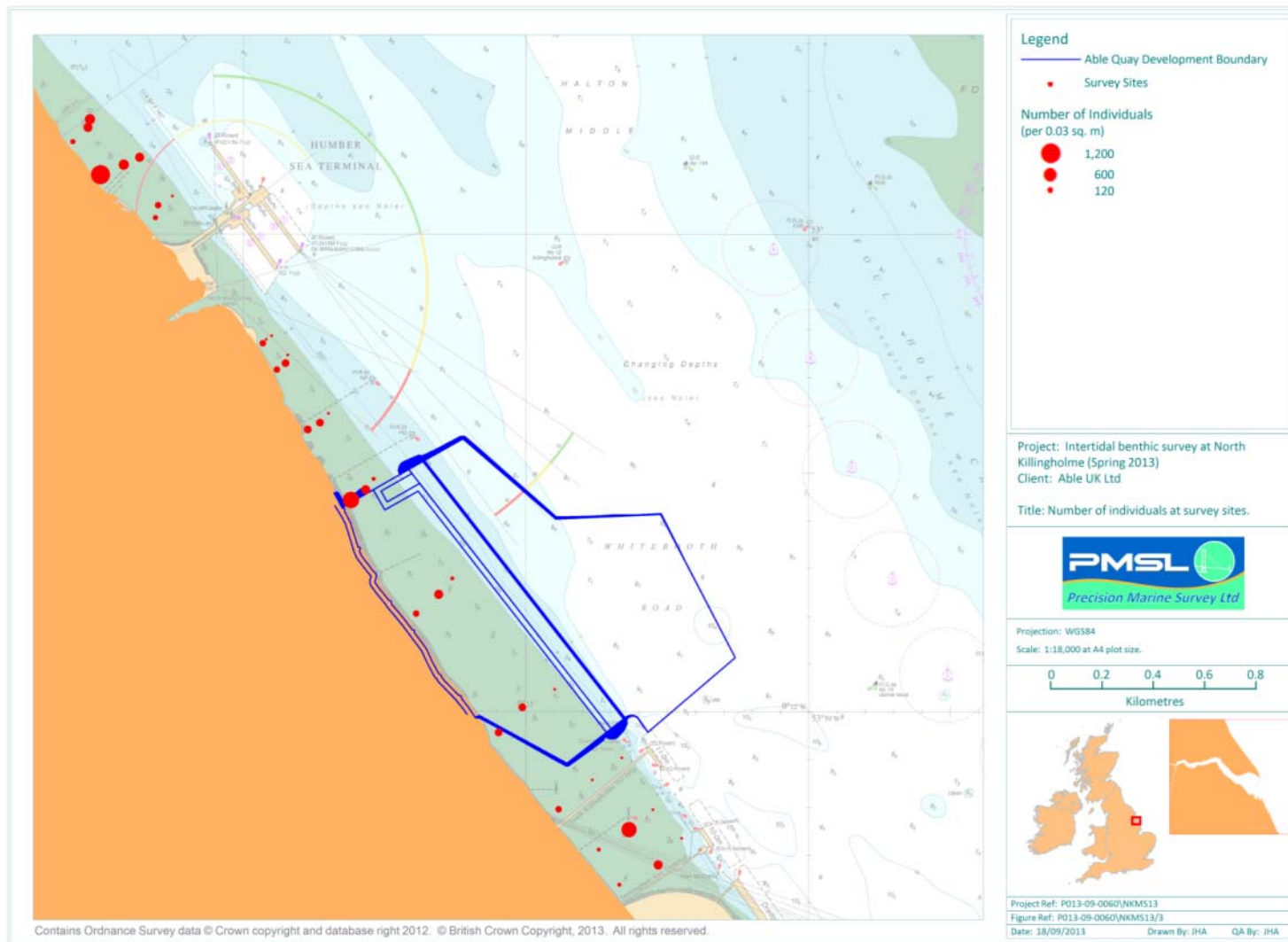
Figure 4.   Numbers of individuals per 0.03m² at the survey sites.
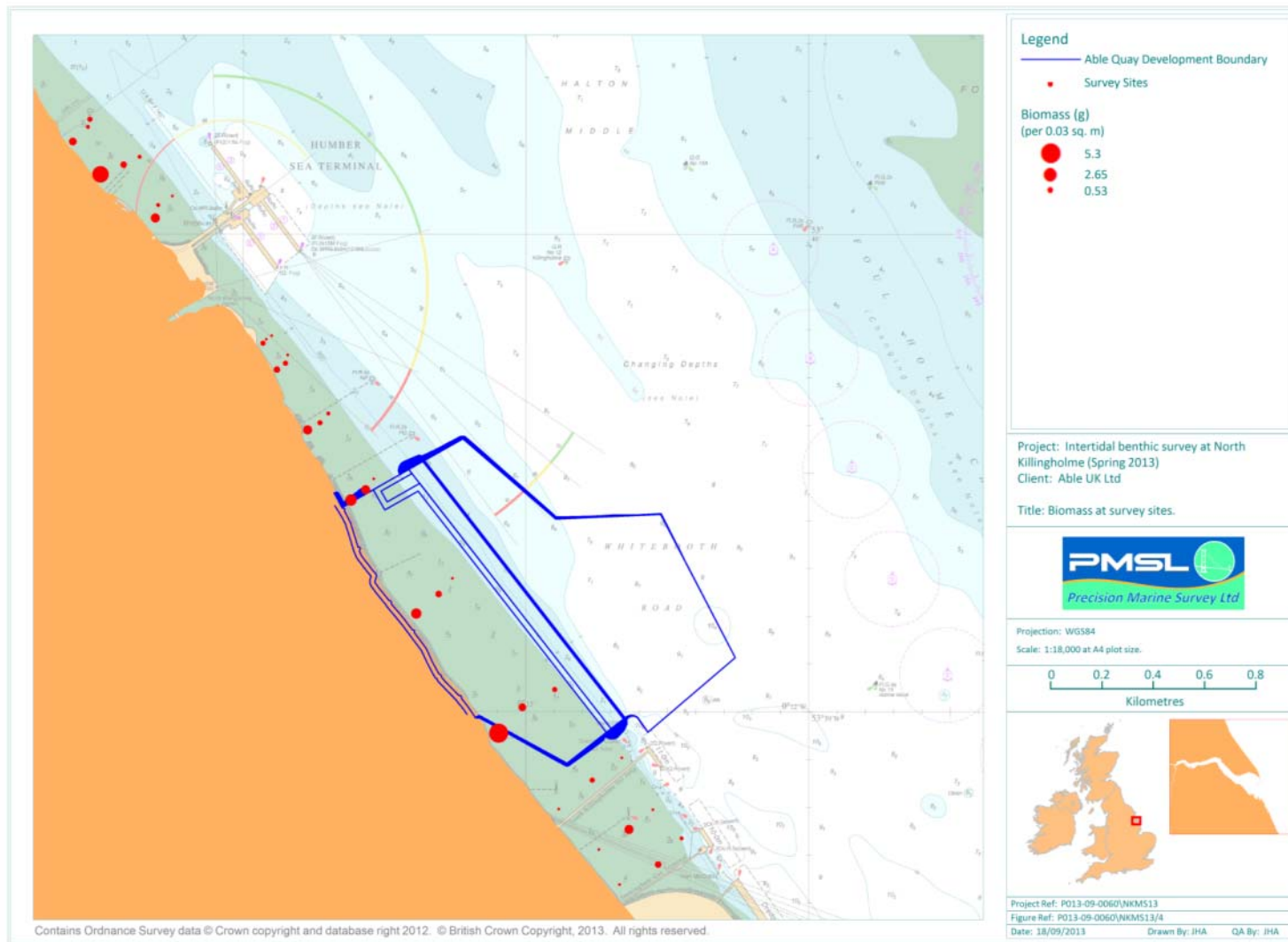
Figure 5.   Biomass (g per 0.03m^2) at the survey sites.
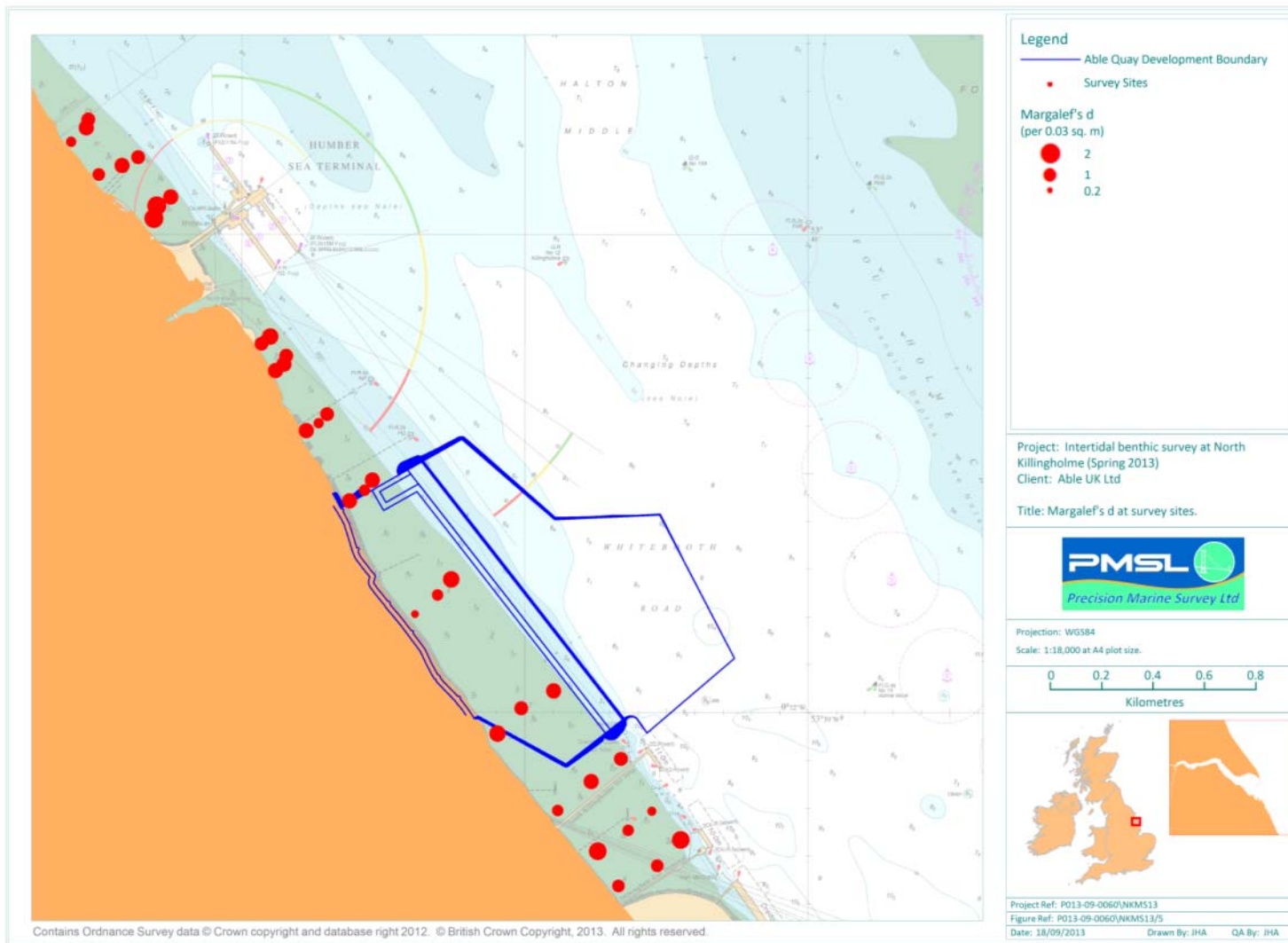
Figure 6.   Margalef's d at the survey sites (per 0.03m^2).
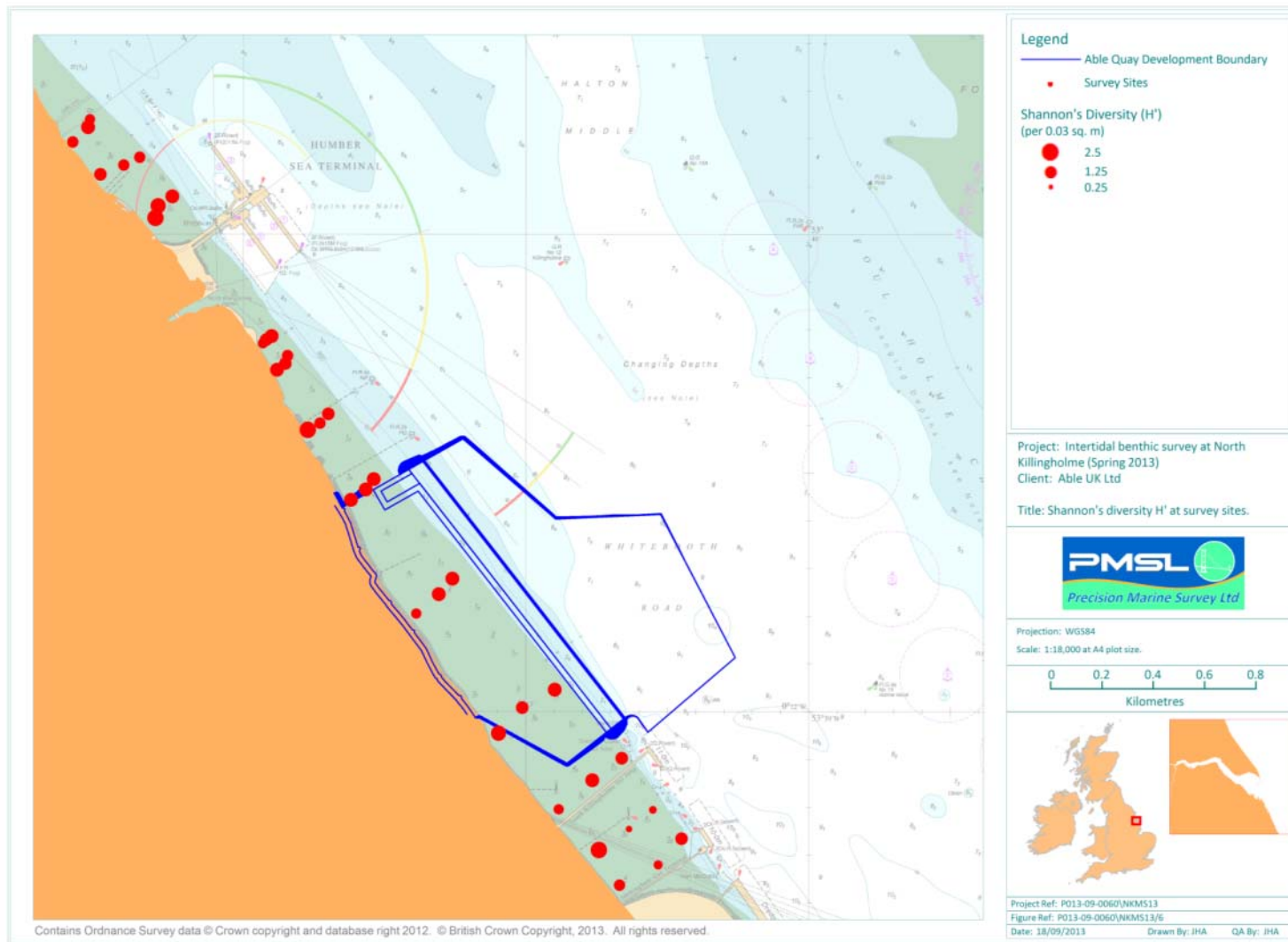
Figure 7.   Shannon's diversity H' at the survey sites (per 0.03m^2).
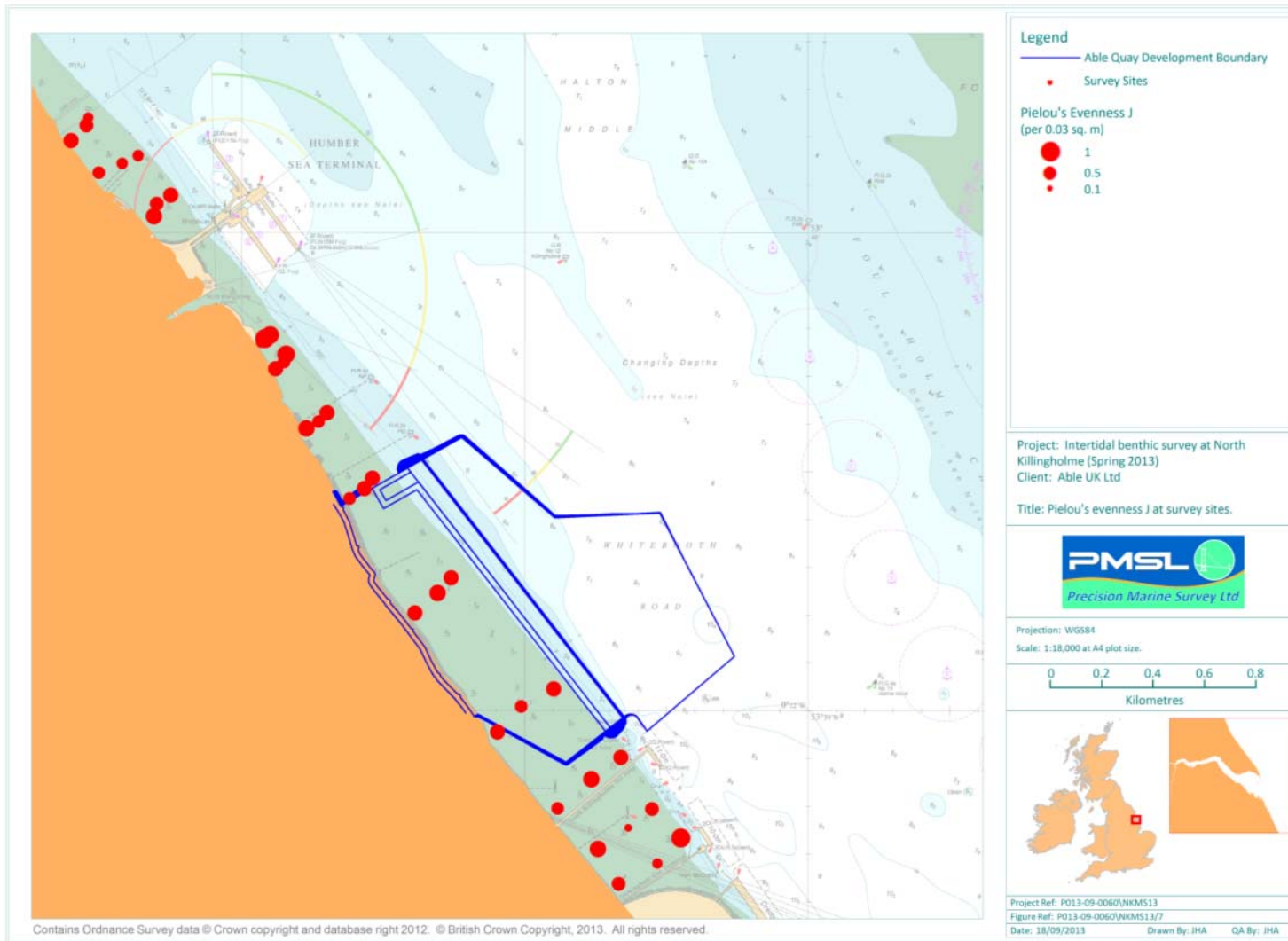
Figure 8.   Pielou's evenness J at the survey sites (per 0.03m^2).
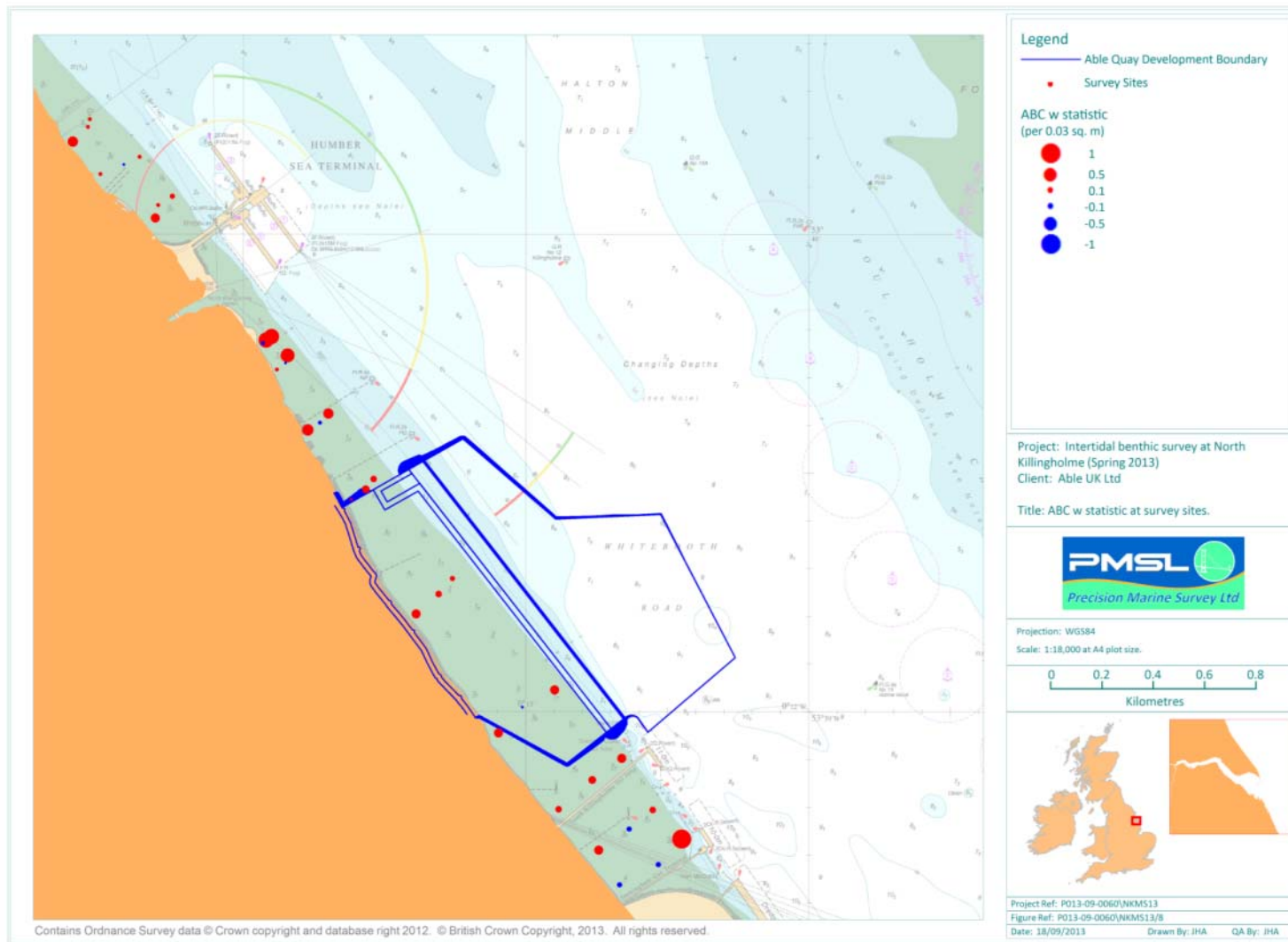
Figure 9.   ABC w statistic at the survey sites (per 0.03m^2).

3.2   Species composition of benthic communities

A summary of the dominant taxa by abundance and biomass has been provided based on pooled data at each site. The average abundances and biomass per site (0.03m^2) across the entire survey area are provided in Table 4 whilst Tables 5 to 8 shows average abundance and biomass of taxa for each shore level from the four survey areas. 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* and *Macoma balthica* along with *Corophium volutator* accounted for the majority of the biomass (85% of total).

Table 4.   Ranked average abundance and biomass for the full survey area.

| Taxa	Average Abundance	% of sites	% Cont.	Taxa	Average Biomass	% of sites	% Cont.
Tubificoides benedii	74.22	94.44	32.98	Hediste diversicolor	0.4305	63.89	51.90
Corophium volutator	60.89	83.33	60.03	Macoma balthica	0.1385	77.78	68.59
Tubificoides agg. (pseudogaster)	26.81	36.11	71.94	Corophium volutator	0.1352	83.33	84.88
Hediste diversicolor	17.33	63.89	79.64	Tubificoides benedii	0.0757	94.44	94.01
Streblospio shrubsolii	16.06	72.22	86.77	Tubificoides agg. (pseudogaster)	0.0305	36.11	97.69
Enchytraeidae	9.56	27.78	91.02	Enchytraeidae	0.0081	27.78	98.66
Nematoda	9.17	72.22	95.09	Streblospio shrubsolii	0.0056	72.22	99.33
Collembola sp.	5.31	16.67	97.45	Diptera sp.	0.0019	19.44	99.56
Macoma balthica	2.31	77.78	98.47	Nephtys hombergii	0.0018	5.56	99.79
Tubificoides swirencoides	0.94	8.33	98.89	Lekanesphaera hookeri	0.0004	2.78	99.84
Pygospio elegans	0.83	36.11	99.26	Coleoptera sp.	0.0004	5.56	99.88
Diptera sp.	0.56	19.44	99.51	Tubificoides swirencoides	0.0002	8.33	99.91
Manayunkia aestuarina	0.50	16.67	99.73	Tharyx sp.	0.0002	13.89	99.94
Tharyx sp.	0.28	13.89	99.85	Nematoda	0.0002	72.22	99.96
Nephtys hombergii	0.08	5.56	99.89	Collembola sp.	0.0001	16.67	99.98
Coleoptera sp.	0.08	5.56	99.93	Pygospio elegans	0.0001	36.11	99.99
Nemertea	0.03	2.78	99.94	Nemertea	0.0000	2.78	99.99
Eteone longa/flava agg.	0.03	2.78	99.95	Manayunkia aestuarina	0.0000	16.67	100.00
Naididae	0.03	2.78	99.96	Tellinacea juv.	0.0000	2.78	100.00
Dipolydora coeca	0.03	2.78	99.98	Eteone longa/flava agg.	0.0000	2.78	100.00
Lekanesphaera hookeri	0.03	2.78	99.99	Naididae	0.0000	2.78	100.00
Tellinacea juv.	0.03	2.78	100.00	Spionidae sp.	0.0000	2.78	100.00
Spionidae sp.	P	2.78		Dipolydora coeca	0.0000	2.78	100.00

The summaries of dominant taxa within the different shore levels in each survey area (Tables 5 to 7) highlight a broadly similar pattern with taxa such as *Corophium volutator*, *Tubificoides* spp. and S*treblospio shrubsolii* generally dominating in varying degrees in all areas with species such as *Streblospio shrubsolii* generally more prevalent on the low shore. Upper shore sites 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. The maps shown in Figures 11 to 15 highlight the distribution of key taxa such as *Hediste diversicolor*, *Macoma balthica*, *Corophium volutator, Streblospio shrubsolii* and oligochaetes across the survey area. These highlight a number of spatial trends such as the widespread coverage by *Corophium volutator*, particularly in the northern indirect impact area and control area. *Streblospio shrubsolii* is particularly common in lower shore areas whilst *Hediste diversicolor* is more common in upper shore sites. *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.

Table 5. **Average ranked abundance and biomass (per 0.03m^2) for the low shore sites.**

Control North Low Shore			Direct Impact Low Shore			Indirect Impact North Low Shore			Indirect Impact South Low Shore		
Taxa	Average A	% of sites	Taxa	Average A	% of sites	Taxa	Average A	% of sites	Taxa	Average A	% of sites
Corophium volutator	176.67	100.00	Streblospio shrubsolii	30.33	100.00	Streblospio shrubsolii	6.67	100.00	Tubificoides swirencoides	6.00	33.33
Streblospio shrubsolii	52.00	100.00	Nematoda	16.67	66.67	Tubificoides benedii	4.33	100.00	Streblospio shrubsolii	4.67	33.33
Nematoda	10.00	100.00	Tubificoides benedii	11.00	100.00	Macoma balthica	1.67	100.00	Tubificoides benedii	2.67	100.00
Tubificoides benedii	8.33	100.00	Tubificoides swirencoides	5.33	66.67	Nematoda	0.33	33.33	Corophium volutator	1.00	66.67
Macoma balthica	1.67	100.00	Macoma balthica	2.67	100.00	Corophium volutator	0.33	33.33	Macoma balthica	0.67	66.67
Hediste diversicolor	0.67	66.67	Pygospio elegans	1.00	66.67	Tellinacea juv.	0.33	33.33	Nephtys hombergii	0.67	33.33
Pygospio elegans	0.67	66.67	Corophium volutator	0.67	66.67	Spionidae sp.	P	33.33			
Tubificoides agg. (pseudogaster)	0.33	33.33	Tharyx sp.	0.67	33.33						
Enchytraeidae	0.33	33.33	Hediste diversicolor	0.33	33.33						
Dipolydora coeca	0.33	33.33	Nephtys hombergii	0.33	33.33						
			Diptera sp.	0.33	33.33						

Control North Low Shore			Direct Impact Low Shore			Indirect Impact North Low Shore			Indirect Impact South Low Shore		
Taxa	Average B	% of sites	Taxa	Average B	% of sites	Taxa	Average B	% of sites	Taxa	Average B	% of sites
Corophium volutator	0.2627	100.00	Macoma balthica	0.1335	100.00	Macoma balthica	0.1912	100.00	Macoma balthica	0.0830	66.67
Streblospio shrubsolii	0.0233	100.00	Hediste diversicolor	0.0286	33.33	Tubificoides benedii	0.0031	100.00	Nephtys hombergii	0.0099	33.33
Macoma balthica	0.0120	100.00	Nephtys hombergii	0.0121	33.33	Streblospio shrubsolii	0.0018	100.00	Tubificoides swirencoides	0.0018	33.33
Tubificoides benedii	0.0045	100.00	Streblospio shrubsolii	0.0085	100.00	Tellinacea juv.	0.0002	33.33	Corophium volutator	0.0008	66.67
Hediste diversicolor	0.0018	66.67	Tubificoides benedii	0.0057	100.00	Corophium volutator	0.0001	33.33	Tubificoides benedii	0.0005	100.00
Nematoda	0.0003	100.00	Corophium volutator	0.0047	66.67	Nematoda	0.0000	33.33	Streblospio shrubsolii	0.0004	33.33
Pygospio elegans	0.0001	66.67	Tubificoides swirencoides	0.0010	66.67	Spionidae sp.	0.0000	33.33			
Tubificoides agg. (pseudogaster)	0.0000	33.33	Nematoda	0.0002	66.67						
Enchytraeidae	0.0000	33.33	Pygospio elegans	0.0001	66.67						
Dipolydora coeca	0.0000	33.33	Tharyx sp.	0.0001	33.33						
			Diptera sp.	0.0000	33.33						

Table 6.   Average ranked abundance and biomass (per 0.03m²) for the mid shore sites.

Control North Mid Shore			Direct Impact Mid Shore			Indirect Impact North Mid Shore			Indirect Impact South Mid Shore		
Taxa	Average A	% of sites	Taxa	Average A	% of sites	Taxa	Average A	% of sites	Taxa	Average A	% of sites
Corophium volutator	161.33	100.00	Tubificoides benedii	161.33	100.00	Corophium volutator	85.00	100.00	Tubificoides benedii	350.00	100.00
Tubificoides benedii	70.00	100.00	Corophium volutator	57.00	100.00	Tubificoides benedii	76.33	100.00	Streblospio shrubsolii	13.33	66.67
Nematoda	20.33	100.00	Streblospio shrubsolii	38.00	100.00	Streblospio shrubsolii	5.00	33.33	Hediste diversicolor	10.67	100.00
Streblospio shrubsolii	9.33	100.00	Nematoda	14.67	100.00	Nematoda	2.67	66.67	Corophium volutator	5.67	100.00
Enchytraeidae	9.00	100.00	Macoma balthica	10.33	100.00	Hediste diversicolor	2.00	100.00	Nematoda	4.67	66.67
Pygospio elegans	6.00	100.00	Tharyx sp.	2.00	66.67	Diptera sp.	2.00	66.67	Manayunkia aestuarina	4.00	33.33
Macoma balthica	4.33	100.00	Pygospio elegans	0.67	66.67	Macoma balthica	1.67	66.67	Macoma balthica	1.33	100.00
Hediste diversicolor	3.00	100.00	bificoides agg. (pseudogast	0.67	33.33	Tharyx sp.	0.67	33.33	Pygospio elegans	0.67	66.67
Tubificoides agg. (pseudogaster)	0.67	33.33	Hediste diversicolor	P	66.67	Coleoptera sp.	0.67	33.33	bificoides agg. (pseudogast	0.67	33.33
Nemertea	0.33	33.33									
Manayunkia aestuarina	0.33	33.33									
Naididae	0.33	33.33									
Coleoptera sp.	0.33	33.33									
Tharyx sp.	P	33.33									

Control North Mid Shore			Direct Impact Mid Shore			Indirect Impact North Mid Shore			Indirect Impact South Mid Shore		
Taxa	Average B	% of sites	Taxa	Average B	% of sites	Taxa	Average B	% of sites	Taxa	Average B	% of sites
Corophium volutator	0.2471	100.00	Macoma balthica	0.7398	100.00	Corophium volutator	0.1793	100.00	Tubificoides benedii	0.4076	100.00
Macoma balthica	0.1925	100.00	Corophium volutator	0.1991	100.00	Tubificoides benedii	0.0991	100.00	Hediste diversicolor	0.3320	100.00
Tubificoides benedii	0.0482	100.00	Tubificoides benedii	0.1593	100.00	Macoma balthica	0.0595	66.67	Macoma balthica	0.0539	100.00
Hediste diversicolor	0.0428	100.00	Hediste diversicolor	0.0201	66.67	Hediste diversicolor	0.0306	100.00	Corophium volutator	0.0282	100.00
Streblospio shrubsolii	0.0024	100.00	Streblospio shrubsolii	0.0143	100.00	Coleoptera sp.	0.0042	33.33	Streblospio shrubsolii	0.0053	66.67
Enchytraeidae	0.0005	100.00	Tharyx sp.	0.0021	66.67	Streblospio shrubsolii	0.0019	33.33	bificoides agg. (pseudogast	0.0012	33.33
Nemertea	0.0005	33.33	Nematoda	0.0003	100.00	Diptera sp.	0.0017	66.67	Nematoda	0.0001	66.67
Coleoptera sp.	0.0004	33.33	Pygospio elegans	0.0001	66.67	Tharyx sp.	0.0005	33.33	Pygospio elegans	0.0001	66.67
Pygospio elegans	0.0003	100.00	bificoides agg. (pseudogast	0.0001	33.33	Nematoda	0.0002	66.67	Manayunkia aestuarina	0.0001	33.33
Nematoda	0.0002	100.00									
Tharyx sp.	0.0000	33.33									
Manayunkia aestuarina	0.0000	33.33									
Naididae	0.0000	33.33									
Tubificoides agg. (pseudogaster)	0.0000	33.33									

Table 7.   Average ranked abundance and biomass (per 0.03m^2) for the upper shore sites.

Control North Upper Shore			Direct Impact Upper Shore			Indirect Impact North Upper Shore			Indirect Impact South Upper Shore		
Taxa	Average A	% of sites	Taxa	Average A	% of sites	Taxa	Average A	% of sites	Taxa	Average A	% of sites
Tubificoides agg. (pseudogaster)	264.00	100.00	Tubificoides benedii	186.67	100.00	Corophium volutator	117.33	100.00	Collembola sp.	44.33	100.00
Enchytraeidae	96.33	66.67	Corophium volutator	102.00	100.00	Hediste diversicolor	38.00	100.00	bificoides agg. (pseudogast	37.67	100.00
Hediste diversicolor	53.67	100.00	Hediste diversicolor	99.67	100.00	Streblospio shrubsolii	16.33	100.00	Tubificoides benedii	9.33	100.00
Corophium volutator	21.67	100.00	Nematoda	17.00	66.67	ficoides agg. (pseudoga	10.00	66.67	Nematoda	4.33	66.67
Collembola sp.	18.67	33.33	Streblospio shrubsolii	15.00	66.67	Tubificoides benedii	9.67	100.00	Diptera sp.	3.33	100.00
Nematoda	14.67	100.00	bificoides agg. (pseudogast	7.67	33.33	Enchytraeidae	8.67	100.00	Corophium volutator	2.00	33.33
Tubificoides benedii	1.00	33.33	Manayunkia aestuarina	1.00	66.67	Nematoda	4.67	100.00	Streblospio shrubsolii	1.33	33.33
Diptera sp.	1.00	33.33	Macoma balthica	1.00	33.33	Macoma balthica	1.00	100.00	Macoma balthica	0.67	33.33
Manayunkia aestuarina	0.67	66.67	Collembola sp.	0.67	66.67				Lekanesphaera hookeri	0.33	33.33
Streblospio shrubsolii	0.67	33.33	Pygospio elegans	0.67	33.33						
Macoma balthica	0.67	33.33	Eteone longa/flava agg.	0.33	33.33						
Pygospio elegans	0.33	33.33	Enchytraeidae	0.33	33.33						

| Control North Upper Shore			Direct Impact Upper Shore			Indirect Impact North Upper Shore			Indirect Impact South Upper Shore		
Taxa	Average B	% of sites	Taxa	Average B	% of sites	Taxa	Average B	% of sites	Taxa	Average B	% of sites
Hediste diversicolor	1.7134	100.00	Hediste diversicolor	2.4079	100.00	Hediste diversicolor	0.5889	100.00	Macoma balthica	0.0467	33.33
Tubificoides agg. (pseudogaster)	0.3123	100.00	Corophium volutator	0.4052	100.00	Corophium volutator	0.2393	100.00	bificoides agg. (pseudogast	0.0416	100.00
Enchytraeidae	0.0954	66.67	Tubificoides benedii	0.1600	100.00	Macoma balthica	0.0599	100.00	Corophium volutator	0.0139	33.33
Macoma balthica	0.0731	33.33	Macoma balthica	0.0165	33.33	Tubificoides benedii	0.0091	100.00	Diptera sp.	0.0122	100.00
Corophium volutator	0.0415	100.00	bificoides agg. (pseudogast	0.0041	33.33	ficoides agg. (pseudoga	0.0064	66.67	Tubificoides benedii	0.0116	100.00
Diptera sp.	0.0093	33.33	Streblospio shrubsolii	0.0038	66.67	Streblospio shrubsolii	0.0036	100.00	Lekanesphaera hookeri	0.0053	33.33
Collembola sp.	0.0008	33.33	Nematoda	0.0002	66.67	Enchytraeidae	0.0009	100.00	Streblospio shrubsolii	0.0007	33.33
Streblospio shrubsolii	0.0006	33.33	Manayunkia aestuarina	0.0001	66.67	Nematoda	0.0002	100.00	Collembola sp.	0.0007	100.00
Pygospio elegans	0.0005	33.33	Collembola sp.	0.0001	66.67				Nematoda	0.0001	66.67
Nematoda	0.0003	100.00	Eteone longa/flava agg.	0.0000	33.33						
Tubificoides benedii	0.0001	33.33	Pygospio elegans	0.0000	33.33						
Manayunkia aestuarina	0.0001	66.67	Enchytraeidae	0.0000	33.33						
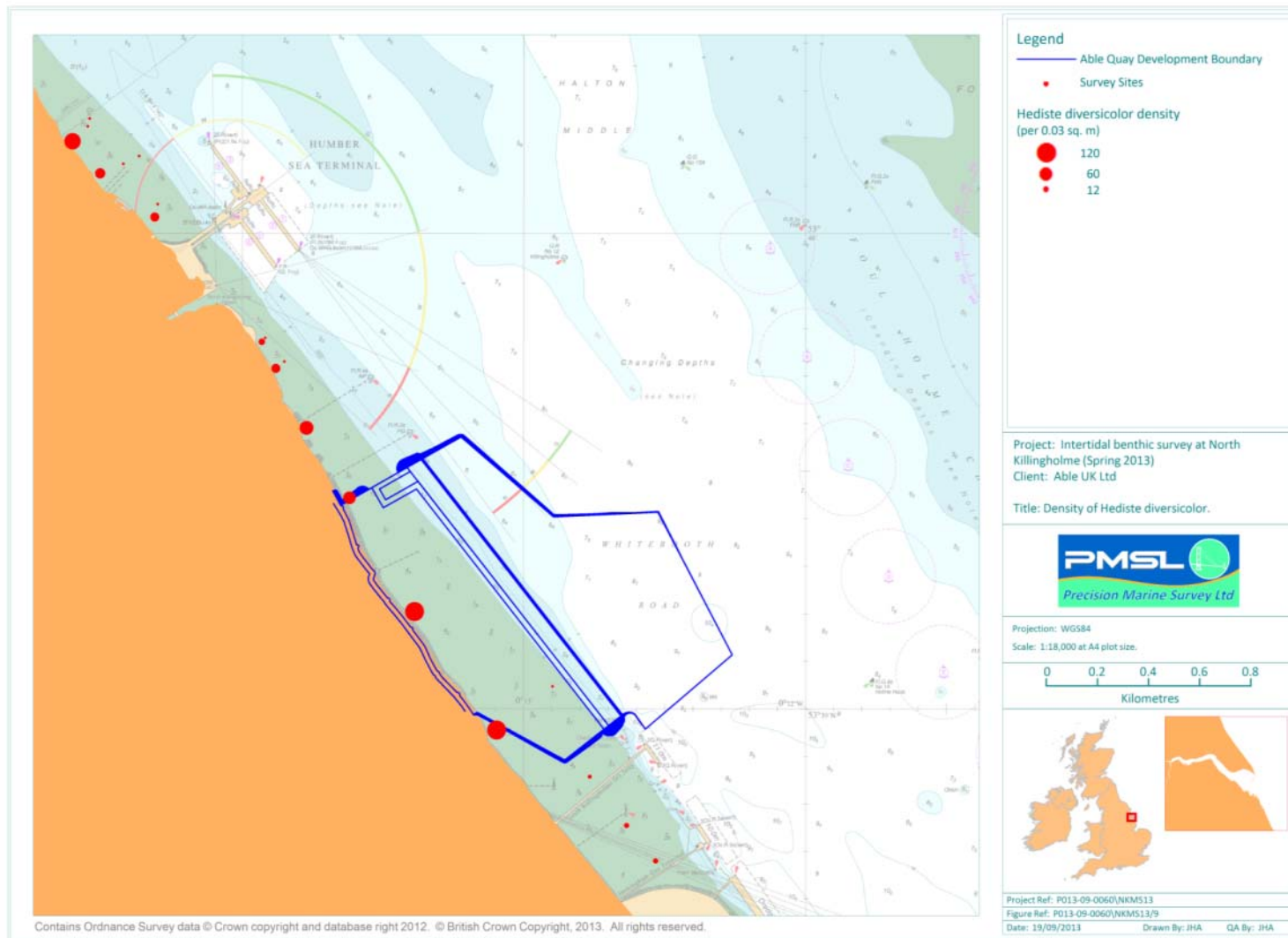
Figure 10.   Spatial distribution in numbers of *Hediste diversicolor*.
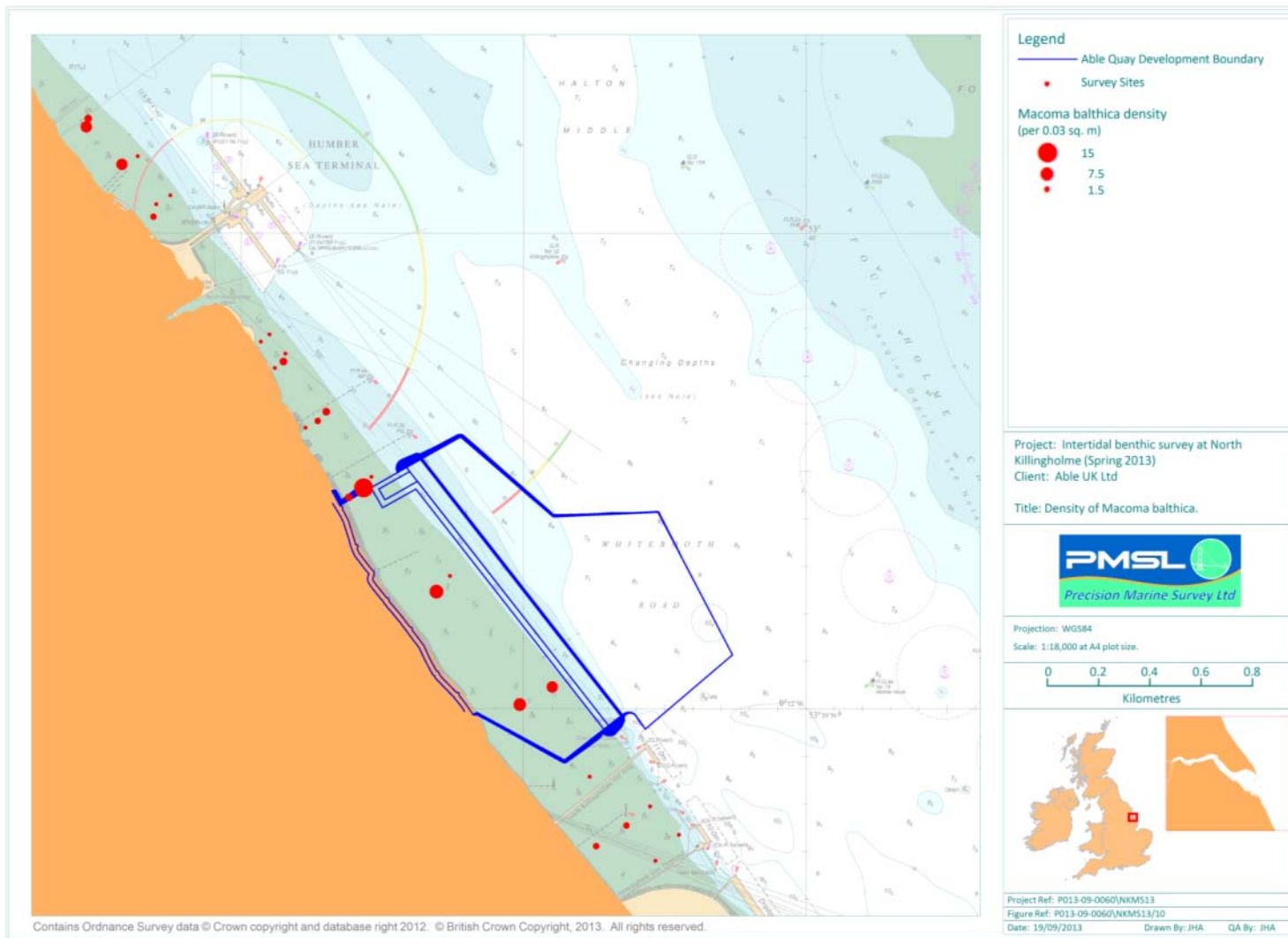
Figure 11.   Spatial distribution in numbers of *Macoma balthica*.
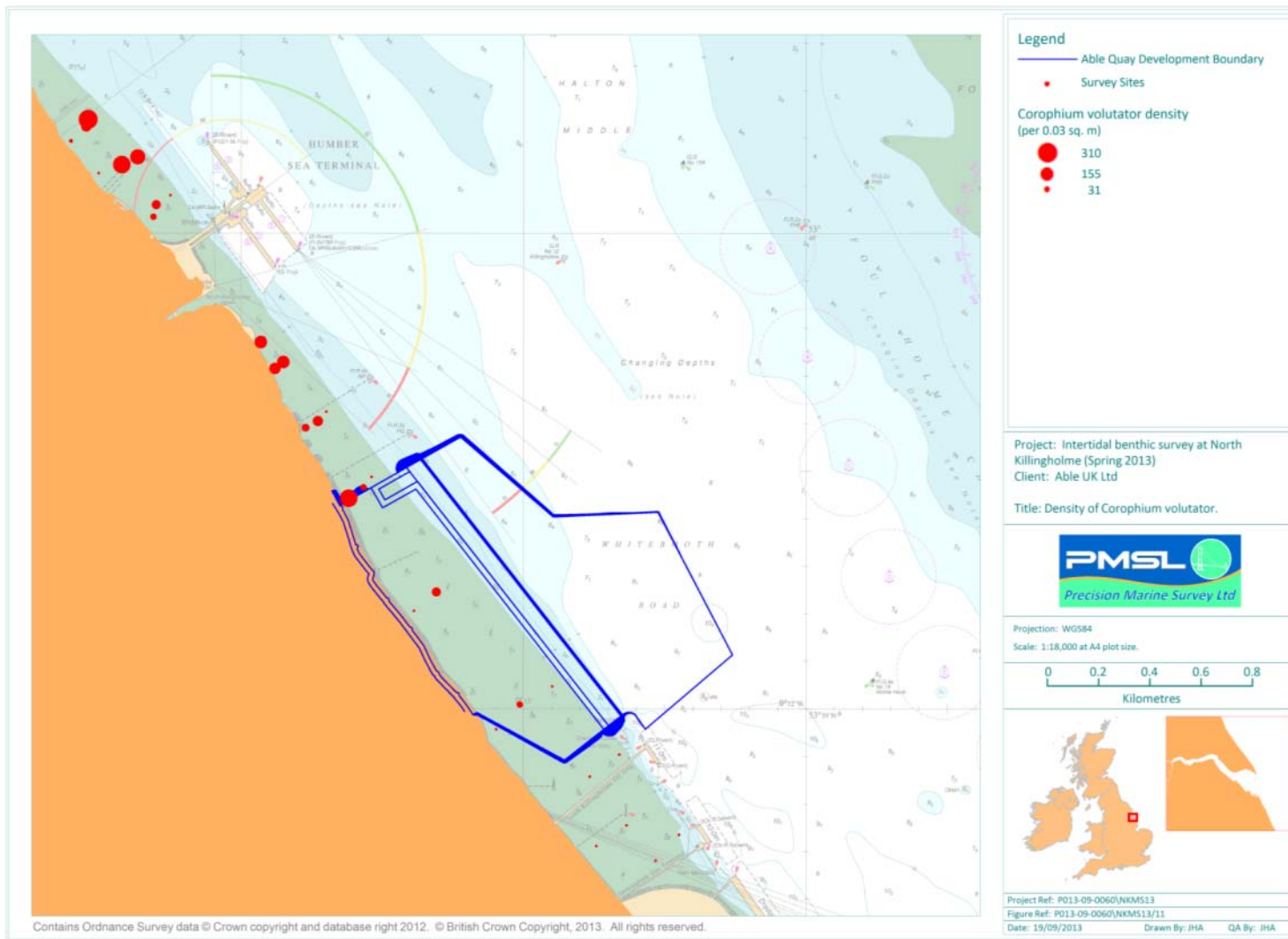
Figure 12. Spatial distribution in numbers of *Corophium volutator*.
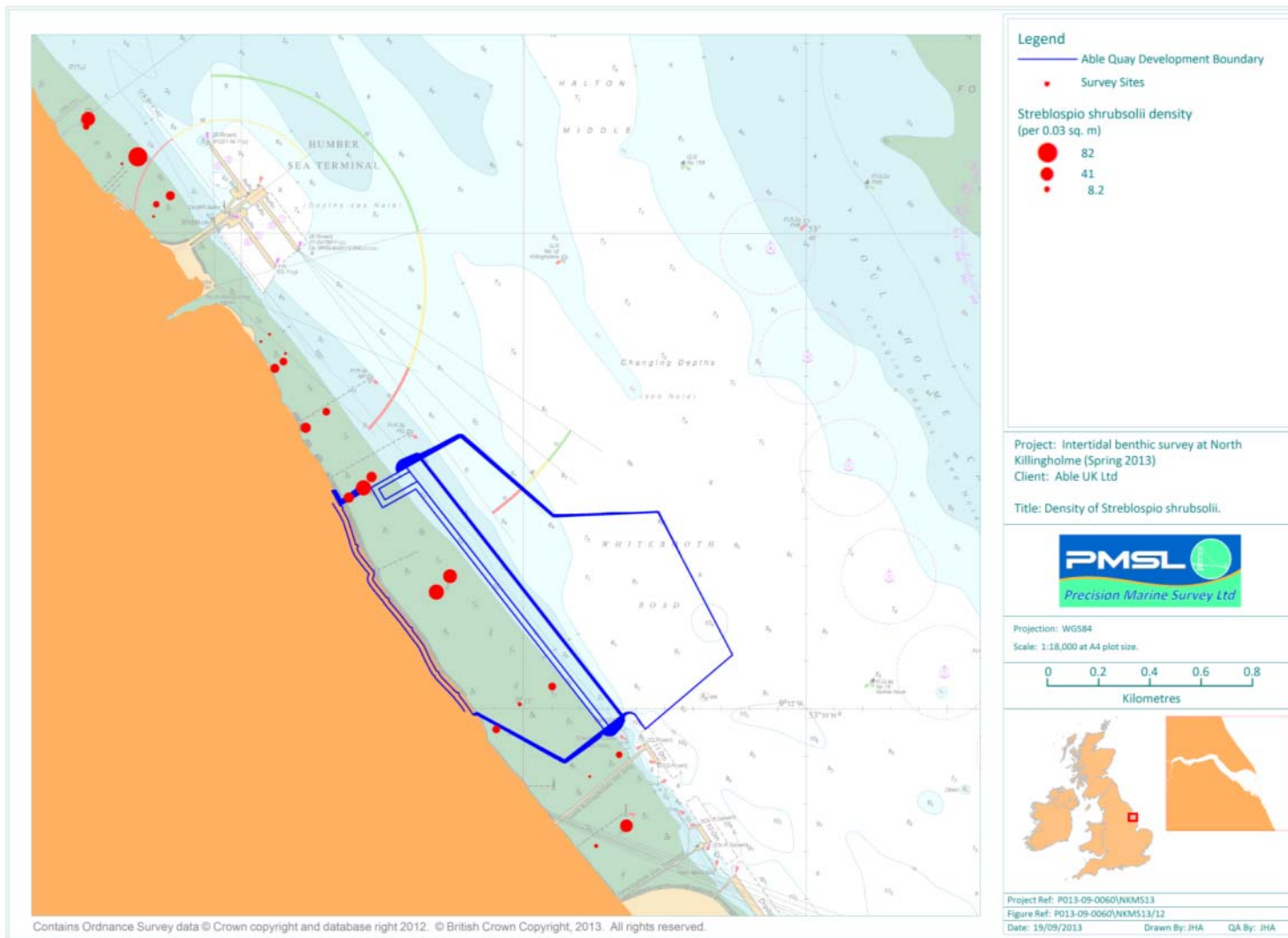
Figure 13. Spatial distribution in numbers of *Streblospio shrubsolii*.
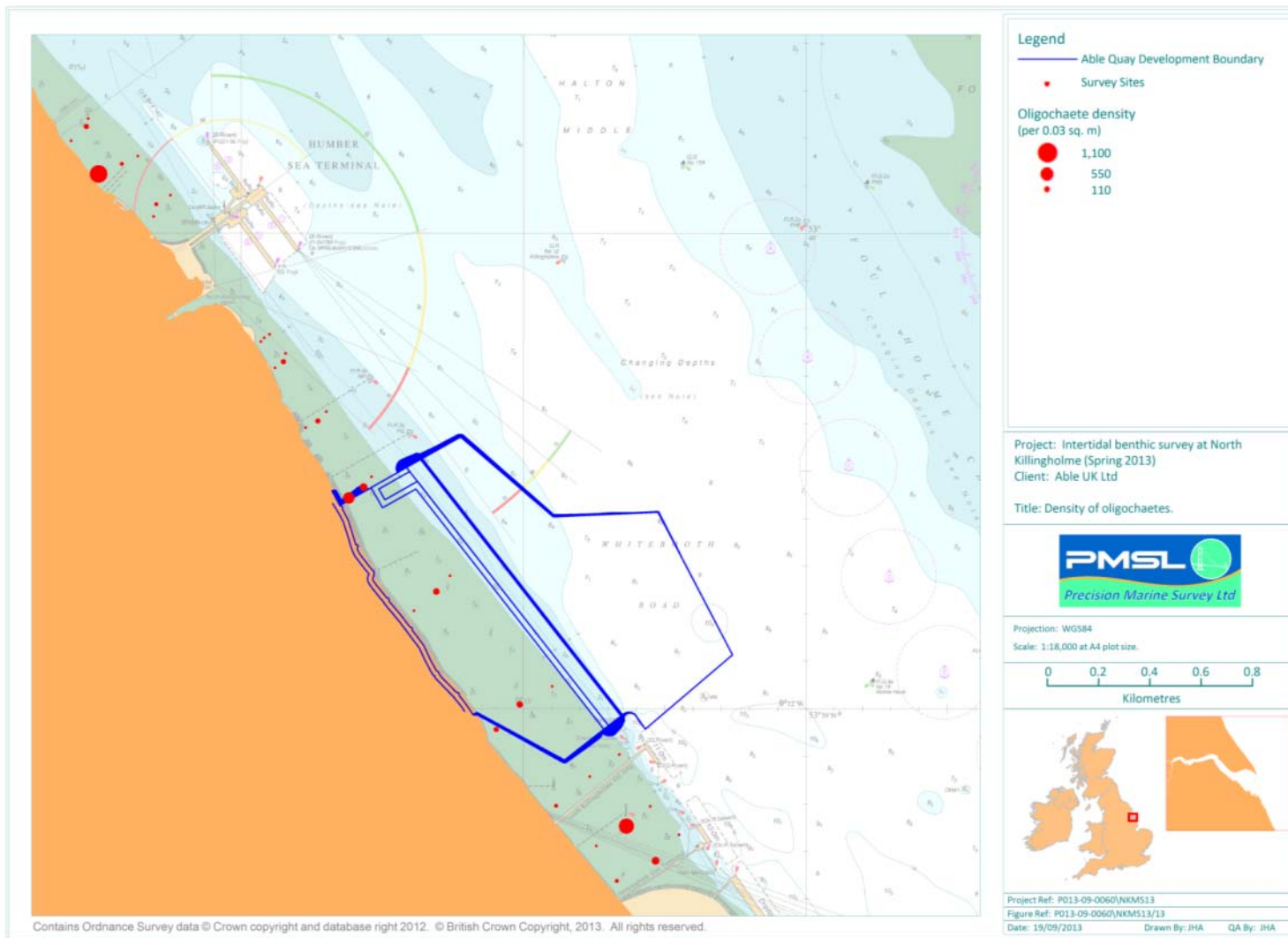
Figure 14.   Spatial distribution in numbers of *oligochaete taxa*.

3.3   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. 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.

The results of multivariate analysis on the replicate data (Figures 15 to 18) highlight a degree of variability across the area with some outlier samples in groups a to c which include single samples with no taxa recorded and the remainder falling into 8 groups at varying levels of similarly ranging from 10% to over 80%. For the most part replicate samples from the same sites fall into the same broad groups although there is a degree of intra-site variability as is usually the case, particularly in dynamic estuarine environments. Figures 15 to 18 highlight the distribution of samples in the dendrograms and MDS plots by survey area and shore level and it is apparent that whilst there appears to be some grouping by area shore level appears to be the dominant factor.

A broader assessment of the main patterns in the species data is provided by undertaking multivariate analysis of the site (pooled) data which integrates small scale variability/noise at the sites and provides a simpler interpretation of similarities between sites (Figures 19 and 20). These results indicate similarities between sites ranging from just under 20% to over 80% and 5 main groups of sites were derived using the SIMPROF test.

The characteristic taxa at the sites within each SIMPROF group are illustrated in Table 9 and the spatial distribution of site groups is shown in Figure 21. Group A includes a few relatively impoverished and variable sites on the upper in the northern control area and southern indirect impact site (CN2U, IS1U and IS3U) which are separated from the remaining sites at around 20% similarity. These sites were characterised by species such as *Tubificoides* agg. (*pseudogaster*) and *Tubificoides benedii*, terrestrial taxa such as *Collembola* sp. and *Diptera* sp. along with Nematoda and other taxa such as *Hediste diversicolor*, *Manayunkia aestuarina* and Enchytraeidae which occur in moderate numbers at individual sites.

Group B includes impoverished low shore sites at the northern and southern indirect impact sites (IN2L, IN3L, IS1L and IS2L) and characterised by taxa such as *Tubificoides benedii* and *Macoma balthica* along with occasional *Streblospio shrubsolii*, Nematoda and *Corophium volutator*. Group C is primarily composed of low shore sites from a variety of areas (CN1L, DI1L, DI2L, DI3L, IN1L, IS3L) and one upper shore site (IS2U). These sites are characterised by moderate numbers of *Streblospio shrubsolii* and *Tubificoides benedii* (all sites) and sporadic or occasional numbers of taxa such as *Corophium volutator*, *Macoma balthica*, Nematoda, *Tubificoides swirencoides*, *Pygospio elegans* and *Nephtys hombergii*.

Group D forms the largest group of sites which are separated at over 50% similarity indicating a relatively similar species composition and includes primarily mid and upper shore sites from both the direct impact and control area and also indirect impact sites (CN1M, CN1U, CN2M, CN3M, DI1M, DI2M, DI3M, DI3U, IN1M, IN1U, IN2M, IN2U, IN3U, IS1M and IS2M) including two low shore sites from the control area (CN2L and CN3L). These sites are characterised by *Corophium volutator*, *Tubificoides benedii*, *Streblospio shrubsolii*, Nematoda, *Macoma balthica* and *Hediste diversicolor* in addition to a variety of other taxa.

Group E comprises of five upper and mid shore sites (CN3U, DI1U, DI2U, IN3M and IS3M) which are characterised by moderate to low numbers of *Hediste diversicolor*, *Corophium volutator* and *Tubificoides benedii* along with occasional *Tubificoides* agg. (*pseudogaster*), Nematoda and *Streblospio shrubsolii*.

Project ref: P013-09-0060\NKMS13
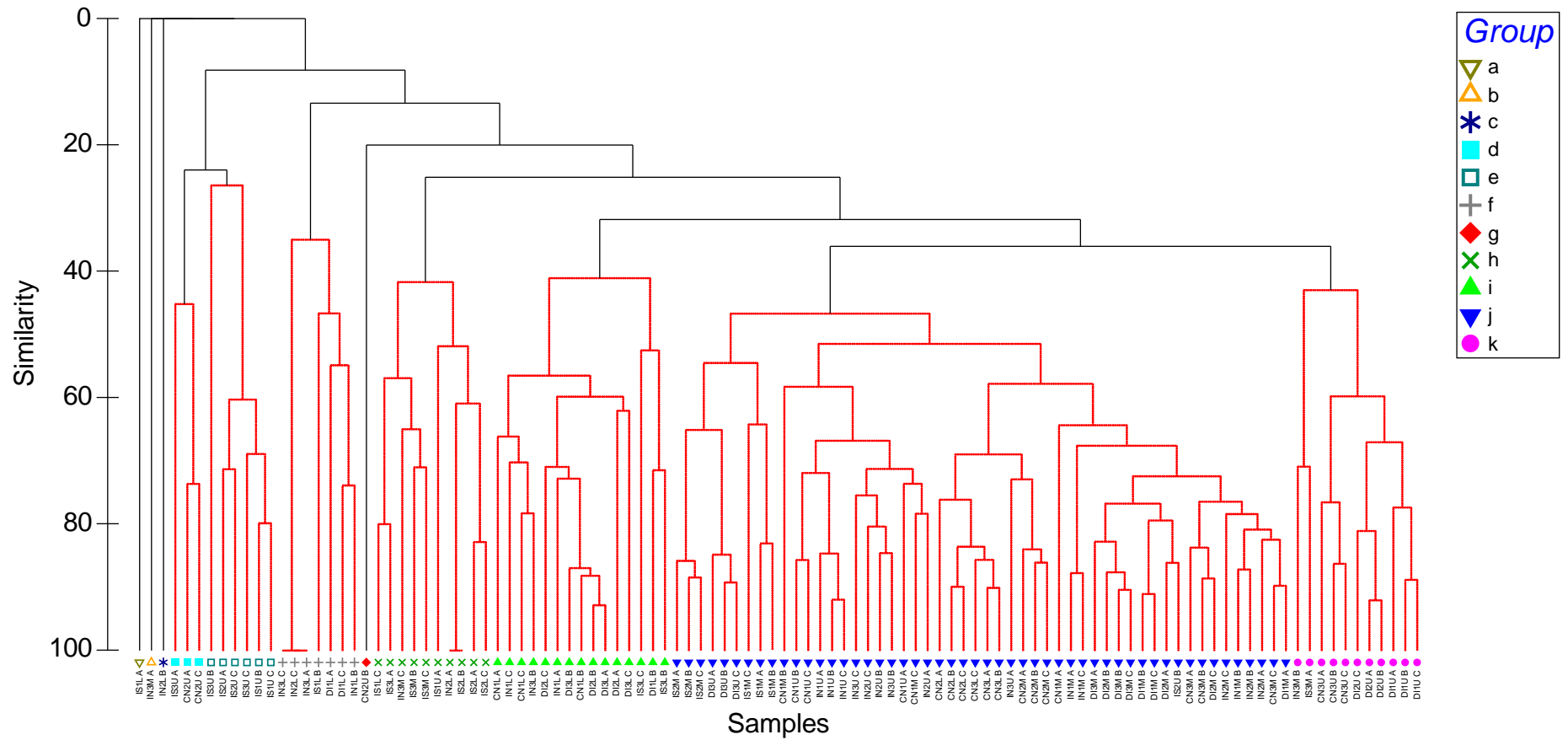
Figure 15. Results of cluster analysis on replicate data (samples highlighted by group).
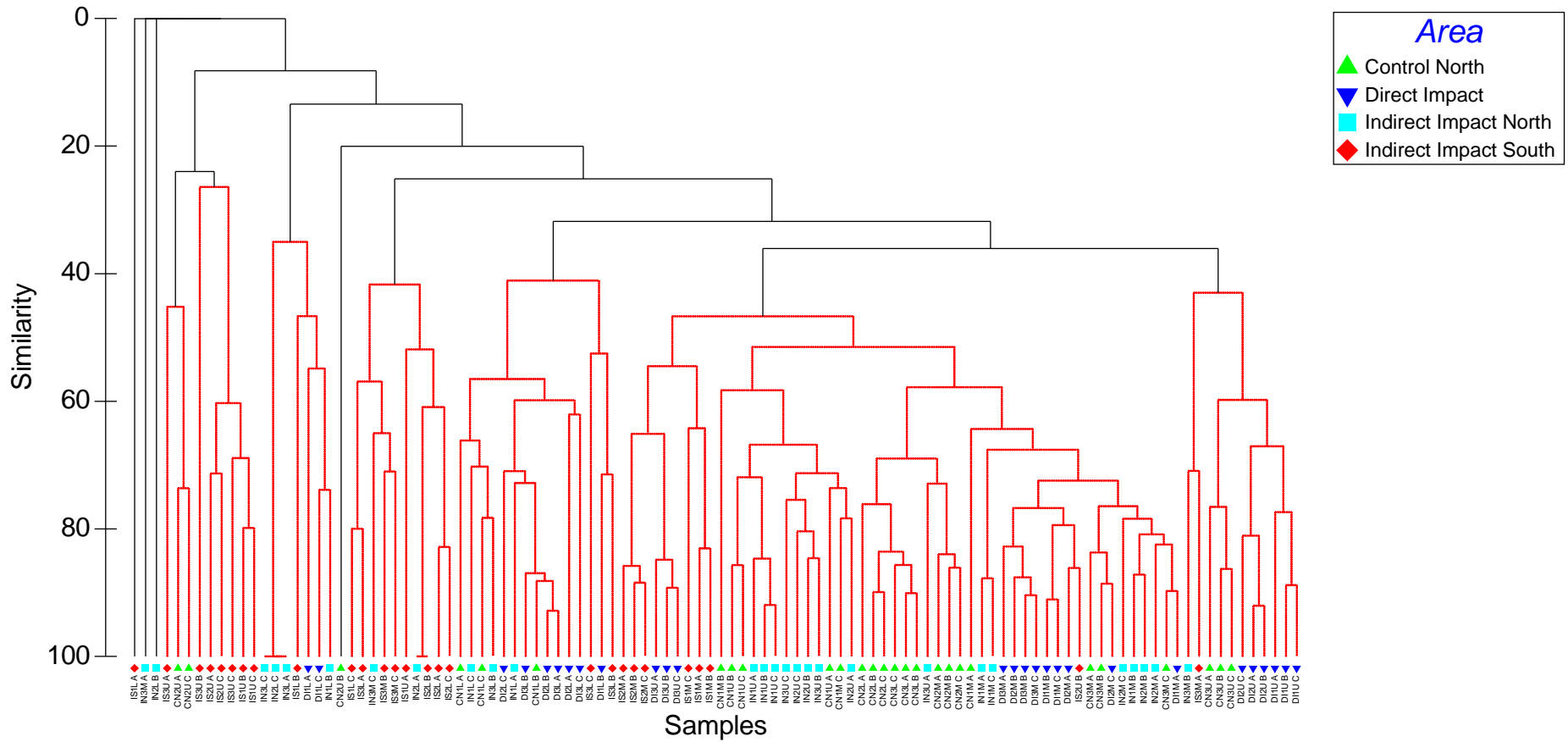
Figure 16. Results of cluster analysis on replicate data (samples highlighted by area).
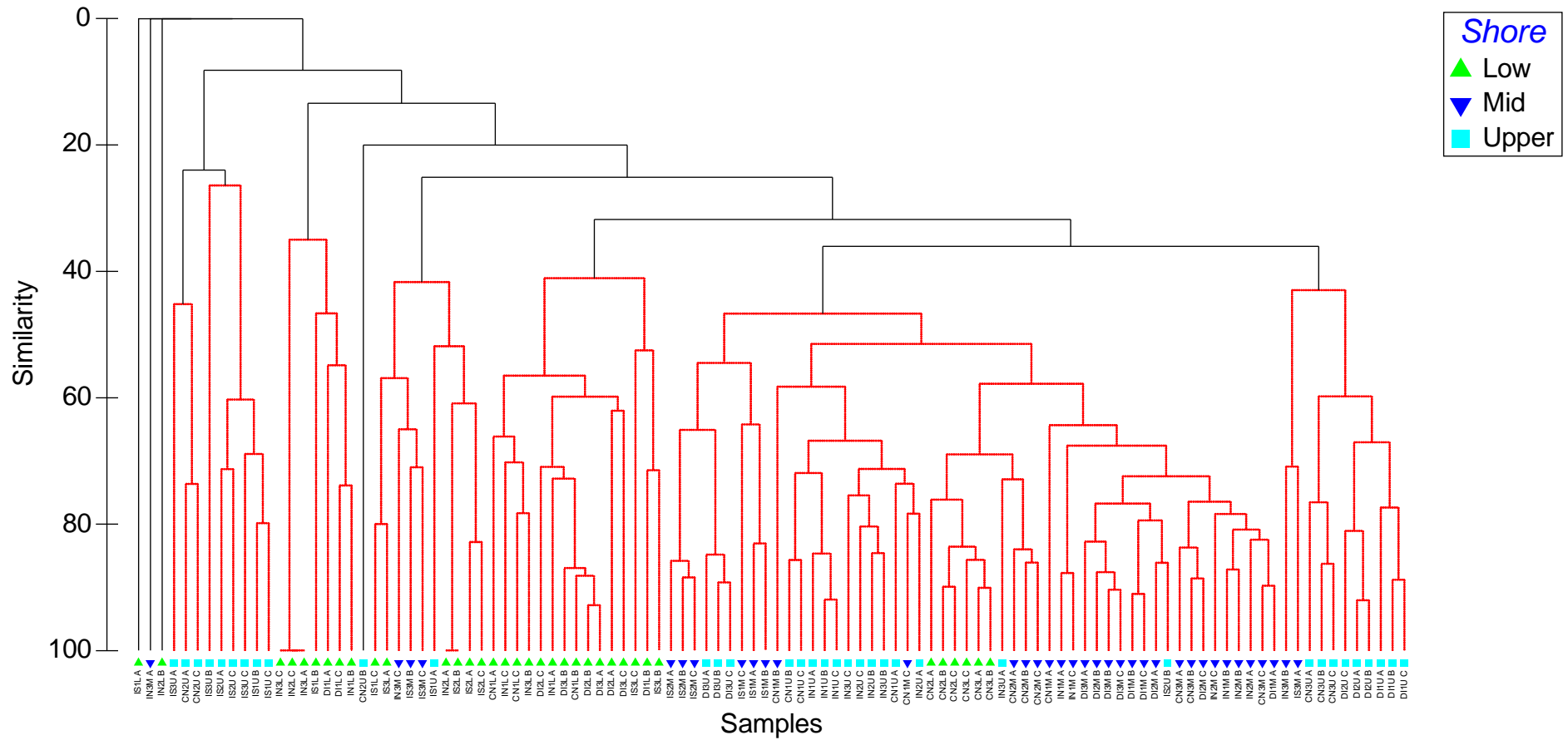
Figure 17. Results of cluster analysis on replicate data (samples highlighted by shore level).
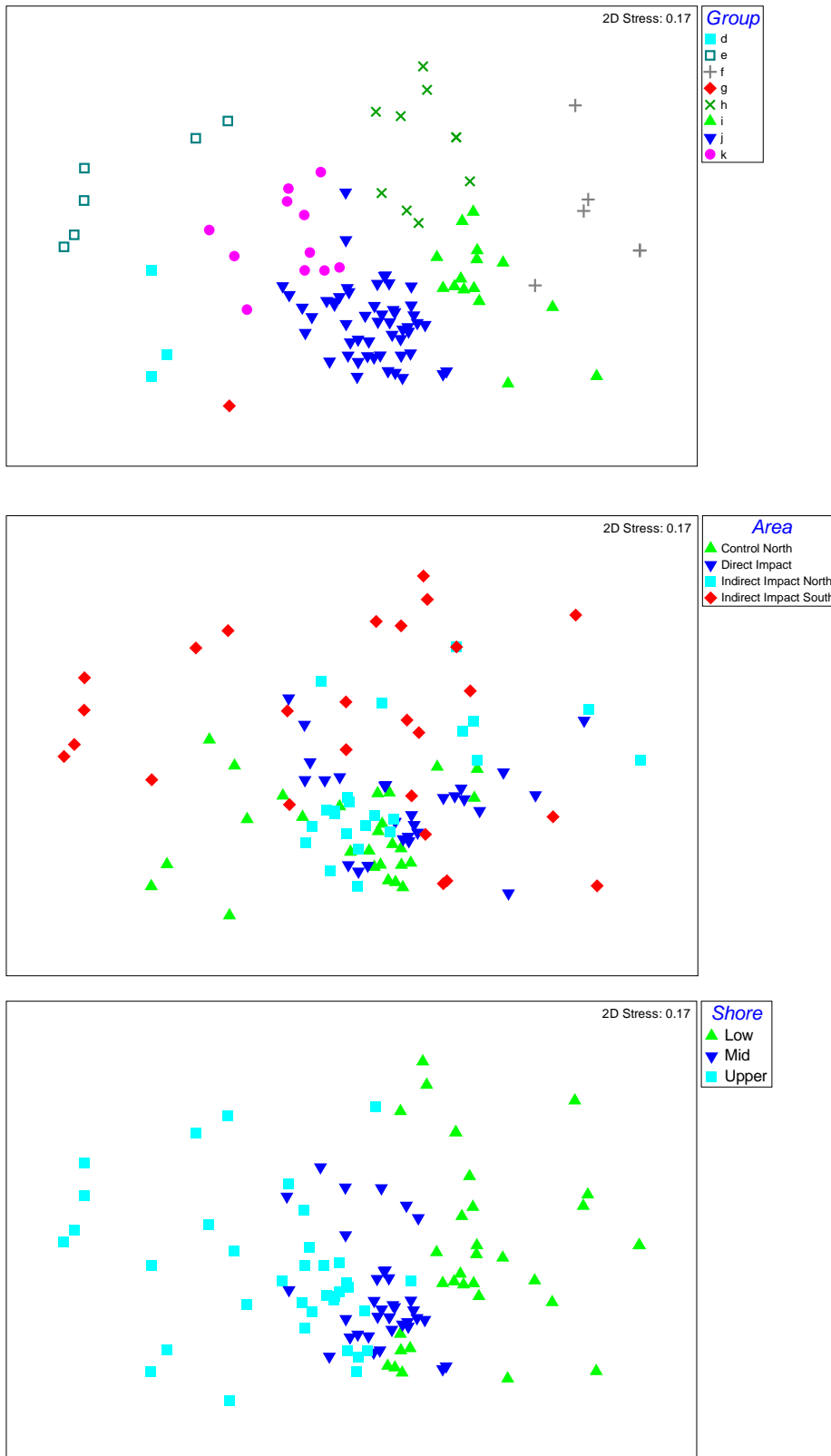
Figure 18. Results of nMDS on replicate data with samples highlighted by group, area and shore level (outlier groups a to c omitted).
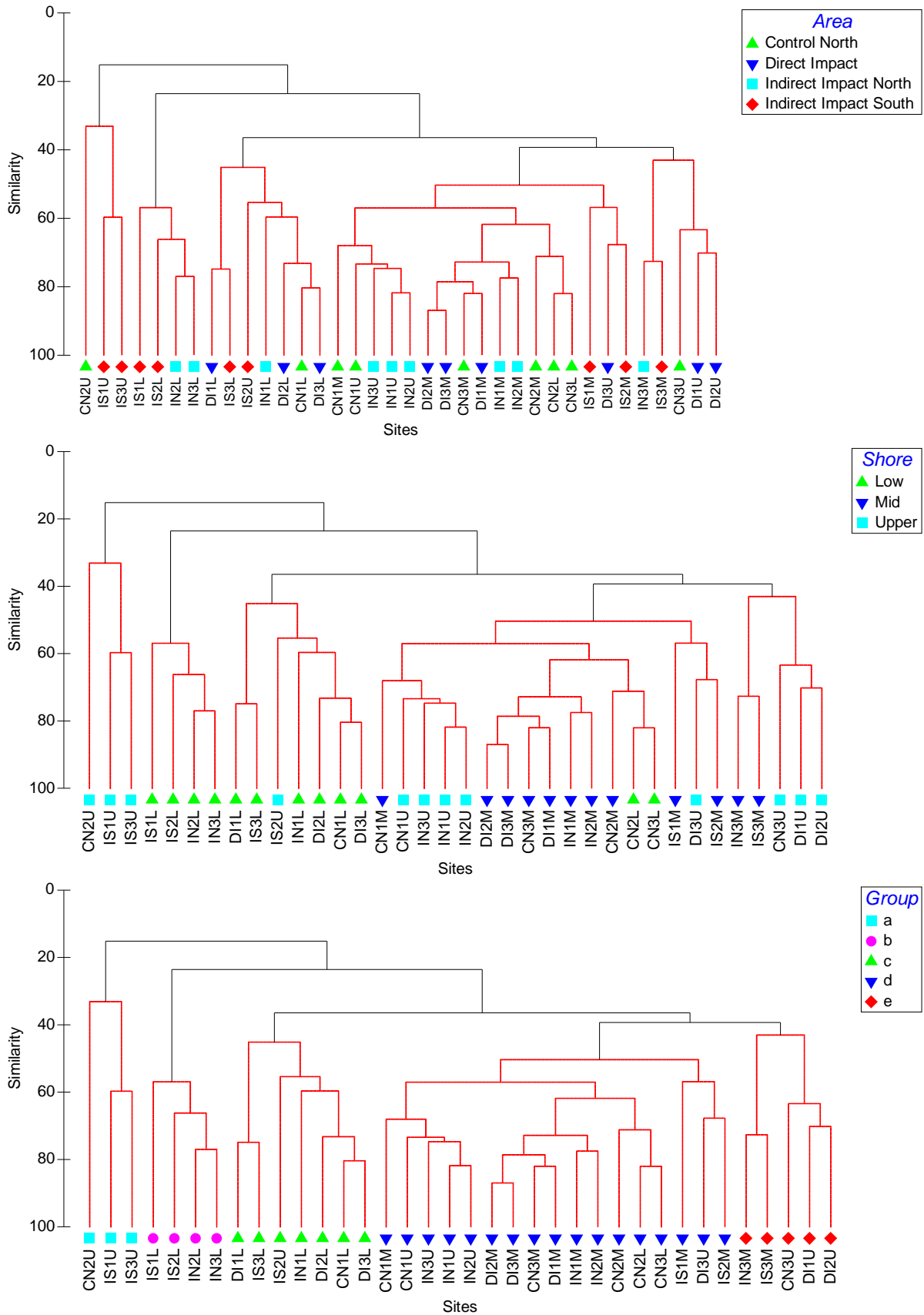
Figure 19.   Results of cluster analysis on pooled site data (sites highlighted by area, shore level and SIMPROF group).
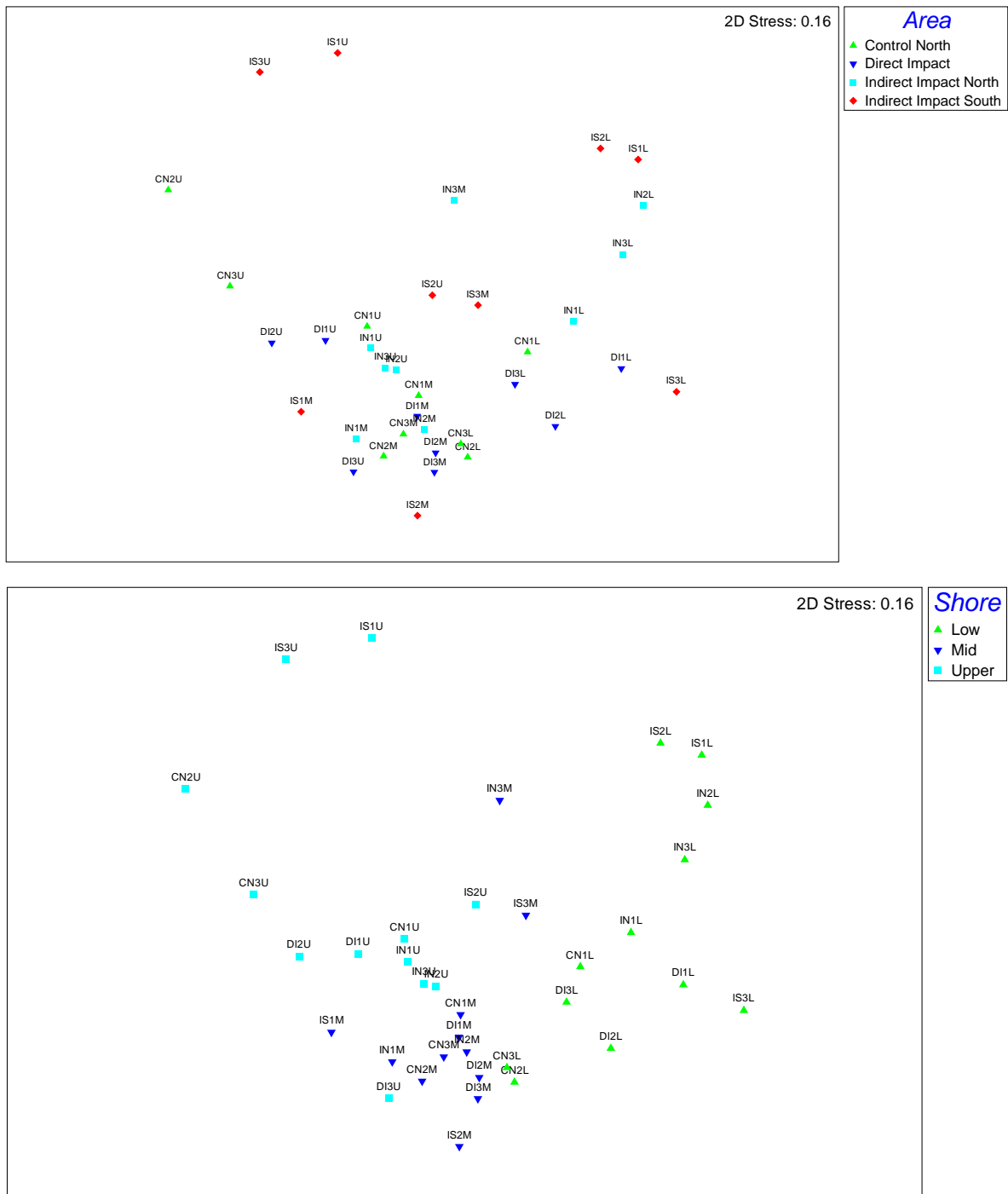
Figure 20.   Results of nMDS on pooled site data (sites highlighted by area and shore level).

Table 8. **Characteristic taxa from site groups derived from cluster analysis on pooled data.**

SIMPROF Cluster	Sites	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
Group a Average similarity: 41.92	CN2U	Tubificoides agg. (pseudogaster)	288.00	100.00	56.11	56.11
	IS1U	Collembola sp.	62.67	100.00	26.86	82.97
	IS3U	Diptera sp.	3.33	100.00	9.3	92.27
		Tubificoides benedii	2.00	66.67	4.22	96.49
		Nematoda	11.33	66.67	3.51	100
		Hediste diversicolor	12.67	33.33	0	100
		Manayunkia aestuarina	0.33	33.33	0	100
		Enchytraeidae	91.00	33.33	0	100
		Corophium volutator	1.33	33.33	0	100
		Lekanesphaera hookeri	0.33	33.33	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group b Average similarity: 63.28	IN2L	Tubificoides benedii	3.00	100.00	52.22	52.22
	IN3L	Macoma balthica	1.00	100.00	41.85	94.07
	IS1L	Streblospio shrubsolii	1.00	50.00	5.93	100
	IS2L	Nematoda	0.25	25.00	0	100
		Corophium volutator	0.25	25.00	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group c Average similarity: 54.87	CN1L	Streblospio shrubsolii	21.14	100.00	42.66	42.66
	DI1L	Tubificoides benedii	10.14	100.00	22.52	65.18
	DI2L	Corophium volutator	1.86	85.71	9.75	74.93
	DI3L	Macoma balthica	2.00	85.71	9.22	84.15
	IN1L	Nematoda	9.86	57.14	9.09	93.25
	IS2U	Tubificoides swirencoides	4.86	42.86	4.33	97.57
	IS3L	Pygospio elegans	0.57	42.86	1.44	99.02
		Nephtys hombergii	0.43	28.57	0.54	99.55
		Diptera sp.	0.57	28.57	0.45	100
		Hediste diversicolor	0.14	14.29	0	100
		Tharyx sp.	0.29	14.29	0	100
		Tubificoides agg. (pseudogaster)	1.14	14.29	0	100
		Tellinacea juv.	0.14	14.29	0	100
		Collembola sp.	0.14	14.29	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group d Average similarity: 59.24	CN1M	Corophium volutator	124.94	100.00	35.73	35.73
	CN1U	Tubificoides benedii	144.06	100.00	25.98	61.71
	CN2L	Streblospio shrubsolii	24.00	88.24	11.48	73.19
	CN2M	Nematoda	12.59	100.00	10.2	83.39
	CN3L	Macoma balthica	3.76	100.00	6.16	89.55
	CN3M	Hediste diversicolor	14.24	76.47	5.53	95.08
	DI1M	Enchytraeidae	4.18	52.94	2.19	97.27
	DI2M	Pygospio elegans	1.47	52.94	1.29	98.55
	DI3M	Tubificoides agg. (pseudogaster)	2.59	41.18	1.12	99.67
	DI3U	Manayunkia aestuarina	0.88	23.53	0.2	99.87
	IN1M	Tharyx sp.	0.47	11.76	0.05	99.92
	IN1U	Diptera sp.	0.35	11.76	0.04	99.96
	IN2M	Coleoptera sp.	0.18	11.76	0.04	100
	IN2U	Nemertea	0.06	5.88	0	100
	IN3U	Naididae	0.06	5.88	0	100
	IS1M	Dipolydora coeca	0.06	5.88	0	100
	IS2M	Collembola sp.	0.06	5.88	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group e Average similarity: 52.72	CN3U	Hediste diversicolor	68.60	100.00	42.8	42.8
	DI1U	Corophium volutator	10.00	100.00	29.44	72.24
	DI2U	Tubificoides benedii	26.80	80.00	22.08	94.32
	IN3M	Tubificoides agg. (pseudogaster)	9.80	40.00	3.14	97.46
	IS3M	Nematoda	2.40	40.00	1.46	98.92
		Streblospio shrubsolii	3.60	40.00	1.08	100
		Eteone longa/flava agg.	0.20	20.00	0	100
		Pygospio elegans	0.20	20.00	0	100
		Manayunkia aestuarina	0.40	20.00	0	100
		Macoma balthica	0.20	20.00	0	100
		Collembola sp.	0.20	20.00	0	100

Figure 21. Distribution of site groups derived from cluster analysis on pooled data.

4. Autumn Intertidal Invertebrate Survey (Interim Summary)

As outlined in the MEMMP an autumn intertidal survey was proposed to survey the mudflats inside and outside the proposed development area at a higher level of spatial resolution (but with single replicates) in order to provide a greater understanding of the distribution of invertebrate communities in this area in relation to avifaunal prey availability. This survey was undertaken in September 2013 following a similar methodology to that employed for the May 2013 survey. The samples from this survey are currently being processed but it was agreed that data from a subset of site be presented earlier to allow a preliminary assessment of the data. The location of the survey sites processed to date are shown in Figure 22 and a some preliminary results are presented below.

The biological parameters derived from the interim dataset are shown in Table 10 and average values for key parameters (number of taxa, individuals and biomass) inside and outside the proposed development area are shown in Figure 23 with the spatial distribution of these parameters provided in Figures 24 to 26. The results of the autumn survey (based on the samples processed to date) indicate a similar range of values for numbers of taxa, individuals and biomass to those described in Section 3 for the spring NKM survey and also from other surveys in the middle Humber. A preliminary assessment of the spatial variation indicates relatively differences in terms of numbers of taxa but with some variation in terms of numbers of individuals and biomass in relation to shore position with lower values generally recorded from the low shore, particularly with regard to biomass. There is also some indication of a slight increase in upper shore biomass within the proposed development area.

In terms of characteristic species from the autumn survey the dominant taxa from the samples processed to date are shown in Tables 11 and 12 and Figures 27 to 31. As described for the spring survey the dominant taxa in terms of numbers of individuals are *Corophium volutator* and *Tubificoides benedii* which account for 80% of the total abundance. Other key taxa include *Hediste diversicolor*, *Streblospio shrubsolii*, Enchytraeidae and *Macoma balthica*. In terms of biomass *Hediste diversicolor*, *Corophium volutator* and *Tubificoides benedii* account for over 90% of the total. Similar taxa tend to be dominant at sites inside and outside the proposed development area with any changes rather subtle and generally reflect a re-ordering of supporting taxa rather than major differences. Figures 27 to 31 provide some indication of a slight increase in numbers of *Hediste diversicolor* and *Macoma balthica* on the upper and mid shore respectively within the proposed development area although this may in part reflect greater sampling effort.

The results of preliminary multivariate analysis (Figures 32 to 34 and Table 13) highlight a relatively high level of similarity across the area with most sites exhibiting similarities over 40%. Eight groups were derived from the SIMPROF test including a number of outliers (single samples). As described for the spring survey a relatively clear pattern was evident with regard to shore position whilst differences in relation to position inside or outside the proposed development area were less obvious. The majority of sites fell within a single group which also contained most of the sites in the development area and whilst there appears to be some spatial patterns in community structure the differences in terms of key taxa are relatively minor.
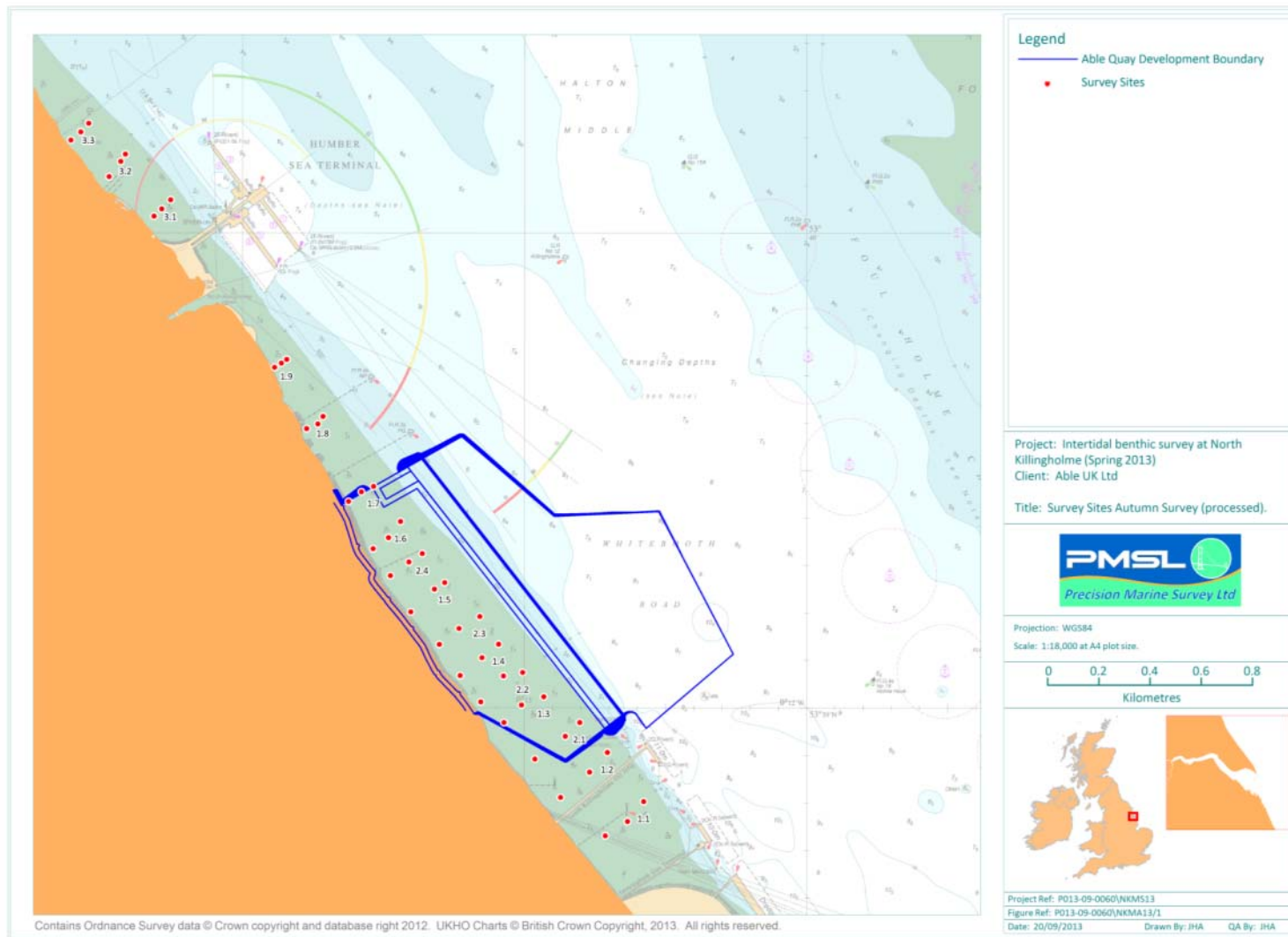
Figure 22. Location of survey sites from autumn survey processed to date.

Table 9.   Biological parameters from autumn survey (per 0.01m^2).

Area	Shore	Sample	No. of Taxa	Numbers of Individuals (0.01m^2)	Biomass (g per 0.01m^2)	Margalef's d	Pielou's J	Shannon's H'
Outside	Low	1.1LB	3	103	0.0373	0.43	0.65	1.04
Outside	Mid	1.1MB	5	357	0.3469	0.68	0.48	1.13
Outside	Upper	1.1UB	5	49	0.07	1.03	0.67	1.56
Outside	Low	1.2LB	6	35	0.0104	1.41	0.82	2.13
Outside	Mid	1.2MB	8	80	0.0601	1.60	0.84	2.51
Outside	Upper	1.2UB	4	32	0.01	0.87	0.80	1.59
Inside	Low	1.3LB	6	192	0.1195	0.95	0.29	0.76
Inside	Mid	1.3MB	8	347	0.1792	1.03	0.39	1.11
Inside	Upper	1.3UB	5	328	0.6915	0.69	0.64	1.48
Inside	Low	1.4LB	4	157	0.0753	0.59	0.56	1.12
Inside	Mid	1.4MB	7	135	0.1054	1.22	0.59	1.64
Inside	Upper	1.4UB	5	261	1.2349	0.72	0.63	1.46
Inside	Low	1.5LB	4	96	0.0409	0.66	0.70	1.40
Inside	Mid	1.5MB	7	125	0.0751	1.24	0.52	1.46
Inside	Upper	1.5UB	4	65	0.7241	0.72	0.76	1.51
Inside	Low	1.6LB	5	24	0.0084	1.26	0.75	1.74
Inside	Mid	1.6MB	10	271	0.2096	1.61	0.43	1.42
Inside	Upper	1.6UB	7	341	1.0275	1.03	0.55	1.55
Inside	Low	1.7LB	5	45	0.0139	1.05	0.81	1.89
Inside	Mid	1.7MB	7	348	0.2545	1.03	0.56	1.58
Inside	Upper	1.7UB	5	456	0.7132	0.65	0.55	1.28
Outside	Low	1.8LB	4	5	0.0057	1.86	0.96	1.92
Outside	Mid	1.8MB	5	241	0.2163	0.73	0.50	1.16
Outside	Upper	1.8UB	6	220	0.5193	0.93	0.75	1.94
Outside	Low	1.9LB	2	3	0.0003	0.91	0.92	0.92
Outside	Mid	1.9MB	6	215	0.1575	0.93	0.41	1.05
Outside	Upper	1.9UB	6	231	0.5116	0.92	0.25	0.65
Inside	Low	2.1LB	8	22	0.0064	2.26	0.89	2.68
Inside	Mid	2.1MB	9	217	0.1065	1.49	0.45	1.41
Inside	Upper	2.1UB	6	116	0.2261	1.05	0.23	0.60
Inside	Low	2.2LB	4	216	0.1103	0.56	0.47	0.93
Inside	Mid	2.2MB	9	262	0.4194	1.44	0.34	1.07
Inside	Upper	2.2UB	5	141	1.3758	0.81	0.66	1.54
Inside	Low	2.3LB	5	152	0.1356	0.80	0.38	0.89
Inside	Mid	2.3MB	7	219	0.1037	1.11	0.56	1.58
Inside	Upper	2.3UB	5	266	0.4422	0.72	0.58	1.35
Inside	Low	2.4LB	7	120	0.0919	1.25	0.29	0.82
Inside	Mid	2.4MB	6	240	0.1225	0.91	0.38	0.98
Inside	Upper	2.4UB	5	104	0.8276	0.86	0.65	1.51
Outside	Low	3.1LB	5	30	0.0061	1.18	0.80	1.85
Outside	Mid	3.1MB	7	242	0.1806	1.09	0.33	0.94
Outside	Upper	3.1UB	7	148	0.4808	1.20	0.64	1.80
Outside	Low	3.2LB	7	128	0.0883	1.24	0.57	1.60
Outside	Mid	3.2MB	7	137	0.4546	1.22	0.47	1.31
Outside	Upper	3.2UB	8	66	0.3168	1.67	0.88	2.64
Outside	Low	3.3LB	8	283	0.2449	1.24	0.46	1.38
Outside	Mid	3.3MB	7	311	0.5361	1.05	0.59	1.65
Outside	Upper	3.3UB	9	394	0.8702	1.34	0.56	1.77

	Inside	Outside
Low	5.33	5.00
Mid	7.78	6.43
Upper	5.22	6.43

	Inside	Outside
Low	113.78	83.86
Mid	240.44	226.14
Upper	230.89	162.86

	Inside	Outside
Low	0.07	0.06
Mid	0.18	0.28
Upper	0.81	0.40

Figure 23. **Average values of biological parameters per 0.01m² inside and outside the proposed development area (autumn survey).**

Figure 24.   Number of taxa across the survey area (autumn survey) per 0.01m².

Figure 25. Numbers of individuals across the survey area (autumn survey) per 0.01m^2.

Figure 26.   Biomass of invertebrates across the survey area (autumn survey) per 0.01m².

Table 10. Dominant taxa for the survey area (autumn survey).

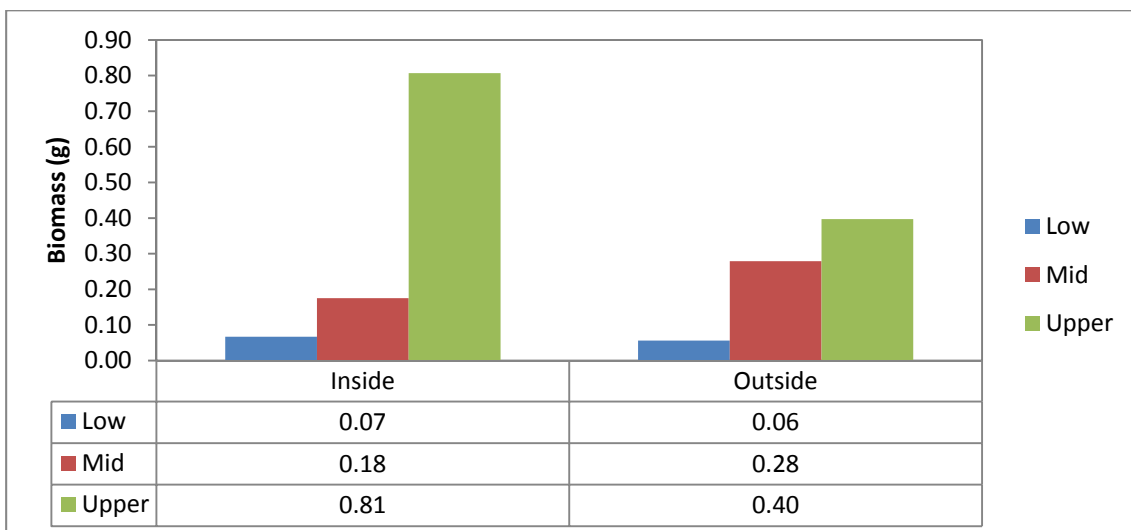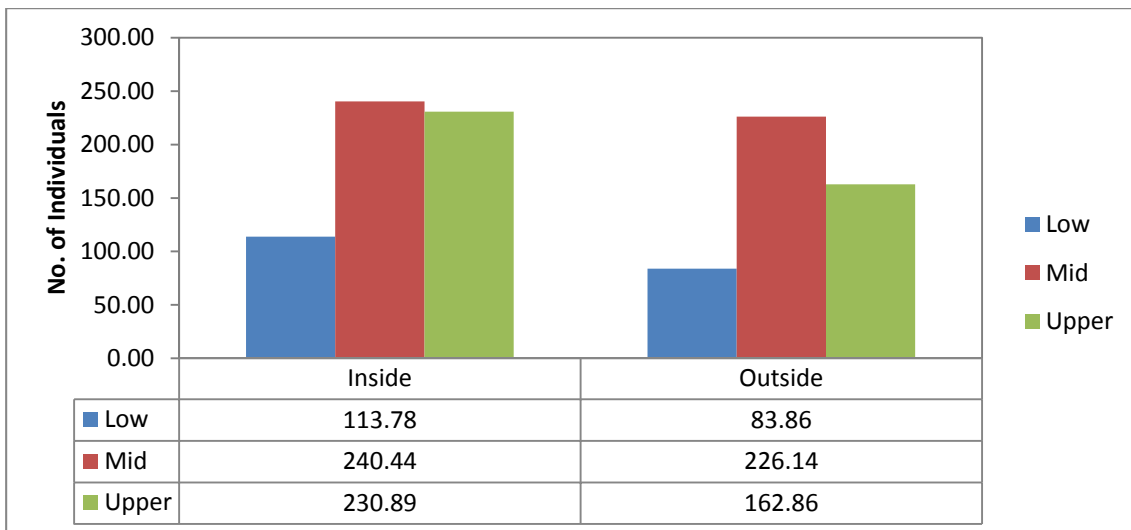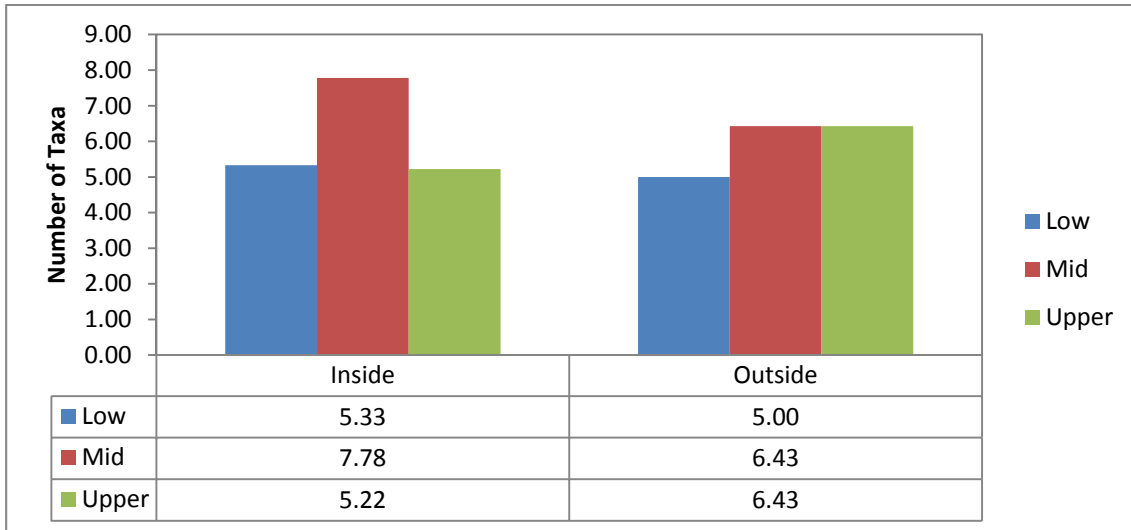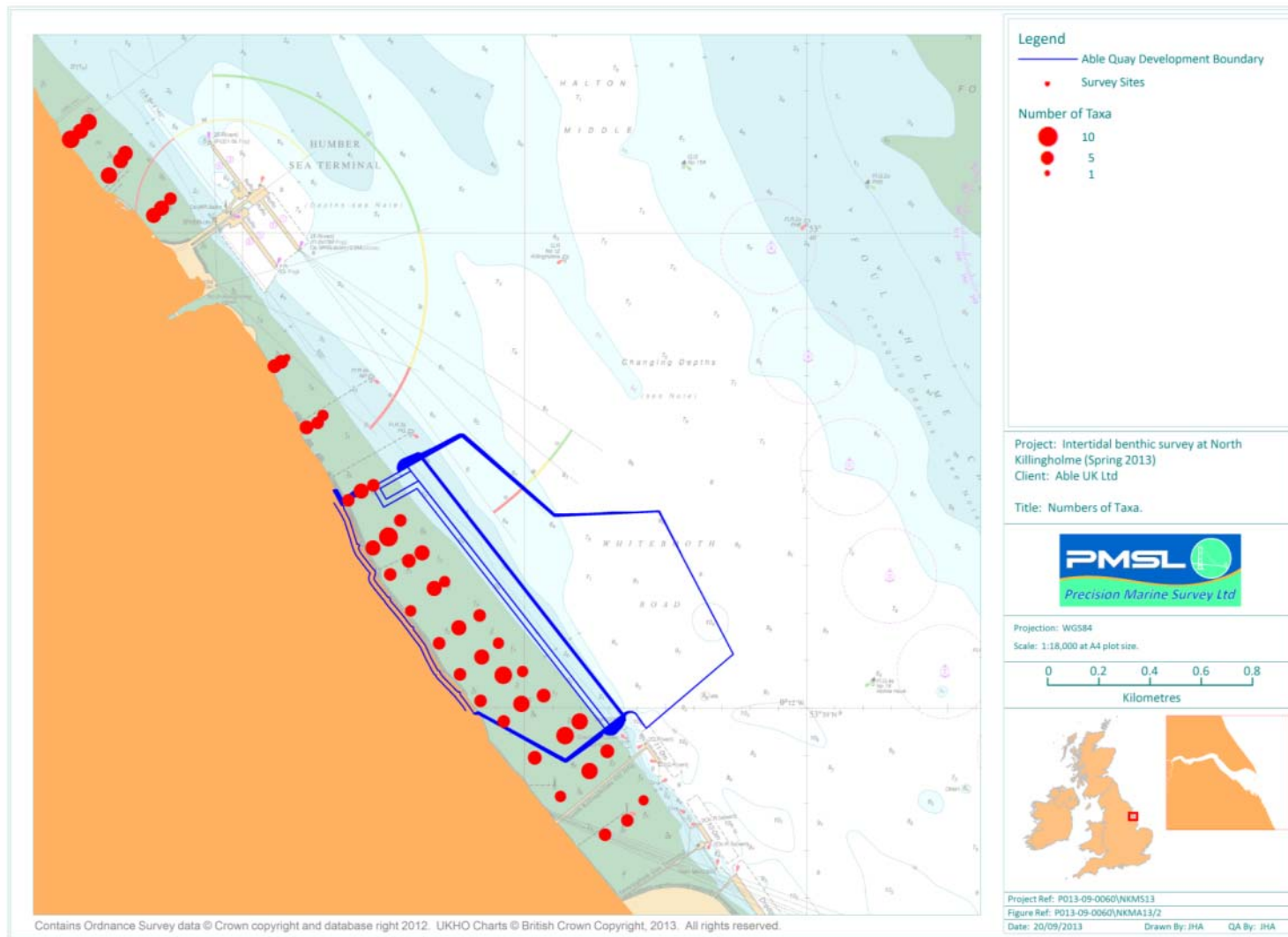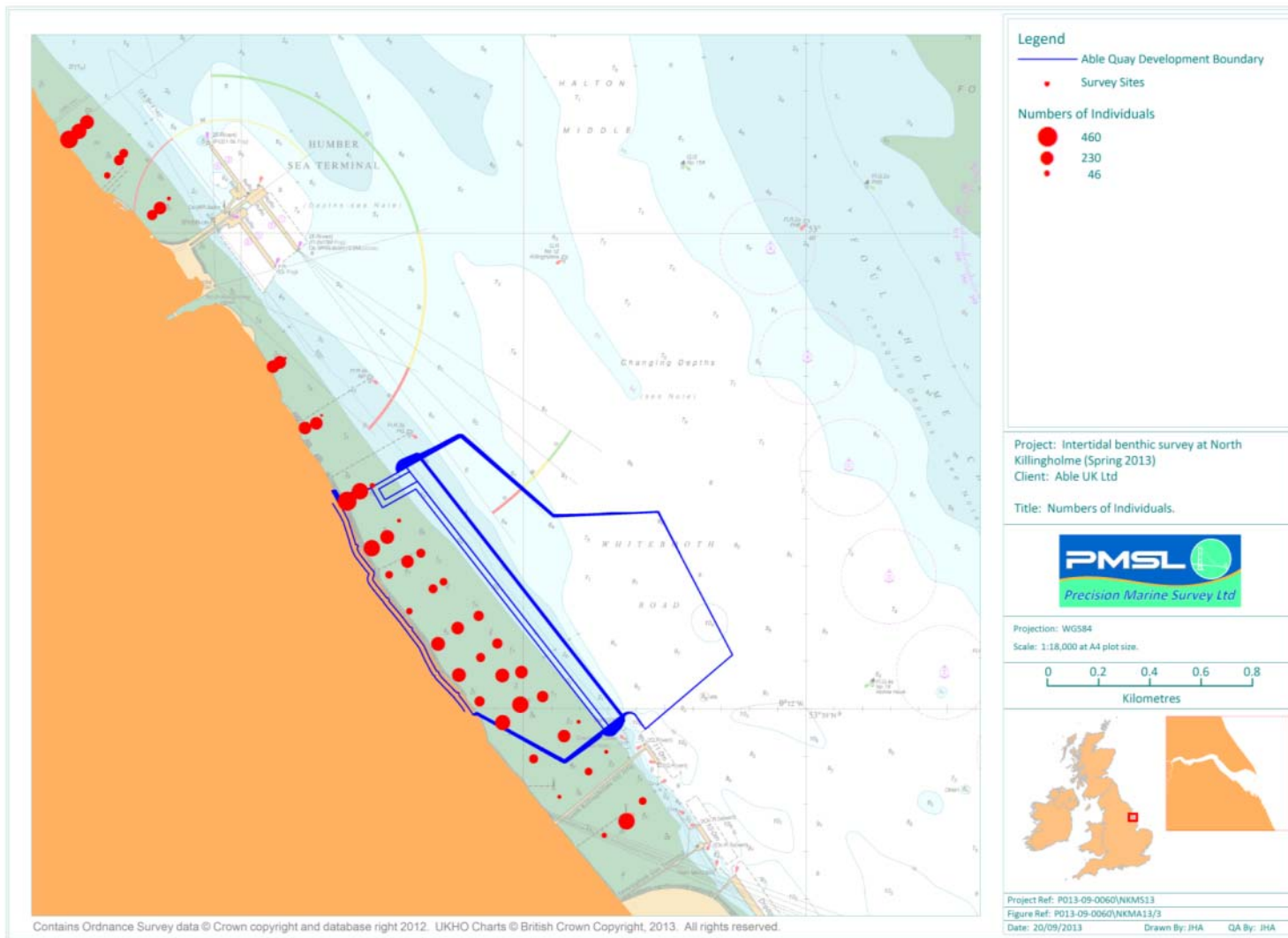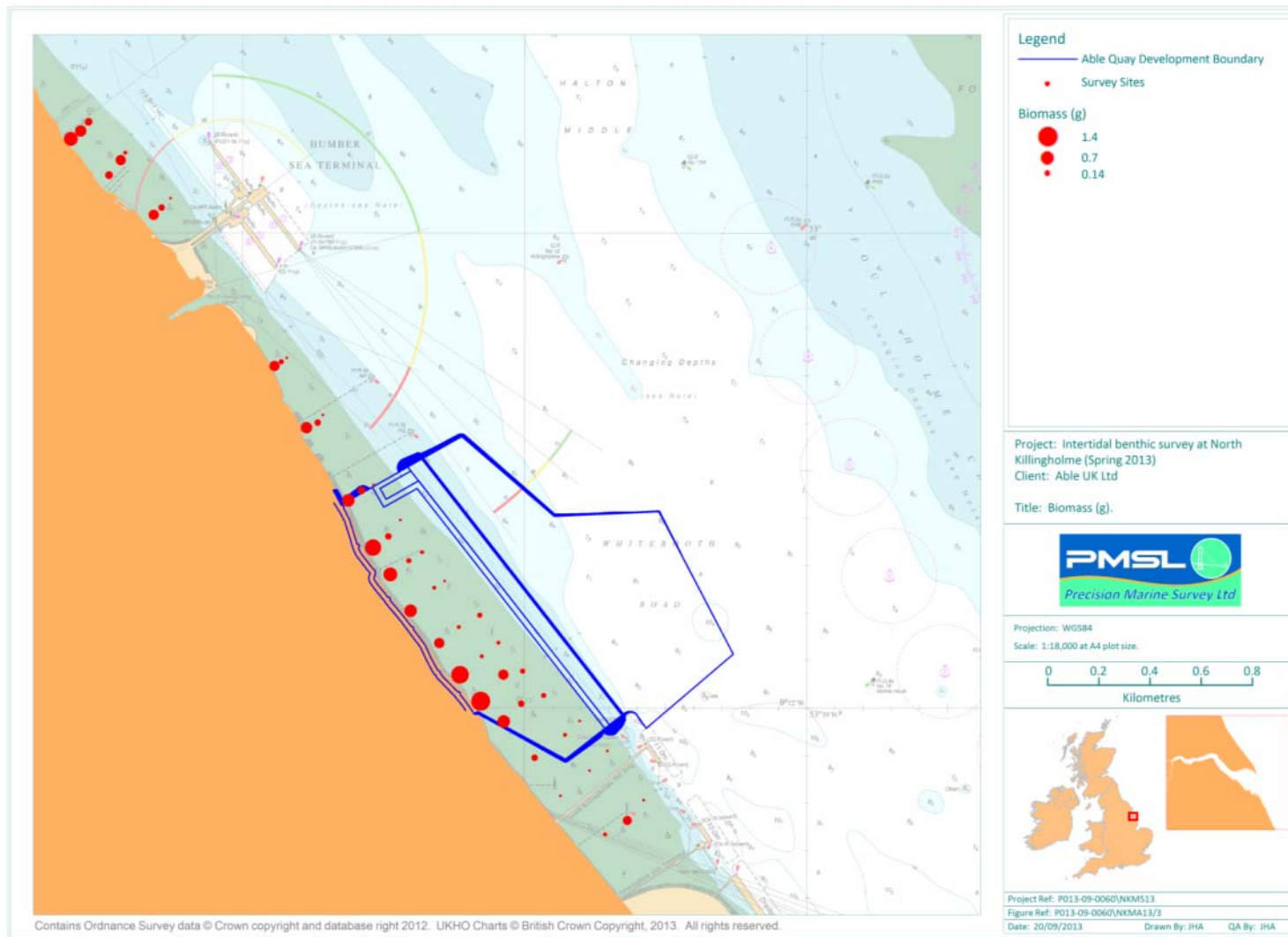| Taxon	Average A	% of Sites	% cont.	Taxon	Average B	% of Sites	% cont.
Corophium volutator	109.04	93.75	61.03	Hediste diversicolor	8.7054	52.08	59.77
Tubificoides benedii	34.75	89.58	80.48	Corophium volutator	3.3627	93.75	82.86
Nematoda	7.46	89.58	84.65	Tubificoides benedii	1.4012	89.58	92.48
Hediste diversicolor	7.02	52.08	88.58	Macoma balthica	0.8462	45.83	98.29
Streblospio shrubsolii	6.96	75.00	92.48	Nematoda	0.0758	89.58	98.81
Enchytraeidae	5.81	18.75	95.73	Streblospio shrubsolii	0.0677	75.00	99.27
Macoma balthica	3.00	45.83	97.41	Diptera larvae	0.0372	14.58	99.53
Collembola sp.	1.92	18.75	98.48	Enchytraeidae	0.0188	18.75	99.66
Tubificoides agg. (pseudogaster)	0.71	10.42	98.88	Tubificoides (pseudogaster) agg.	0.0175	10.42	99.78
Pygospio elegans	0.58	29.17	99.21	Coleoptera sp.	0.0067	2.08	99.82
Diptera sp.	0.56	14.58	99.52	Eteone longa/flava agg.	0.0063	20.83	99.87
Manayunkia aestuarina	0.23	8.33	99.65	Pygospio elegans	0.0056	29.17	99.91
Eteone longa/flava agg.	0.21	20.83	99.77	Tharyx sp.	0.005	10.42	99.94
Nemertea	0.10	10.42	99.83	Nemertea	0.0047	12.50	99.97
Tharyx sp.	0.10	10.42	99.88	Nephtys hombergii	0.002	2.08	99.99
Tubificoides swirencoides	0.08	2.08	99.93	Collembola sp.	0.0011	18.75	99.99
Acarina sp.	0.06	6.25	99.97	Manayunkia aestuarina	0.0004	8.33	100.00
Nephtys hombergii	0.02	2.08	99.98	Acarina	0.0003	6.25	100.00
Coleoptera sp.	0.02	2.08	99.99	Tubificoides swirencoides	0.0001	2.08	100.00
Linyphiidae	0.02	2.08	100.00	Linyphiidae	0.0001	2.08	100.00

Table 11. Dominant taxa inside and outside the proposed development area (autumn survey).

	Inside				Outside		
Taxon	Average A	% of Sites	% cont.	Taxon	Average A	% of Sites	% cont.
Corophium volutator	121.67	96.30	62.38	Corophium volutator	92.81	90.48	58.88
Tubificoides benedii	44.30	100.00	85.09	Tubificoides benedii	22.48	76.19	73.14
Streblospio shrubsolii	9.00	92.59	89.71	Enchytraeidae	13.19	33.33	81.51
Hediste diversicolor	8.89	48.15	94.27	Nematoda	10.38	85.71	88.10
Nematoda	5.19	92.59	96.92	Hediste diversicolor	4.62	57.14	91.03
Macoma balthica	3.89	37.04	98.92	Streblospio shrubsolii	4.33	52.38	93.78
Pygospio elegans	0.74	37.04	99.30	Collembola sp.	3.95	23.81	96.28
Collembola sp.	0.33	14.81	99.47	Macoma balthica	1.86	57.14	97.46
Eteone longa/flava agg.	0.26	25.93	99.60	Tubificoides agg. (pseudogaster)	1.57	19.05	98.46
Nemertea	0.19	18.52	99.70	Diptera sp.	1.05	23.81	99.12
Tharyx sp.	0.19	18.52	99.79	Manayunkia aestuarina	0.43	14.29	99.40
Diptera sp.	0.19	7.41	99.89	Pygospio elegans	0.38	19.05	99.64
Enchytraeidae	0.07	7.41	99.92	Tubificoides swirencoides	0.19	4.76	99.76
Manayunkia aestuarina	0.07	3.70	99.96	Eteone longa/flava agg.	0.14	14.29	99.85
Tubificoides agg. (pseudogaster)	0.04	3.70	99.98	Acarina sp.	0.14	14.29	99.94
Coleoptera sp.	0.04	3.70	100.00	Nephtys hombergii	0.05	4.76	99.97
				Linyphiidae	0.05	4.76	100.00

	Inside				Outside		
Taxon	Average B	% of Sites	% cont.	Taxon	Average B	% of Sites	% cont.
Hediste diversicolor	0.2242	48.15	64.13	Hediste diversicolor	0.1262	57.14	51.74
Corophium volutator	0.0751	96.30	85.61	Corophium volutator	0.0635	90.48	77.79
Tubificoides benedii	0.0361	100.00	95.93	Macoma balthica	0.0261	57.14	88.48
Macoma balthica	0.0111	37.04	99.09	Tubificoides benedii	0.0203	76.19	96.81
Streblospio shrubsolii	0.0018	92.59	99.60	Nematoda	0.0035	85.71	98.23
Diptera larvae	0.0003	7.41	99.69	Diptera larvae	0.0014	23.81	98.79
Coleoptera sp.	0.0002	3.70	99.76	Streblospio shrubsolii	0.0009	52.38	99.18
Eteone longa/flava agg.	0.0002	25.93	99.82	Enchytraeidae	0.0009	33.33	99.54
Tharyx sp.	0.0002	18.52	99.87	Tubificoides (pseudogaster) agg.	0.0008	19.05	99.88
Nemertea	0.0002	22.22	99.92	Nephtys hombergii	0.0001	4.76	99.92
Pygospio elegans	0.0001	37.04	99.96	Pygospio elegans	0.0001	19.05	99.96
Nematoda	0.0001	92.59	99.99	Eteone longa/flava agg.	0.0000	14.29	99.97
Collembola sp.	0.0000	14.81	100.00	Collembola sp.	0.0000	23.81	99.98
Enchytraeidae	0.0000	7.41	100.00	Manayunkia aestuarina	0.0000	14.29	99.99
Manayunkia aestuarina	0.0000	3.70	100.00	Acarina	0.0000	14.29	100.00
Tubificoides (pseudogaster) agg.	0.0000	3.70	100.00	Tubificoides swirencoides	0.0000	4.76	100.00
				Linyphiidae	0.0000	4.76	100.00
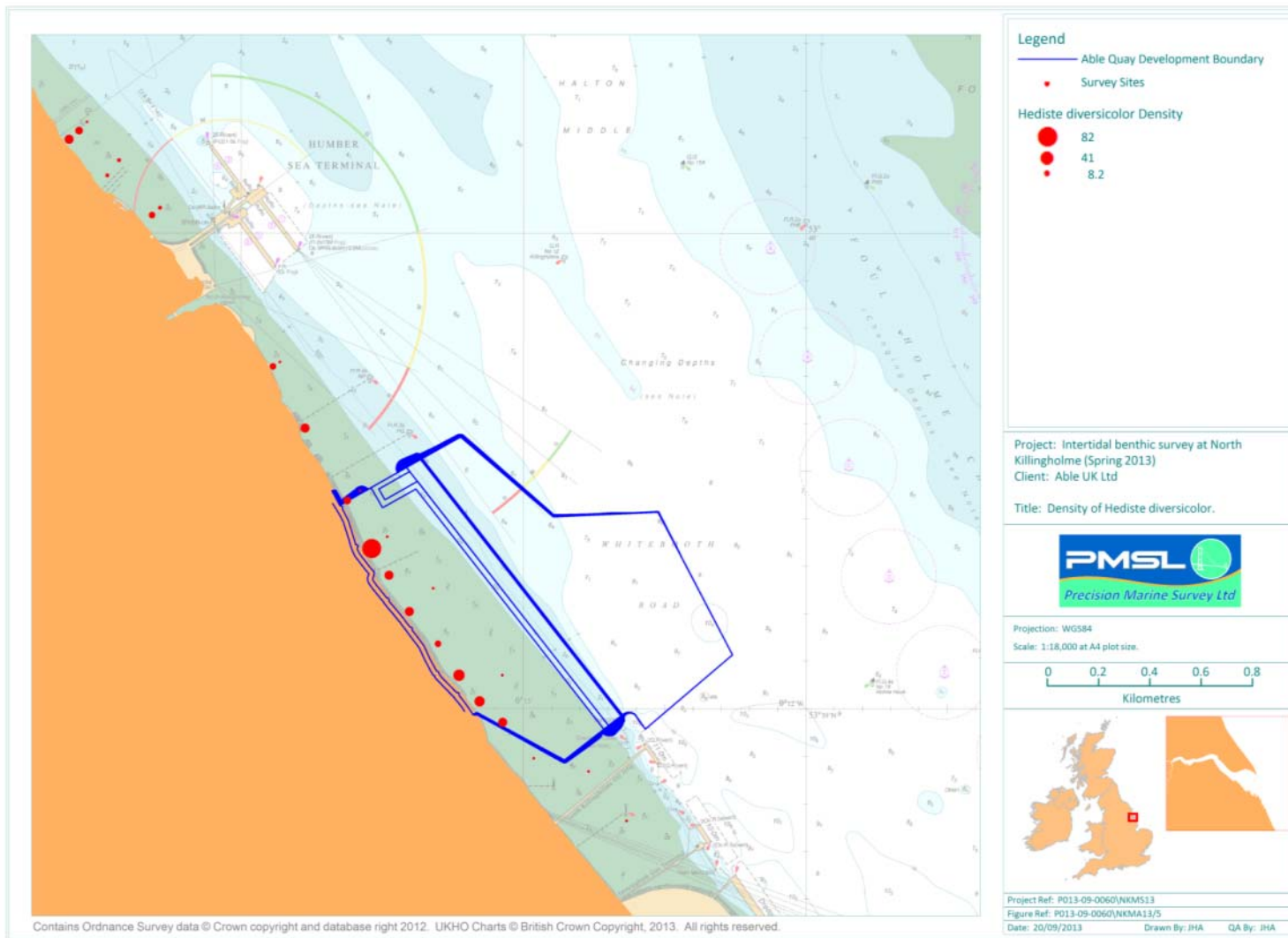
Figure 27. Distribution of *Hediste diversicolor* (autumn survey).
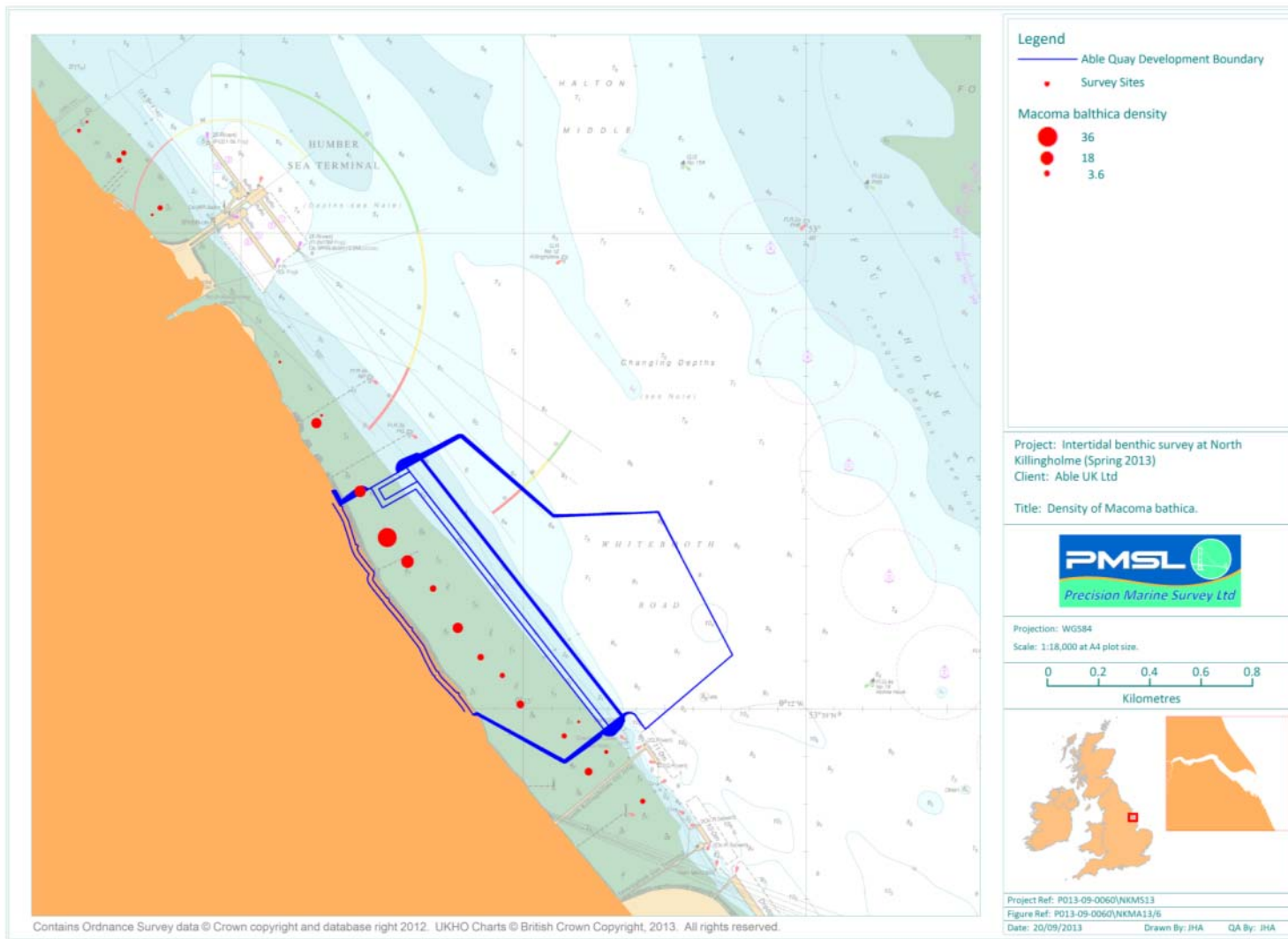
Figure 28.   Distribution of *Macoma balthica* (autumn survey).
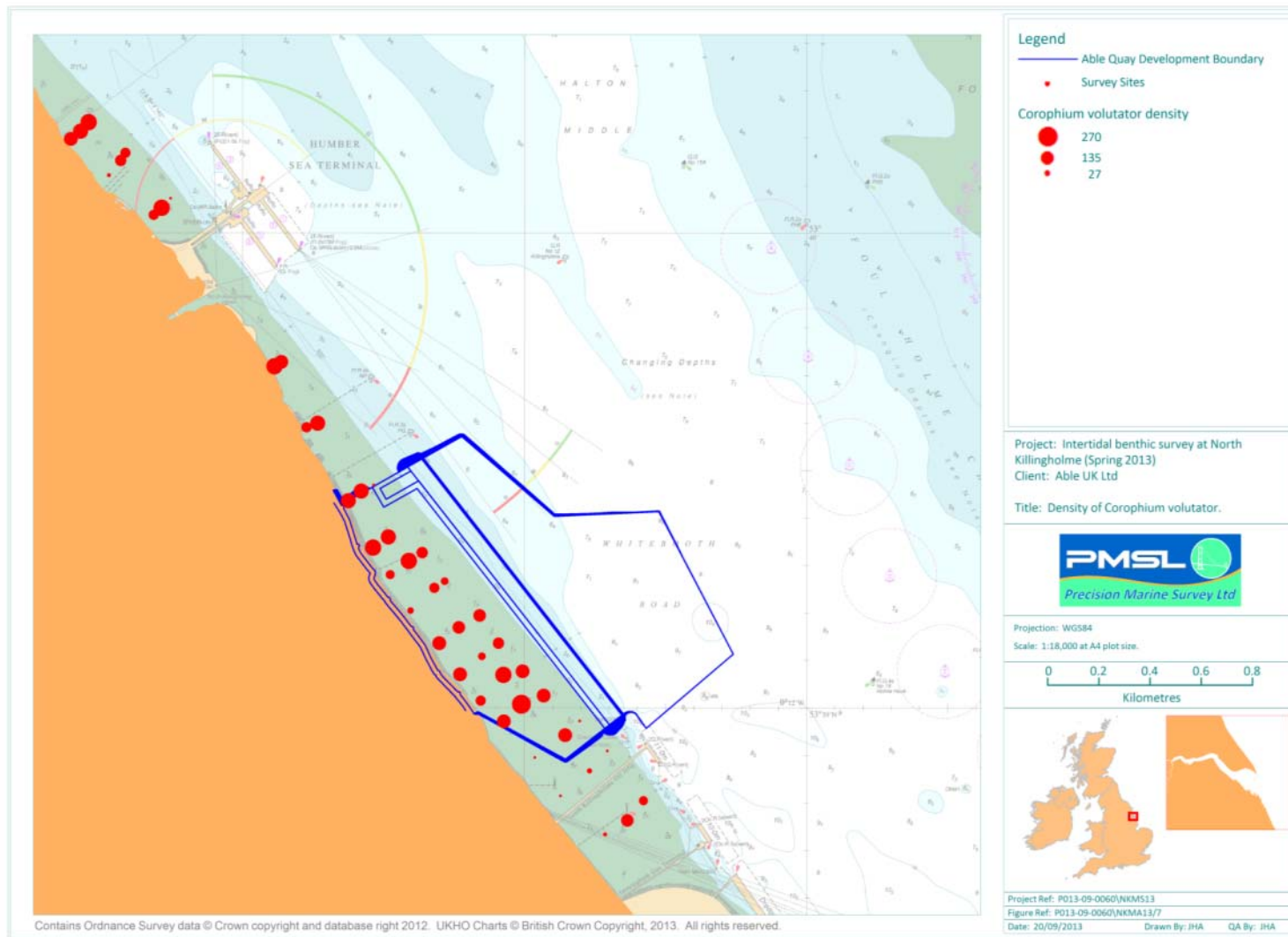
Figure 29. Distribution of *Corophium volutator* (autumn survey).
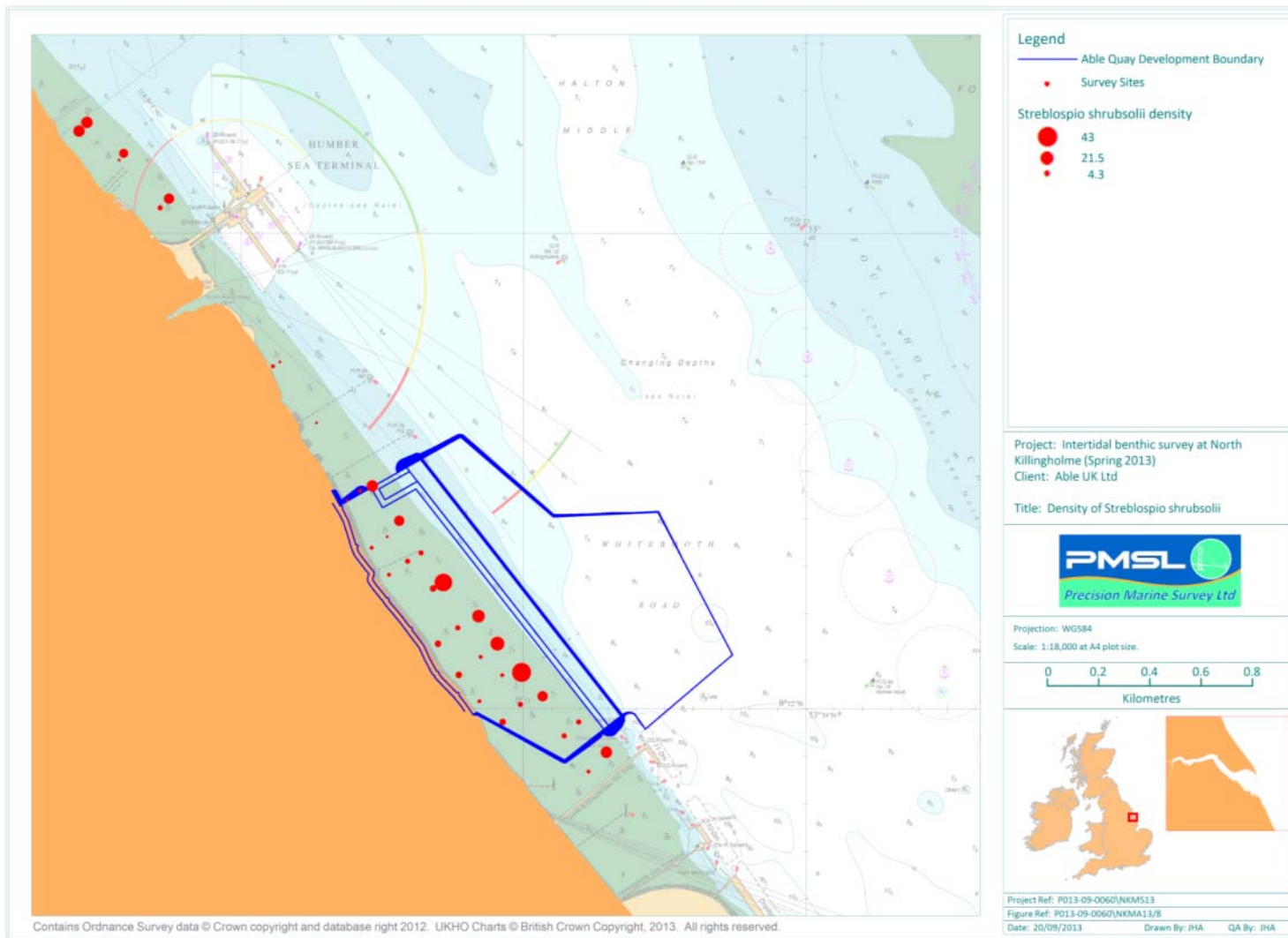
Figure 30.   Distribution of *Streblospio shrubsolii* (autumn survey).
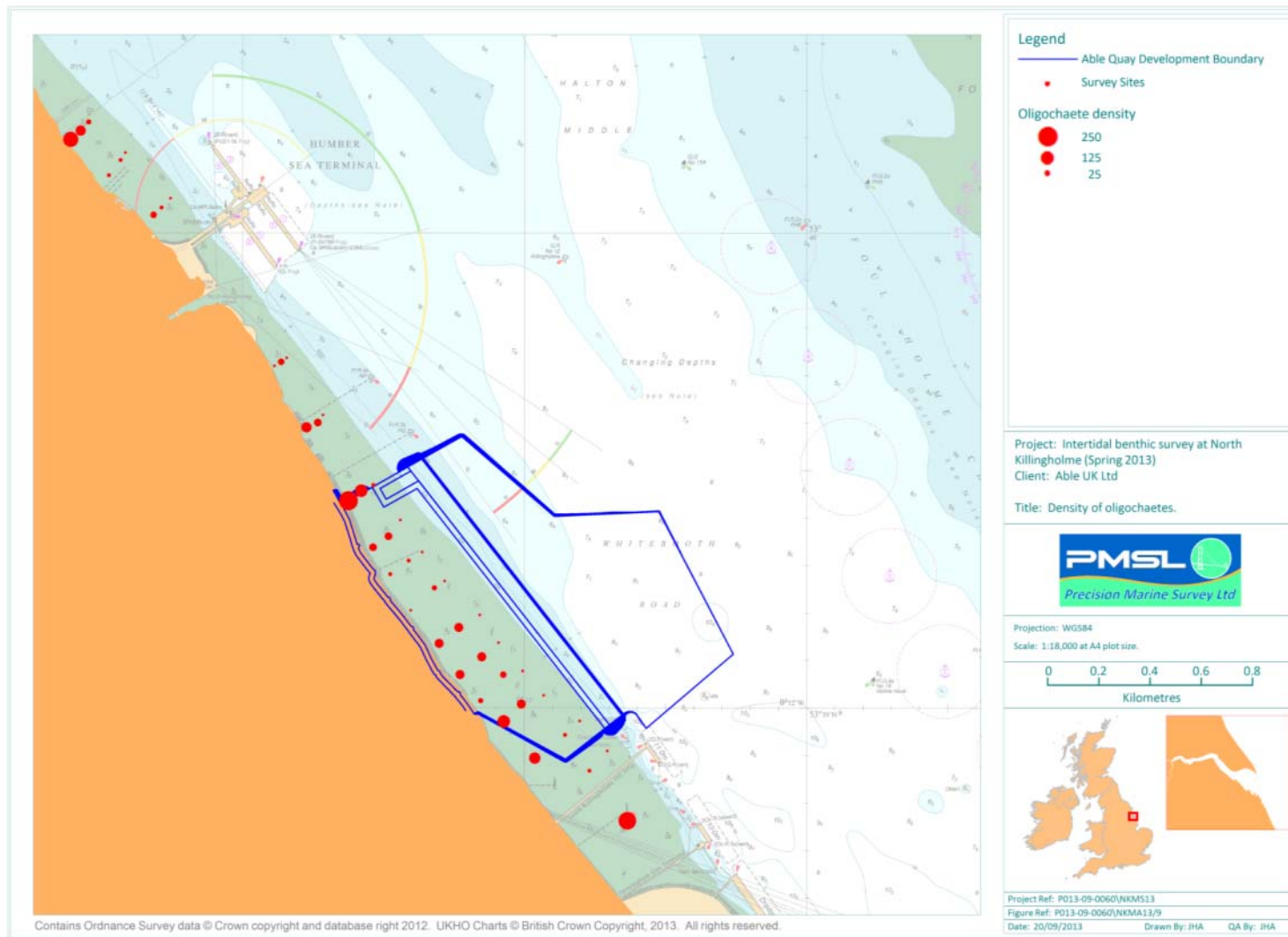
Figure 31.   Distribution of oligochaetes (autumn survey).
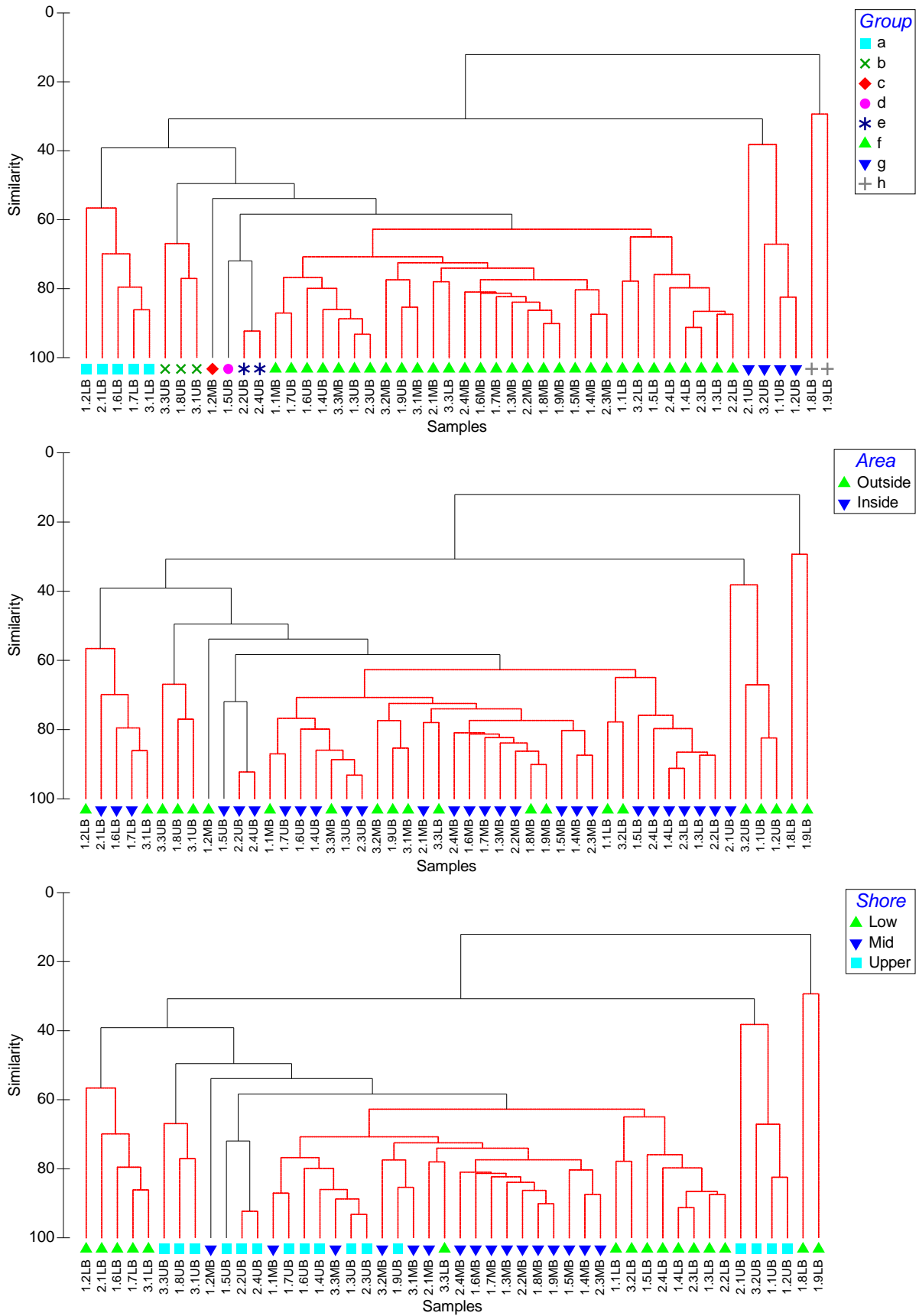
Figure 32. Results of cluster analysis (samples highlighted by group, area and shore level)
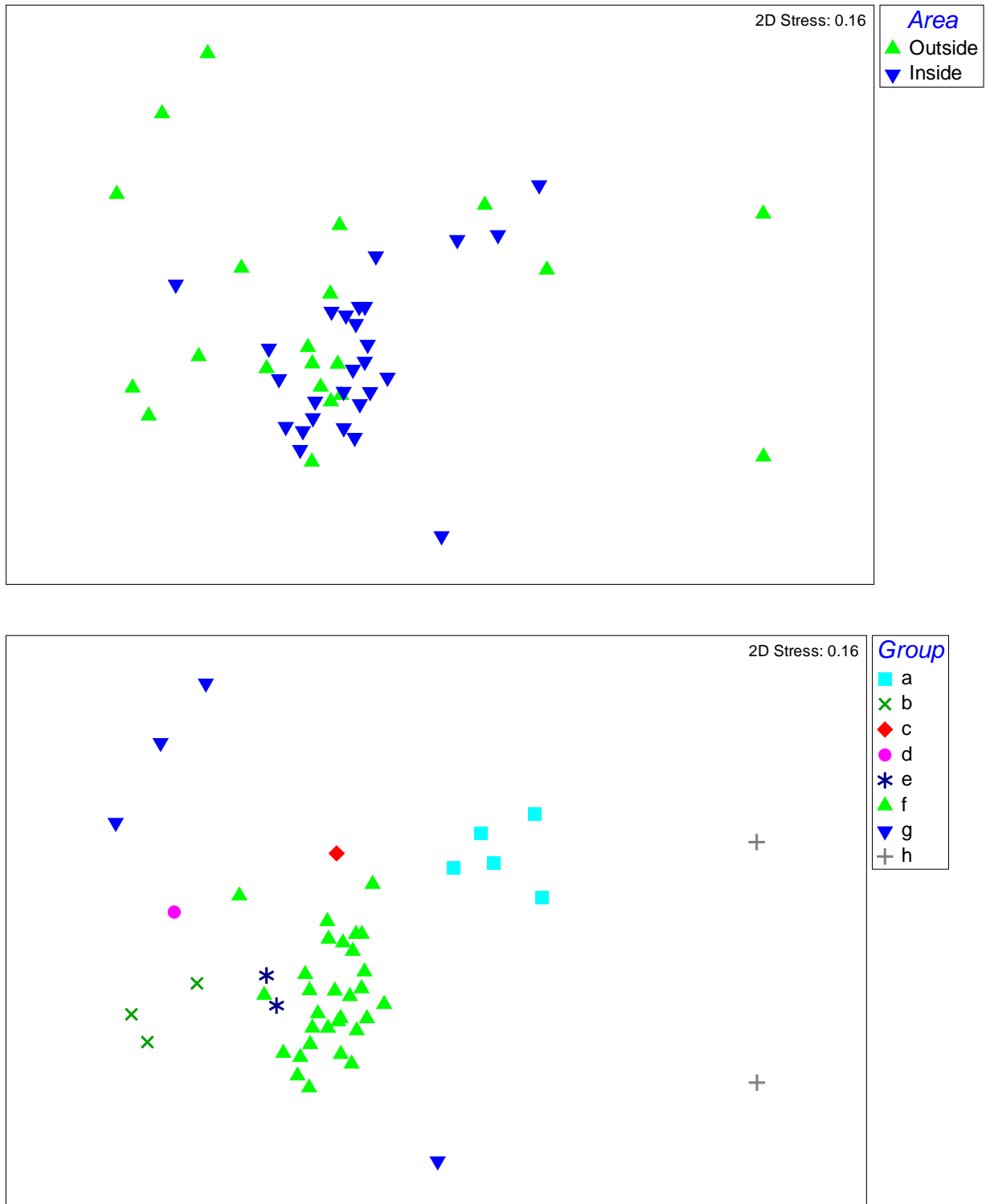
Figure 33. Results of nMDS (sites highlighted by area, shore level and group)

2D Stress: 0.16
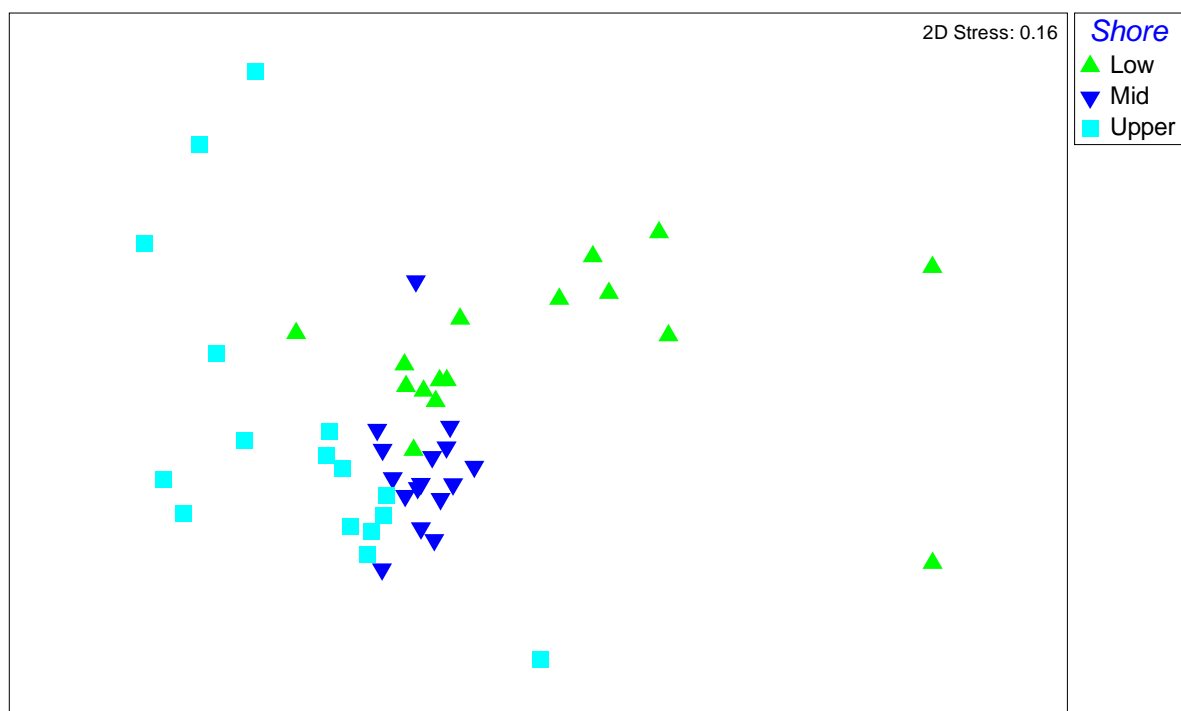
Shore
▲ Low
▼ Mid
■ Upper

Figure 33 (cont.). Results of nMDS (sites highlighted by area, shore level and group).

Table 12.   Characteristic taxa from cluster groups derived from SIMPROF

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
	1.2LB	Streblospio shrubsolii	13.00	100.00	37.99	37.99
	1.6LB	Tubificoides benedii	8.20	100.00	28.25	66.23
	1.7LB	Nematoda	3.80	80.00	14.26	80.5
	2.1LB	Corophium volutator	2.80	80.00	9.24	89.74
Group a	3.1LB	Eteone longa/flava agg.	0.80	80.00	7.52	97.26
Average similarity: 68.08		Pygospio elegans	0.80	40.00	1.6	98.87
		Macoma balthica	0.60	40.00	1.13	100
		Tharyx sp.	0.20	20.00	0	100
		Tubificoides swirencoides	0.80	20.00	0	100
		Collembola sp.	0.20	20.00	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
	1.8UB	Corophium volutator	113.33	100.00	40.77	40.77
	3.1UB	Enchytraeidae	88.67	100.00	24.35	65.12
	3.3UB	Hediste diversicolor	17.00	100.00	15.2	80.32
		Nematoda	20.67	100.00	13.98	94.29
		Tubificoides agg. (pseudogaster)	8.67	66.67	4.34	98.63
Group b		Tubificoides benedii	1.00	66.67	1.37	100
Average similarity: 70.23		Manayunkia aestuarina	2.33	33.33	0	100
		Macoma balthica	0.33	33.33	0	100
		Collembola sp.	0.67	33.33	0	100
		Diptera sp.	0.67	33.33	0	100
		Acarina sp.	0.33	33.33	0	100
		Linyphiidae	0.33	33.33	0	100

SIMPROF Cluster	Site	Species	A
Group c	1.2MB	Corophium volutator	24.00
		Collembola sp.	24.00
		Tubificoides benedii	11.00
		Macoma balthica	7.00
		Nematoda	6.00
		Pygospio elegans	3.00
		Streblospio shrubsolii	3.00
		Hediste diversicolor	2.00

SIMPROF Cluster	Site	Species	A
Group d	1.5UB	Corophium volutator	37.00
		Hediste diversicolor	19.00
		Tubificoides benedii	5.00
		Diptera sp.	4.00

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group e Average similarity: 92.24	2.2UB	Corophium volutator	72.50	100.00	41.65	41.65
	2.4UB	Hediste diversicolor	25.50	100.00	24.05	65.7
		Tubificoides benedii	21.00	100.00	21.64	87.33
		Streblospio shrubsolii	2.50	100.00	7.42	94.75
		Nematoda	1.00	100.00	5.25	100

SIMPROF Cluster	Sites		Species	Average A	% of Sites	Contrib%	Cum.%
Group f Average similarity: 69.53	1.1LB	1.9UB	Corophium volutator	154.13	100.00	57.49	57.49
	1.1MB	2.1MB	Tubificoides benedii	48.57	96.67	17.59	75.08
	1.3LB	2.2LB	Nematoda	8.67	96.67	10.46	85.54
	1.3MB	2.2MB	Streblospio shrubsolii	8.70	93.33	8.32	93.86
	1.3UB	2.3LB	Macoma balthica	4.40	56.67	2.88	96.74
	1.4LB	2.3MB	Hediste diversicolor	6.93	53.33	2.22	98.96
	1.4MB	2.3UB	Pygospio elegans	0.63	33.33	0.54	99.5
	1.4UB	2.4LB	Eteone longa/flava agg.	0.17	16.67	0.13	99.64
	1.5LB	2.4MB	Enchytraeidae	0.27	16.67	0.12	99.75
	1.5MB	3.1MB	Nemertea	0.17	16.67	0.12	99.87
	1.6MB	3.2LB	Tharyx sp.	0.13	13.33	0.07	99.94
	1.6UB	3.2MB	Manayunkia aestuarina	0.13	10.00	0.03	99.98
	1.7MB	3.3LB	Tubificoides agg. (pseudogaster)	0.07	6.67	0.01	99.99
	1.7UB	3.3MB	Collembola sp.	0.17	6.67	0.01	100
	1.8MB		Diptera sp.	0.07	3.33	0	100
	1.9MB		Coleoptera sp.	0.03	3.33	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group g Average similarity: 55.15	1.1UB	Collembola sp.	15.00	100.00	35.11	35.11
	1.2UB	Corophium volutator	12.50	100.00	30.16	65.27
	2.1UB	Diptera sp.	4.75	100.00	18.1	83.37
	3.2UB	Nematoda	2.25	100.00	13.31	96.69
		Acarina sp.	0.50	50.00	1.74	98.43
		Hediste diversicolor	1.50	50.00	1.57	100
		Tubificoides benedii	26.50	25.00	0	100
		Tubificoides agg. (pseudogaster)	1.50	25.00	0	100
		Enchytraeidae	1.25	25.00	0	100

SIMPROF Cluster	Sites	Species	Average A	% of Sites	Contrib%	Cum.%
Group h Average similarity: 29.29	1.8LB	Tubificoides benedii	1.50	100.00	100	100
	1.9LB	Eteone longa/flava agg.	0.50	50.00	0	100
		Nephtys hombergii	0.50	50.00	0	100
		Pygospio elegans	1.00	50.00	0	100
		Macoma balthica	0.50	50.00	0	100
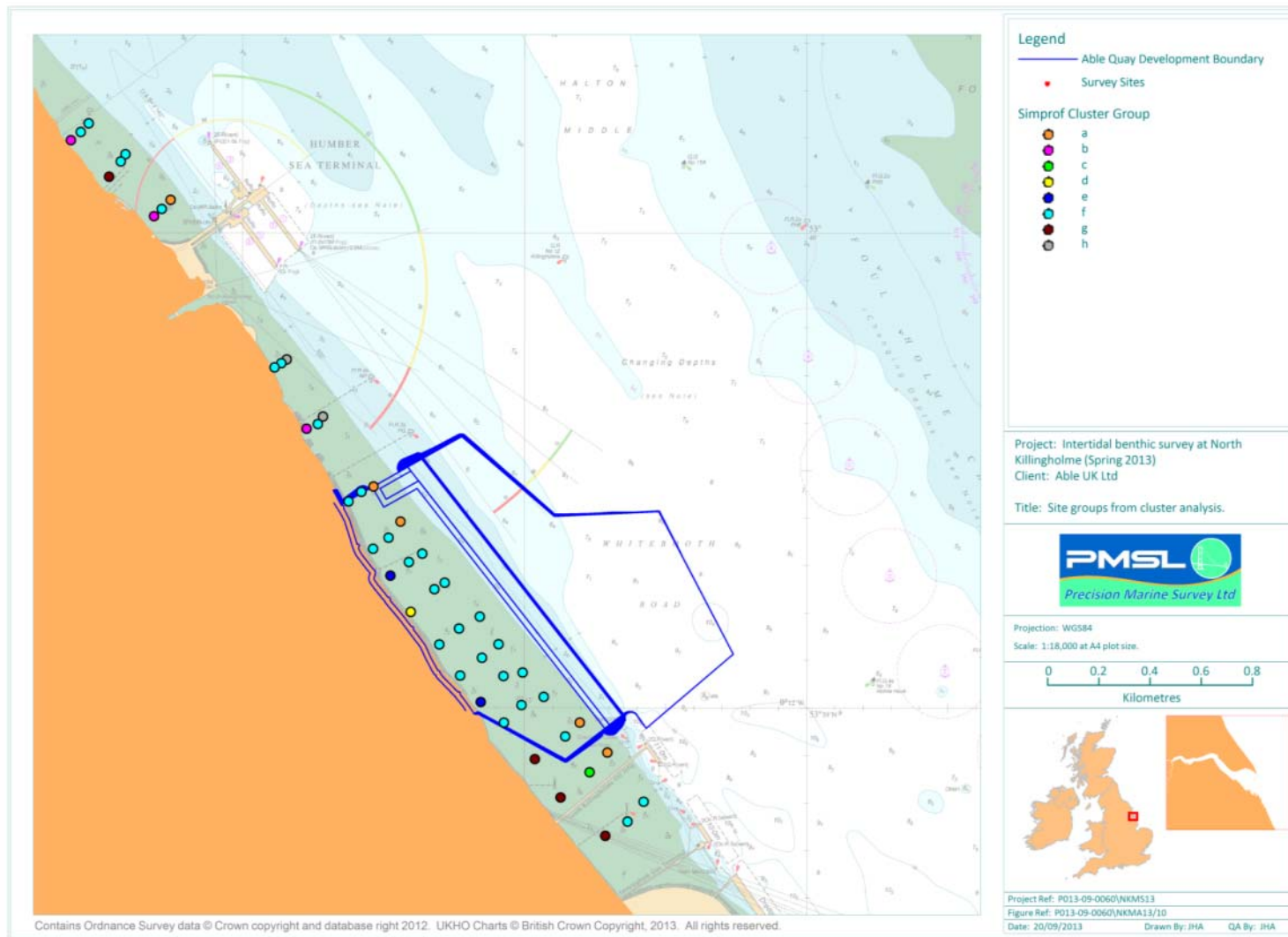
Figure 34.   Distribution of site groups derived from cluster analysis (autumn survey).

5. Summary of Cherry Cobb Sand data

As outlined in the MEMMP intertidal benthic surveys on the Cherry Cobb Sands area on the north bank were required to assess the benthic communities in the area of the proposed mitigation site. This survey was undertaken in May/June 2013 following a similar methodology to that employed for the May NKM 2013 survey. Additional surveys in Autumn using single replicates to assess bird food resources at the control areas at Cherry Cobb Sands has also been undertaken (as described for NKM) and this data is currently being processed. The results of May 2013 CCS survey will be reported separately but it is considered useful to include a brief summary here to put the spring 2013 NKM survey data in context of the wider area. The location of the survey sites processed to date are shown in Figure 35 and a some preliminary results are presented below. 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.

The biological parameters derived from CCS dataset (per sample, average and total) are shown in Tables 14 to 16 with the spatial distribution of total numbers of taxa, individuals and biomass parameters provided in Figures 36 to 38. The results of the CCS survey indicate a broadly similar range of values for numbers of taxa, individuals and biomass to those described in Section 3 for the spring NKM survey and generally correspond to other surveys in the middle Humber. A preliminary assessment of the spatial variation indicates relatively little differences in terms of numbers of taxa between NKM and CCS although a higher total number of taxa were recorded at CCS possibly reflecting the wider range of sediment types. Numbers of individuals and biomass were highly variable with much lower values on the low shore and to a lesser extent at the northern CCS control sites. The remainder of the upper and mid shore CCS sites tend to have higher total numbers of individuals and biomass than recorded at the NKM sites.

In terms of characteristic species from the CCS survey the dominant taxa from all samples and per different survey/shore area are shown in Tables 17 and 18 with the distribution of key taxa (*Hediste diversicolor*, *Macoma balthica*, *Corophium volutator* and oligochaetes spp.) provide in Figures 39 to 42. 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 and 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. Other differences in taxa between NKM and CCS include the reduction in numbers of *Streblospio shrubsolii and an* increase in numbers *of Pygospio elegans*. In terms of biomass *Hediste diversicolor* and *Macoma balthica* account for over 90% of the total. Figures 39 to 42 highlight the spatial distribution of these taxa and highlight similar numbers of *Hediste diversicolor* at NKM and CCS (but with a slightly wider distribution at CCS) whilst *Macoma balthica* occurs in generally higher numbers at CCS on the upper and mid shore particularly at the southern control and impact transects. As stated above *Corophium volutator* is largely absent from the CCS site but much more 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.

The results of preliminary multivariate analysis (Figures 43 to 45 and Table 18) on the NKM and CCS data highlights a relatively complex pattern of communities across the area with the majority of NKM sites separated from the CCS sites at around 30 to 40% similarity. This indicates that whilst there is certain level of agreement between the two areas in terms of community structure (i.e. the majority of taxa occur in both areas) there is a difference in community type which largely reflects the absence of *Corophium volutator* at CCS in conjunction with changes in dominance of certain other supporting taxa (e.g. *Streblospio shrubsolii* and *Pygospio elegans*). Other differences in community structure are likely to reflect changes in the sediment regime and it was noted that a wider range of substrate types was present at CCS in addition to other communities (e.g. *Arenicola* beds) which are not present at NKM and overall the CCS area appears to be slightly more diverse in terms of the range of communities and total numbers of species present.
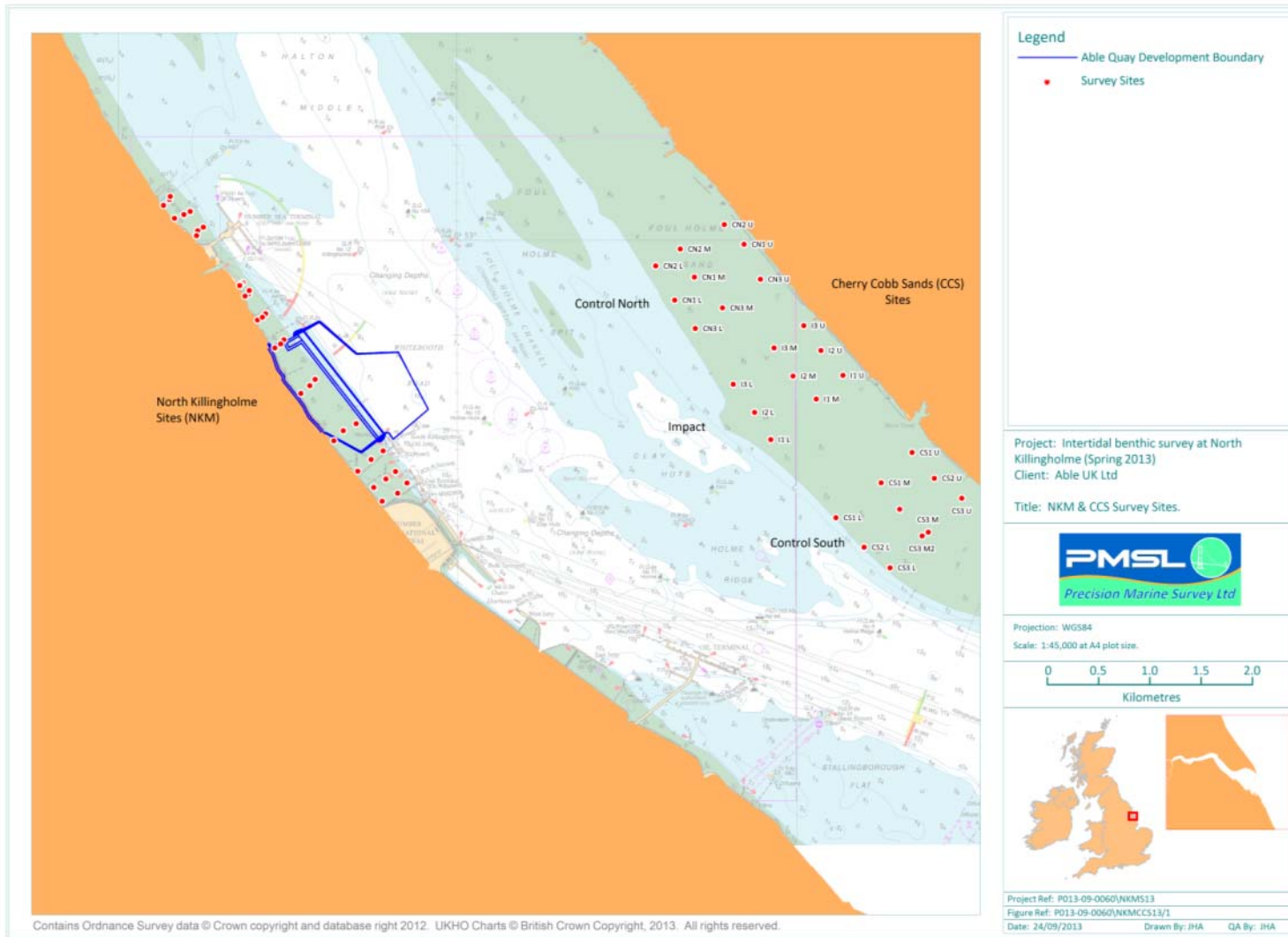
Figure 35. Location of Cherry Cobb Sand Sites (north bank) in relation to NKM sites.

Table 13.   Biological parameters from Cherry Cobb Sands survey.

Area	Sample	Shore	No. of Taxa	Numbers of Individuals	Biomass (g)	Margalef's d	Pielou's J	Shannon's H
	CN1L A	Low	1	3	0.1855	0.00	-	0.00
	CN1L B	Low	1	4	0.1523	0.00	-	0.00
	CN1L C	Low	1	3	0.0075	0.00	-	0.00
	CN1M A	Mid	6	65	0.1175	1.20	0.61	1.57
	CN1M B	Mid	5	118	0.1198	0.84	0.76	1.77
	CN1M C	Mid	3	25	0.3239	0.62	0.90	1.43
	CN1U A	Upper	5	27	0.6061	1.21	0.66	1.53
	CN1U B	Upper	3	27	0.7461	0.61	0.79	1.25
	CN1U C	Upper	7	67	0.5109	1.43	0.73	2.05
	CN2L A	Low	2	3	0.0338	0.91	0.92	0.92
	CN2L B	Low	6	10	0.0775	2.17	0.95	2.45
	CN2L C	Low	1	1	0.0224	-	-	0.00
	CN2M A	Mid	9	168	0.6228	1.56	0.51	1.62
Control North	CN2M B	Mid	8	158	0.2968	1.38	0.49	1.47
	CN2M C	Mid	6	169	0.3353	0.97	0.65	1.67
	CN2U A	Upper	9	405	1.371	1.33	0.47	1.49
	CN2U B	Upper	8	341	0.9617	1.20	0.44	1.33
	CN2U C	Upper	8	374	0.5139	1.18	0.57	1.72
	CN3L A	Low	1	2	0.251	0.00		0.00
	CN3L B	Low	4	5	0.2183	1.24	0.86	1.37
	CN3L C	Low	3	4	0.0177	1.44	0.95	1.50
	CN3M A	Mid	6	83	0.8643	1.13	0.64	1.66
	CN3M B	Mid	7	93	0.4936	1.32	0.64	1.81
	CN3M C	Mid	7	81	0.1931	1.37	0.64	1.78
	CN3U A	Upper	4	35	0.4248	0.84	0.77	1.54
	CN3U B	Upper	4	15	0.2692	1.11	0.78	1.56
	CN3U C	Upper	4	117	0.3231	0.63	0.62	1.24
	CS1L A	Low	1	0	0.005	-	-	0.00
	CS1L B	Low	3	6	0.0181	1.12	1.00	1.58
	CS1L C	Low	3	4	0.0711	1.44	0.95	1.50
	CS1M A	Mid	6	229	1.5169	0.92	0.43	1.12
	CS1M B	Mid	8	268	3.1156	1.25	0.51	1.53
	CS1M C	Mid	7	179	2.3451	1.16	0.53	1.50
	CS1U A	Upper	7	216	3.9571	1.12	0.49	1.37
	CS1U B	Upper	7	291	3.2146	1.06	0.55	1.54
	CS1U C	Upper	8	212	2.7591	1.31	0.43	1.28
	CS2L A	Low	1	1	0.0062	-	-	0.00
	CS2L B	Low	1	1	0.0035	-	-	0.00
	CS2L C	Low	0	0	0	-	-	0.00
	CS2M A	Mid	10	100	0.9538	1.95	0.61	2.02
	CS2M B	Mid	11	111	1.5164	2.12	0.47	1.64
Control South	CS2M C	Mid	10	107	1.8216	1.93	0.59	1.95
	CS2U A	Upper	8	186	2.6792	1.34	0.52	1.57
	CS2U B	Upper	10	252	2.9905	1.45	0.45	1.44
	CS2U C	Upper	7	204	3.2222	1.13	0.48	1.35
	CS3L A	Low	1	1	0.0044	-	-	0.00
	CS3L B	Low	0	0	0	-	-	0.00
	CS3L C	Low	2	2	0.0107	1.44	1.00	1.00
	CS3M A	Mid	5	17	0.1019	1.41	0.80	1.85
	CS3M B	Mid	5	19	0.2766	1.36	0.87	2.02
	CS3M C	Mid	6	25	0.8258	1.55	0.65	1.68
	CS3M2 A	Mid	4	13	0.4002	1.17	0.87	1.74
	CS3M2 B	Mid	6	20	0.6562	1.67	0.74	1.92
	CS3M2 C	Mid	6	26	0.9174	1.53	0.72	1.85
	CS3U A	Upper	9	165	3.1345	1.57	0.57	1.81
	CS3U B	Upper	6	139	2.6659	1.01	0.64	1.65
	CS3U C	Upper	6	205	3.2608	0.94	0.74	1.92

Area	Sample	Shore	No. of Taxa	Numbers of Individuals	Biomass (g)	Margalef's d	Pielou's J	Shannon's H
	I1L A	Low	2	2	0.0103	1.44	1.00	1.00
	I1L B	Low	3	3	0.1014	0.91	0.92	0.92
	I1L C	Low	3	5	0.1062	1.24	0.86	1.37
	I1M A	Mid	9	323	2.8903	1.38	0.51	1.62
	I1M B	Mid	7	367	3.7551	1.02	0.62	1.74
	I1M C	Mid	8	354	2.6165	1.19	0.68	2.04
	I1U A	Upper	6	370	1.3964	0.85	0.37	0.96
	I1U B	Upper	7	329	1.4711	1.04	0.45	1.27
	I1U C	Upper	10	396	1.4888	1.50	0.53	1.78
	I2L A	Low	1	2	0.4831	0.00	-	0.00
	I2L B	Low	2	3	0.0472	0.91	0.92	0.92
	I2L C	Low	3	3	0.0398	1.82	1.00	1.58
	I2M A	Mid	7	362	1.7448	1.02	0.52	1.45
Impact	I2M B	Mid	8	292	1.7914	1.23	0.74	2.23
	I2M C	Mid	9	340	1.8594	1.37	0.59	1.87
	I2U A	Upper	6	18	0.185	1.73	0.89	2.29
	I2U B	Upper	7	13	0.177	2.34	0.91	2.57
	I2U C	Upper	5	14	0.1221	1.52	0.85	1.99
	I3L A	Low	3	3	0.0164	1.82	1.00	1.58
	I3L B	Low	5	7	0.1143	2.06	0.92	2.13
	I3L C	Low	5	6	0.0726	2.23	0.97	2.25
	I3M A	Mid	7	285	1.6417	1.06	0.49	1.38
	I3M B	Mid	7	261	2.1649	1.08	0.72	2.03
	I3M C	Mid	8	338	1.1013	1.20	0.57	1.71
	I3U A	Upper	7	213	0.8225	1.12	0.62	1.74
	I3U B	Upper	6	161	1.1269	0.98	0.68	1.75
	I3U C	Upper	8	258	1.7403	1.26	0.59	1.77

Table 14.   Mean biological parameters from Cherry Cobb Sands survey.

Area	Shore	Site	Mean Numbers of Taxa	Mean Numbers of Individuals	Mean Biomass (g)	Mean Margalef's d	Mean Pielou's J	Mean Shannon's H'
	Low	CN1L	1.00	3.33	0.12	0.00	-	0.00
	Mid	CN1M	4.67	69.33	0.19	0.89	0.76	1.59
	Upper	CN1U	5.00	40.33	0.62	1.08	0.73	1.61
	Low	CN2L	3.00	4.67	0.04	1.54	0.93	1.12
Control North	Mid	CN2M	7.67	165.00	0.42	1.31	0.55	1.59
	Upper	CN2U	8.33	373.33	0.95	1.24	0.50	1.51
	Low	CN3L	2.67	3.67	0.16	0.90	0.91	0.96
	Mid	CN3M	6.67	85.67	0.52	1.27	0.64	1.75
	Upper	CN3U	4.00	55.67	0.34	0.86	0.72	1.45
	Low	CS1L	2.33	3.33	0.03	1.28	0.97	1.03
	Mid	CS1M	7.00	225.33	2.33	1.11	0.49	1.38
	Upper	CS1U	7.33	239.67	3.31	1.16	0.49	1.40
	Low	CS2L	0.67	0.67	0.00	-	-	0.00
Control South	Mid	CS2M	10.33	106.00	1.43	2.00	0.56	1.87
	Upper	CS2U	8.33	214.00	2.96	1.30	0.49	1.45
	Low	CS3L	1.00	1.00	0.01	1.44	1.00	0.33
	Mid	CS3M	5.33	20.33	0.40	1.44	0.77	1.85
	Mid	CS3M2	5.33	19.67	0.66	1.46	0.78	1.84
	Upper	CS3U	7.00	169.67	3.02	1.17	0.65	1.79
	Low	I1L	2.67	3.33	0.07	1.20	0.93	1.10
	Mid	I1M	8.00	348.00	3.09	1.20	0.60	1.80
	Upper	I1U	7.67	365.00	1.45	1.13	0.45	1.34
	Low	I2L	2.00	2.67	0.19	0.91	0.96	0.83
Impact	Mid	I2M	8.00	331.33	1.80	1.21	0.62	1.85
	Upper	I2U	6.00	15.00	0.16	1.86	0.88	2.28
	Low	I3L	4.33	5.33	0.07	2.04	0.96	1.99
	Mid	I3M	7.33	294.67	1.64	1.11	0.59	1.70
	Upper	I3U	7.00	210.67	1.23	1.12	0.63	1.75

Table 15. Total biological parameters (per 0.03m^2) from Cherry Cobb Sands survey.

| Area	Shore	Site	No. of Taxa	Numbers of Individuals (0.03m^2)	Numbers of Individuals per m^2	Biomass (g per 0.03m^2)	Biomass (g per m^2)	Margalef's d	Pielou's J	Shannon's H
	Low	CN1L	2	10	333.33	0.3453	11.51	0.43	0.88	0.88
	Mid	CN1M	7	208	6933.33	0.5612	18.71	1.12	0.67	1.87
	Upper	CN1U	8	121	4033.33	1.8632	62.11	1.46	0.66	1.99
	Low	CN2L	6	14	466.67	0.1337	4.46	1.89	0.86	2.22
Control North	Mid	CN2M	10	495	16500.00	1.2549	41.83	1.45	0.50	1.65
	Upper	CN2U	9	1120	37333.33	2.8466	94.89	1.14	0.49	1.56
	Low	CN3L	5	11	366.67	0.487	16.23	1.25	0.75	1.49
	Mid	CN3M	8	257	8566.67	1.551	51.70	1.26	0.63	1.89
	Upper	CN3U	5	167	5566.67	1.0171	33.90	0.78	0.65	1.50
	Low	CS1L	5	10	333.33	0.0942	3.14	1.30	0.99	1.97
	Mid	CS1M	10	676	22533.33	6.9776	232.59	1.38	0.42	1.41
	Upper	CS1U	10	719	23966.67	9.9308	331.03	1.37	0.45	1.48
	Low	CS2L	1	2	66.67	0.0097	0.32	0.00	-	0.00
Control South	Mid	CS2M	15	318	10600.00	4.2918	143.06	2.43	0.51	1.98
	Upper	CS2U	10	642	21400.00	8.8919	296.40	1.39	0.45	1.50
	Low	CS3L	3	3	100.00	0.0151	0.50	1.82	1.00	1.58
	Mid	CS3M	8	61	2033.33	1.2043	40.14	1.70	0.77	2.31
	Mid2	CS3M2	8	59	1966.67	1.9738	65.79	1.72	0.67	2.02
	Upper	CS3U	10	509	16966.67	9.0612	302.04	1.44	0.57	1.88
	Low	I1L	5	10	333.33	0.2179	7.26	1.30	0.79	1.57
	Mid	I1M	10	1044	34800.00	9.2619	308.73	1.29	0.56	1.86
	Upper	I1U	11	1095	36500.00	4.3563	145.21	1.43	0.41	1.41
	Low	I2L	4	8	266.67	0.5701	19.00	1.44	0.77	1.55
Impact	Mid	I2M	11	994	33133.33	5.3957	179.86	1.45	0.56	1.92
	Upper	I2U	10	45	1500.00	0.4841	16.14	2.36	0.82	2.72
	Low	I3L	8	16	533.33	0.2033	6.78	2.52	0.90	2.70
	Mid	I3M	8	884	29466.67	4.9079	163.60	1.03	0.58	1.75
	Upper	I3U	9	632	21066.67	3.6897	122.99	1.24	0.58	1.83
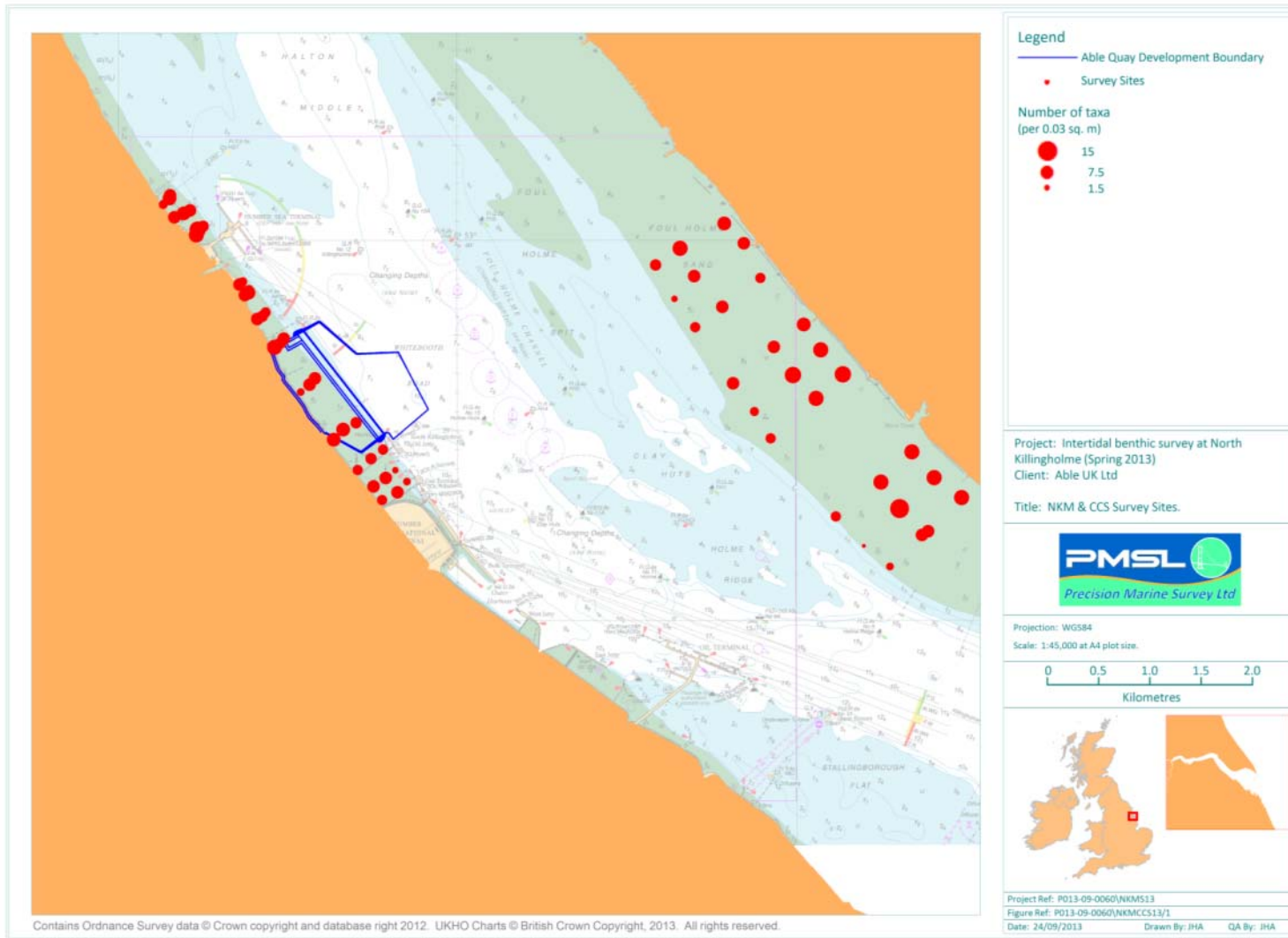
Figure 36. Total number of taxa recorded during the NKM and CCS spring survey.
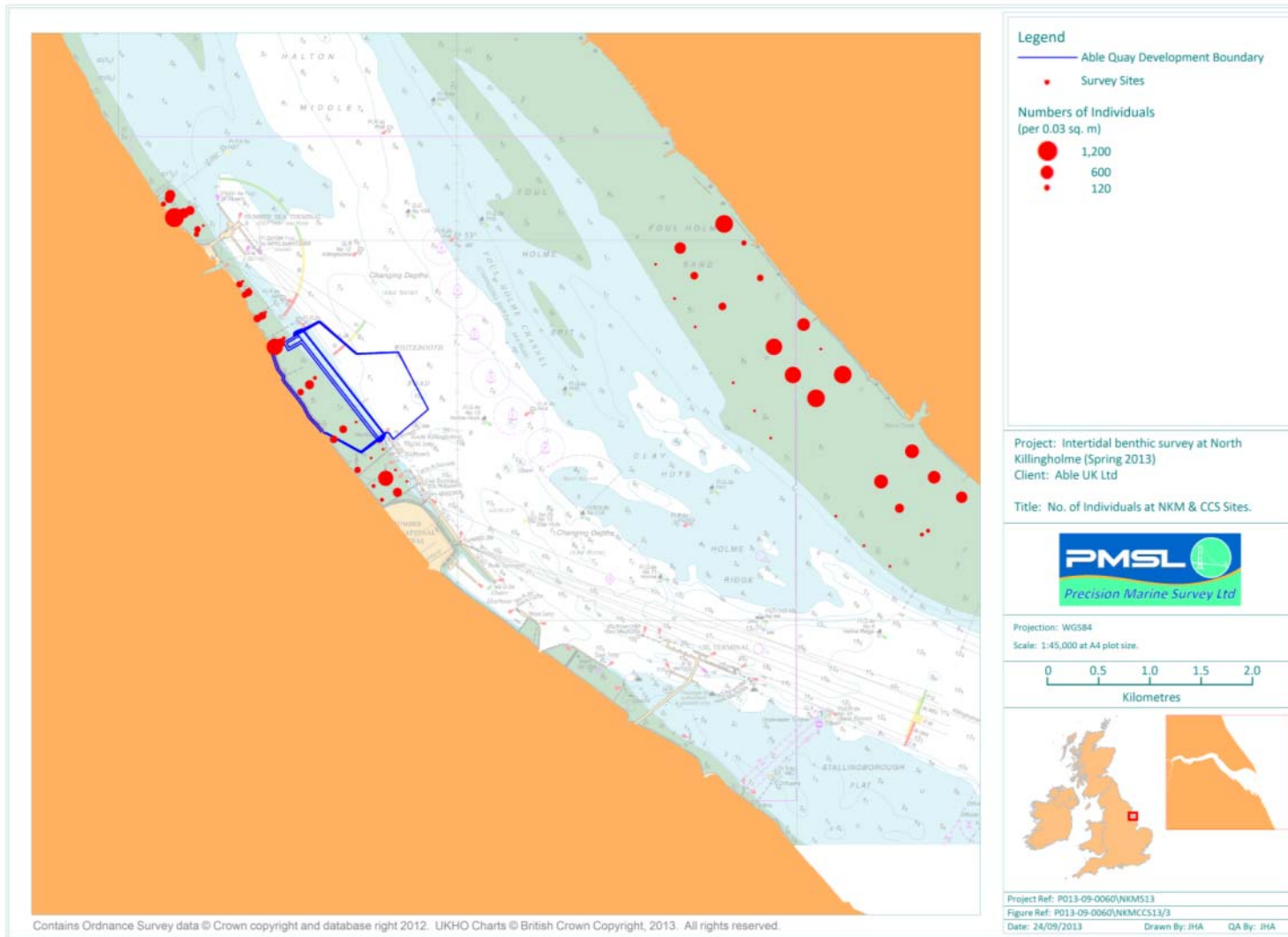
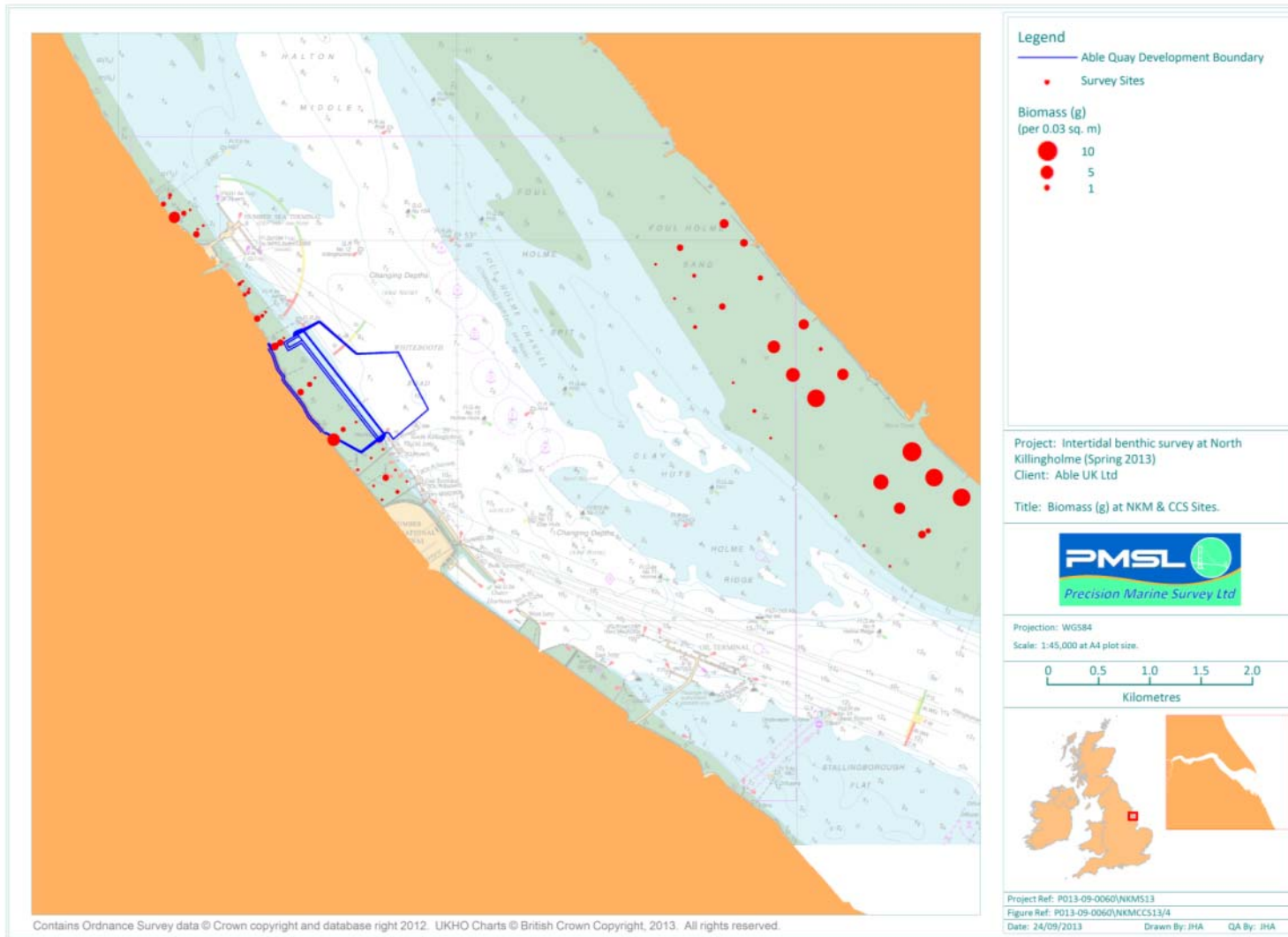**Figure 37.   Total numbers of individuals recorded during the NKM and CCS spring survey.**

Figure 38.   Total biomass of invertebrates recorded during the NKM and CCS spring survey.

Table 16. Dominant taxa from the CCS survey (all sites).

Taxon	Average A	% of Sites	% Cont.	Taxon	Average B	% of Sites	% Cont.
Tubificoides benedii	181.43	78.57	50.15	Macoma balthica	2.0842	82.14	71.52
Nematoda	47.96	71.43	63.41	Hediste diversicolor	0.5606	67.86	90.76
Macoma balthica	34.64	82.14	72.98	Tubificoides benedii	0.1874	78.57	97.19
Tubificoides agg. (pseudogaster)	29.71	14.29	81.19	Hydrobia ulvae	0.0211	64.29	97.91
Hediste diversicolor	17.89	67.86	86.14	Tubificoides agg. (pseudogaster)	0.0190	14.29	98.56
Pygospio elegans	17.07	71.43	90.86	Nephtys hombergii	0.0178	28.57	99.17
Hydrobia ulvae	12.11	64.29	94.21	Pygospio elegans	0.0059	71.43	99.38
Enchytraeidae	11.07	53.57	97.27	Abra tenuis	0.0042	10.71	99.52
Manayunkia aestuarina	3.71	39.29	98.29	Eteone longa/flava agg.	0.0037	35.71	99.65
Diptera sp.	1.46	21.43	98.70	Diptera sp.	0.0035	21.43	99.77
Eteone longa/flava agg.	0.82	35.71	98.92	Nematoda	0.0019	71.43	99.83
Nephtys hombergii	0.82	28.57	99.15	Corophium volutator	0.0009	7.14	99.87
Streblospio shrubsolii	0.61	28.57	99.32	Enchytraeidae	0.0009	53.57	99.90
Bathyporeia sarsi	0.57	3.57	99.48	Bathyporeia sarsi	0.0007	3.57	99.92
Corophium volutator	0.39	7.14	99.59	Scoloplos armiger	0.0005	3.57	99.94
Collembola sp.	0.36	10.71	99.68	Abra sp.	0.0005	3.57	99.96
Abra tenuis	0.18	10.71	99.73	Scrobicularia plana	0.0003	3.57	99.97
Tharyx sp.	0.18	3.57	99.78	Manayunkia aestuarina	0.0002	39.29	99.97
Cyathura carinata	0.14	14.29	99.82	Spionidae sp.	0.0002	3.57	99.98
Mytilidae juv.	0.14	10.71	99.86	Tharyx sp.	0.0002	3.57	99.99
Alderia modesta	0.07	7.14	99.88	Retusa obtusa	0.0001	3.57	99.99
Acarina sp.	0.07	7.14	99.90	Nereididae sp.	0.0001	3.57	99.99
Dalyelliidae sp.	0.07	3.57	99.92	Cyathura carinata	0.0001	14.29	100.00
Caulleriella killariensis	0.07	3.57	99.94	Collembola sp.	0.0000	10.71	100.00
Nemertea	0.04	3.57	99.95	Streblospio shrubsolii	0.0000	28.57	100.00
Sphaerodoropsis baltica	0.04	3.57	99.96	Mytilidae juv.	0.0000	10.71	100.00
Scoloplos armiger	0.04	3.57	99.97	Alderia modesta	0.0000	7.14	100.00
Retusa obtusa	0.04	3.57	99.98	Acarina sp.	0.0000	7.14	100.00
Abra sp.	0.04	3.57	99.99	Dalyelliidae sp.	0.0000	3.57	100.00
Scrobicularia plana	0.04	3.57	100.00	Nemertea	0.0000	3.57	100.00
Nereididae sp.	P	3.57	100.00	Sphaerodoropsis baltica	0.0000	3.57	100.00
Spionidae sp.	P	3.57	100.00	Caulleriella killariensis	0.0000	3.57	100.00
Ascidiacea sp.	P	3.57	100.00	Ascidiacea sp.	P	3.57	100.00

Table 17. Dominant taxa from the CCS survey areas (by shore level).

Control North Lower			Control North Mid			Control North Upper		
Taxon	Average A	% of Sites	Taxon	Average A	% of Sites	Taxon	Average A	% of Sites
Macoma balthica	6.67	100.00	Nematoda	149.00	100.00	Tubificoides agg. (pseudogaster)	274.33	66.67
Nematoda	1.00	33.33	Tubificoides benedii	100.00	66.67	Nematoda	71.00	100.00
Hydrobia ulvae	1.00	33.33	Hediste diversicolor	18.33	100.00	Enchytraeidae	46.33	66.67
Eteone longa/flava agg.	0.67	66.67	Enchytraeidae	18.33	100.00	Hediste diversicolor	35.33	100.00
Tubificoides benedii	0.67	33.33	Manayunkia aestuarina	10.00	100.00	Manayunkia aestuarina	21.67	66.67
Enchytraeidae	0.67	33.33	Pygospio elegans	8.00	100.00	Diptera sp.	12.33	66.67
Streblospio shrubsolii	0.33	33.33	Hydrobia ulvae	7.67	100.00	Hydrobia ulvae	3.00	33.33
Manayunkia aestuarina	0.33	33.33	Macoma balthica	3.00	66.67	Pygospio elegans	2.33	66.67
Mytilidae juv.	0.33	33.33	Streblospio shrubsolii	3.00	33.33	Tubificoides benedii	1.33	33.33
Ascidiacea sp.	P	33.33	Collembola sp.	2.33	33.33	Collembola sp.	1.00	66.67
			Abra tenuis	0.33	33.33	Streblospio shrubsolii	0.33	33.33
						Acarina sp.	0.33	33.33

Taxon	Average B	% of Sites	Taxon	Average B	% of Sites	Taxon	Average B	% of Sites
Macoma balthica	0.3180	100.00	Hediste diversicolor	0.5912	100.00	Hediste diversicolor	1.7023	100.00
Hydrobia ulvae	0.0025	33.33	Macoma balthica	0.3928	66.67	Tubificoides agg. (pseudogaster)	0.1744	66.67
Eteone longa/flava agg.	0.0011	66.67	Tubificoides benedii	0.0954	66.67	Diptera sp.	0.0175	66.67
Tubificoides benedii	0.0002	33.33	Hydrobia ulvae	0.0218	100.00	Enchytraeidae	0.0054	66.67
Nematoda	0.0001	33.33	Abra tenuis	0.0105	33.33	Hydrobia ulvae	0.0049	33.33
Streblospio shrubsolii	0.00003	33.33	Nematoda	0.0067	100.00	Nematoda	0.0023	100.00
Manayunkia aestuarina	0.00003	33.33	Pygospio elegans	0.0022	100.00	Manayunkia aestuarina	0.0012	66.67
Enchytraeidae	0.00003	33.33	Enchytraeidae	0.0008	100.00	Tubificoides benedii	0.0007	33.33
Mytilidae juv.	0.00003	33.33	Manayunkia aestuarina	0.0004	100.00	Pygospio elegans	0.0001	66.67
Ascidiacea sp.	P	33.33	Collembola sp.	0.0003	33.33	Collembola sp.	0.0001	66.67
			Streblospio shrubsolii	0.0001	33.33	Streblospio shrubsolii	0.00003	33.33
						Acarina sp.	0.00003	33.33

Control South Lower			Control South Mid			Control South Upper		
Taxon	Average A	% of Sites	Taxon	Average A	% of Sites	Taxon	Average A	% of Sites
Nephtys hombergii	2.00	100.00	Tubificoides benedii	131.25	100.00	Tubificoides benedii	396.67	100.00
Tubificoides benedii	1.33	66.67	Macoma balthica	87.25	100.00	Macoma balthica	123.00	100.00
Macoma balthica	1.00	66.67	Pygospio elegans	25.00	100.00	Pygospio elegans	41.33	100.00
Mytilidae juv.	0.67	33.33	Nematoda	11.25	75.00	Nematoda	29.67	100.00
Spionidae sp.	P	33.33	Hediste diversicolor	6.00	75.00	Hediste diversicolor	18.00	100.00
			Bathyporeia sarsi	4.00	25.00	Eteone longa/flava agg.	4.00	100.00
			Nephtys hombergii	3.25	75.00	Hydrobia ulvae	4.00	66.67
			Corophium volutator	2.75	50.00	Tubificoides agg. (pseudogaster)	3.00	66.67
			Eteone longa/flava agg.	1.50	50.00	Abra tenuis	1.33	66.67
			Hydrobia ulvae	1.25	75.00	Dalyelliidae sp.	0.67	33.33
			Enchytraeidae	1.25	50.00	Streblospio shrubsolii	0.33	33.33
			Tharyx sp.	1.25	25.00	Manayunkia aestuarina	0.33	33.33
			Caulleriella killariensis	0.50	25.00	Cyathura carinata	0.33	33.33
			Nemertea	0.25	25.00	Scrobicularia plana	0.33	33.33
			Streblospio shrubsolii	0.25	25.00	Diptera sp.	0.33	33.33
			Sphaerodoropsis baltica	0.25	25.00			
			Scoloplos armiger	0.25	25.00			
			Cyathura carinata	0.25	25.00			
			Retusa obtusa	0.25	25.00			
			Alderia modesta	0.25	25.00			
			Mytilidae juv.	0.25	25.00			

Taxon	Average B	% of Sites	Taxon	Average B	% of Sites	Taxon	Average B	% of Sites
Macoma balthica	0.0206	66.67	Macoma balthica	3.2186	100.00	Macoma balthica	7.8652	100.00
Nephtys hombergii	0.0170	100.00	Hediste diversicolor	0.1385	75.00	Hediste diversicolor	0.9476	100.00
Spionidae sp.	0.0017	33.33	Tubificoides benedii	0.1185	100.00	Tubificoides benedii	0.3901	100.00
Tubificoides benedii	0.0004	66.67	Nephtys hombergii	0.1024	75.00	Abra tenuis	0.0291	66.67
Mytilidae juv.	0.0000	33.33	Pygospio elegans	0.0088	100.00	Eteone longa/flava agg.	0.0238	100.00
			Corophium volutator	0.0066	50.00	Pygospio elegans	0.0229	100.00
			Bathyporeia sarsi	0.0050	25.00	Hydrobia ulvae	0.0051	66.67
			Eteone longa/flava agg.	0.0039	50.00	Diptera sp.	0.0042	33.33
			Scoloplos armiger	0.0038	25.00	Tubificoides agg. (pseudogaster)	0.0030	66.67
			Hydrobia ulvae	0.0030	75.00	Scrobicularia plana	0.0024	33.33
			Tharyx sp.	0.0012	25.00	Nematoda	0.0010	100.00
			Retusa obtusa	0.0009	25.00	Dalyelliidae sp.	0.00003	33.33
			Cyathura carinata	0.0004	25.00	Streblospio shrubsolii	0.00003	33.33
			Nematoda	0.0002	75.00	Manayunkia aestuarina	0.00003	33.33
			Enchytraeidae	0.0001	50.00	Cyathura carinata	0.00003	33.33
			Nemertea	0.00003	25.00			
			Streblospio shrubsolii	0.00003	25.00			
			Sphaerodoropsis baltica	0.00003	25.00			
			Caulleriella killariensis	0.00003	25.00			
			Alderia modesta	0.00003	25.00			
			Mytilidae juv.	0.00003	25.00			

Impact Lower			Impact Mid			Impact Upper		
Taxon	Average A	% of Sites	Taxon	Average A	% of Sites	Taxon	Average A	% of Sites
Macoma balthica	5.00	100.00	Tubificoides benedii	612.67	100.00	Tubificoides benedii	404.67	100.00
Nephtys hombergii	1.33	66.67	Nematoda	112.00	100.00	Nematoda	68.67	100.00
Nematoda	1.33	33.33	Hediste diversicolor	57.33	100.00	Hydrobia ulvae	40.67	100.00
Tubificoides benedii	1.00	100.00	Pygospio elegans	55.67	100.00	Hediste diversicolor	29.67	100.00
Pygospio elegans	1.00	66.67	Macoma balthica	54.67	100.00	Pygospio elegans	17.67	100.00
Hydrobia ulvae	0.67	66.67	Hydrobia ulvae	54.33	100.00	Macoma balthica	13.67	100.00
Hediste diversicolor	0.33	33.33	Enchytraeidae	24.33	100.00	Enchytraeidae	11.67	100.00
Manayunkia aestuarina	0.33	33.33	Streblospio shrubsolii	1.00	66.67	Manayunkia aestuarina	2.00	100.00
Enchytraeidae	0.33	33.33	Eteone longa/flava agg.	0.67	66.67	Diptera sp.	0.67	66.67
Nereididae sp.	P	33.33	Cyathura carinata	0.67	66.67	Eteone longa/flava agg.	0.33	33.33
			Diptera sp.	0.33	33.33	Streblospio shrubsolii	0.33	33.33
			Acarina sp.	0.33	33.33	Alderia modesta	0.33	33.33
						Abra sp.	0.33	33.33

Taxon	Average B	% of Sites	Taxon	Average B	% of Sites	Taxon	Average B	% of Sites
Macoma balthica	0.3128	100.00	Macoma balthica	4.9023	100.00	Macoma balthica	1.3490	100.00
Nephtys hombergii	0.0130	66.67	Hediste diversicolor	0.8641	100.00	Hediste diversicolor	0.9427	100.00
Hydrobia ulvae	0.0036	66.67	Tubificoides benedii	0.6272	100.00	Tubificoides benedii	0.4766	100.00
Nereididae sp.	0.0007	33.33	Hydrobia ulvae	0.1024	100.00	Hydrobia ulvae	0.0526	100.00
Tubificoides benedii	0.0001	100.00	Pygospio elegans	0.0131	100.00	Diptera sp.	0.0077	66.67
Pygospio elegans	0.0001	66.67	Nematoda	0.0049	100.00	Abra sp.	0.0050	33.33
Nematoda	0.0001	33.33	Eteone longa/flava agg.	0.0034	66.67	Pygospio elegans	0.0049	100.00
Hediste diversicolor	0.0000	33.33	Diptera sp.	0.0029	33.33	Nematoda	0.0028	100.00
Manayunkia aestuarina	0.0000	33.33	Enchytraeidae	0.0014	100.00	Eteone longa/flava agg.	0.0011	33.33
Enchytraeidae	0.0000	33.33	Streblospio shrubsolii	0.0001	66.67	Enchytraeidae	0.0008	100.00
			Cyathura carinata	0.0001	66.67	Manayunkia aestuarina	0.0001	100.00
			Acarina sp.	0.00003	33.33	Streblospio shrubsolii	0.00003	33.33
						Alderia modesta	0.00003	33.33
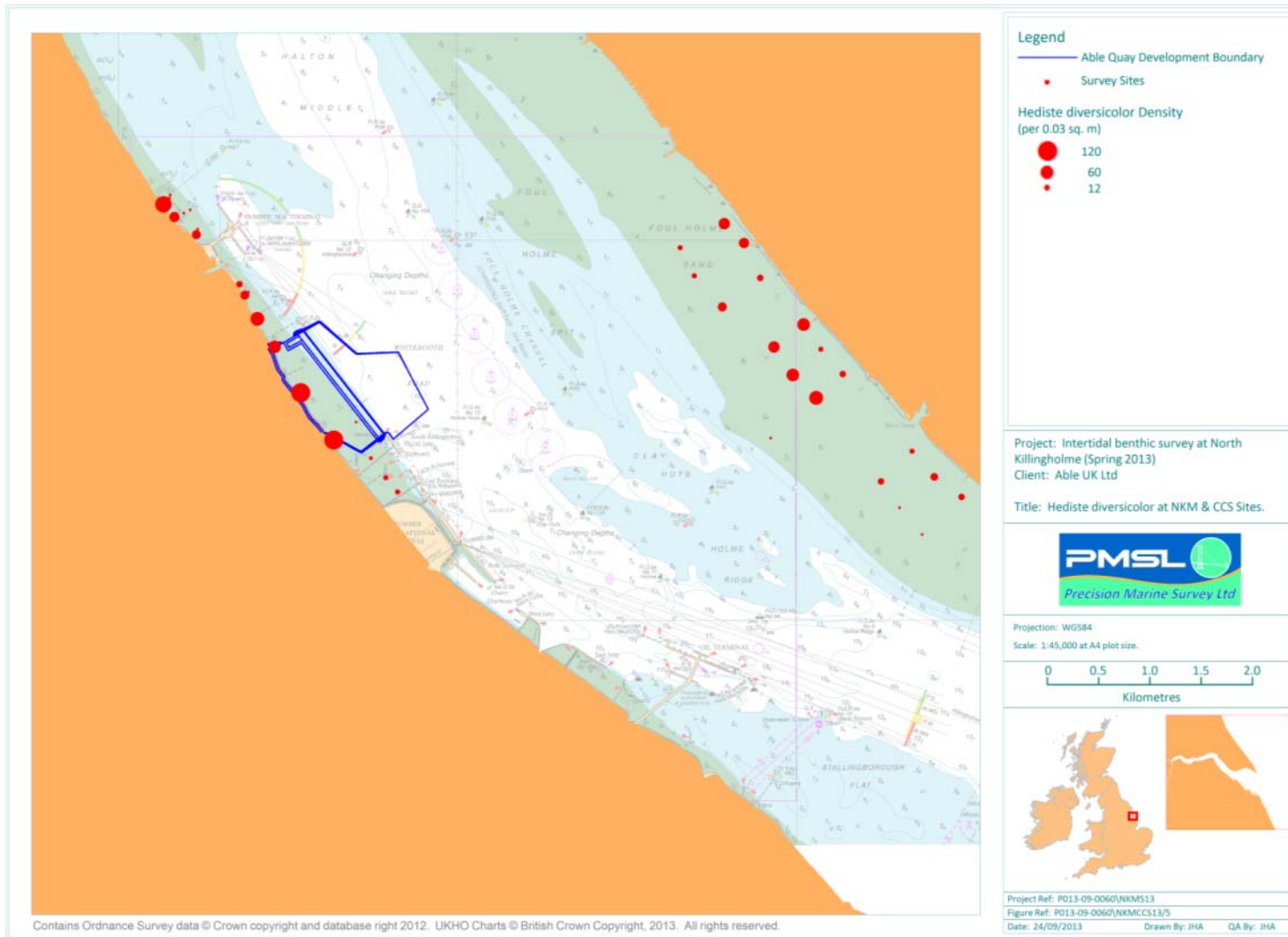
Figure 39.   Distribution of *Hediste diversicolor* from spring NKM and CCS surveys.
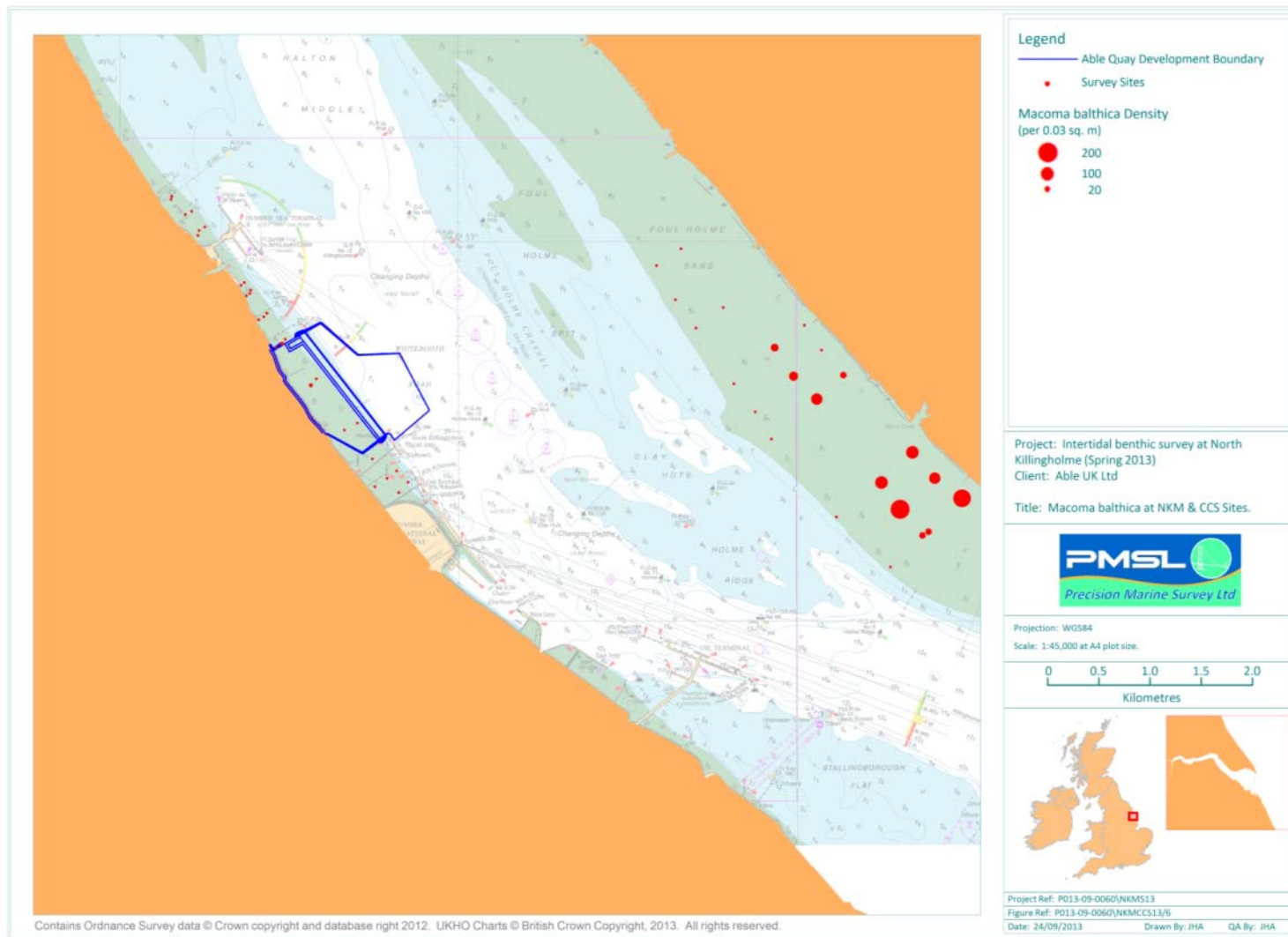
Figure 40.   Distribution of *Macoma balthica* from spring NKM and CCS surveys.

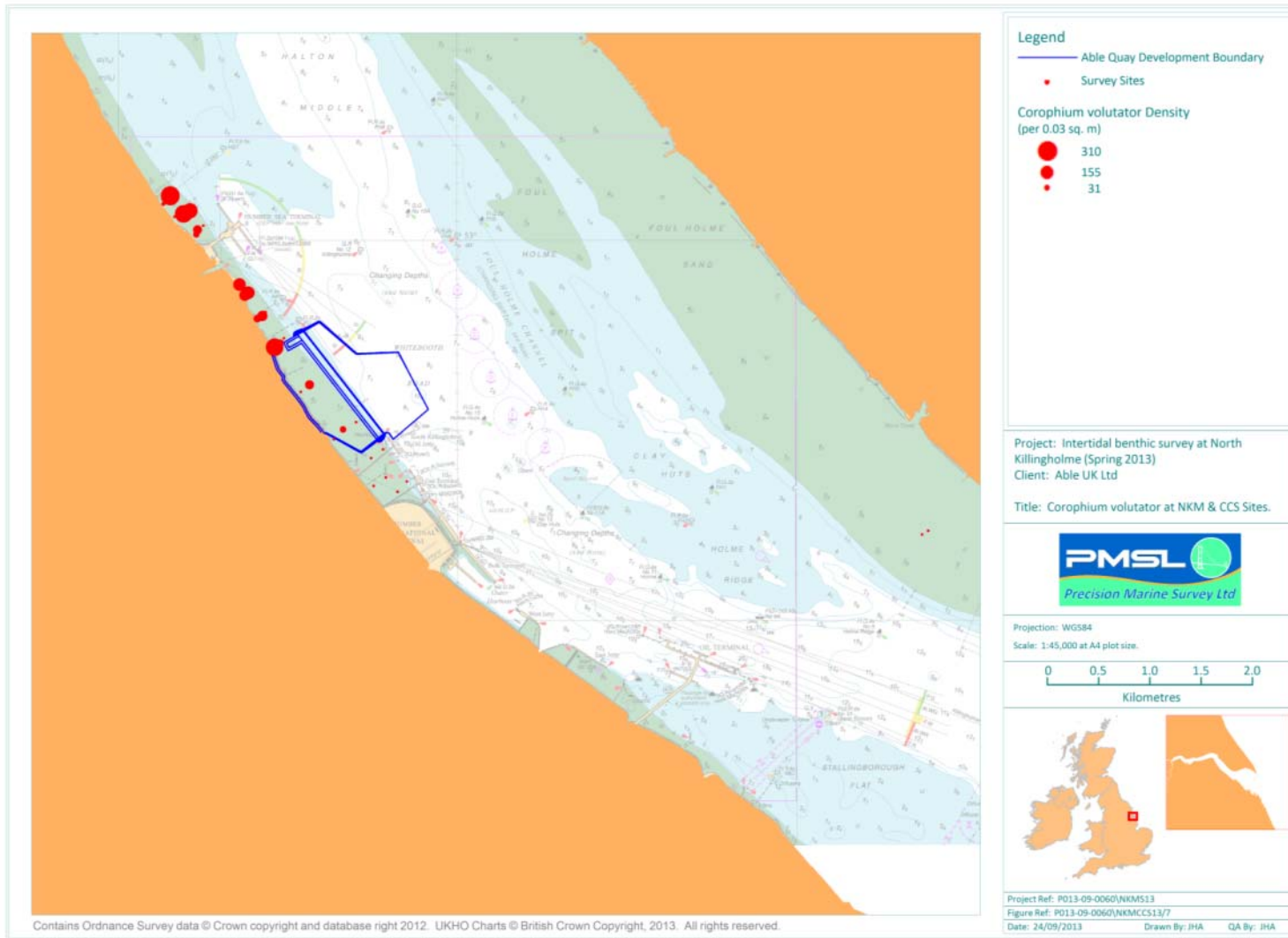**Figure 41.   Distribution of *Corophium volutator* from spring NKM and CCS surveys.**
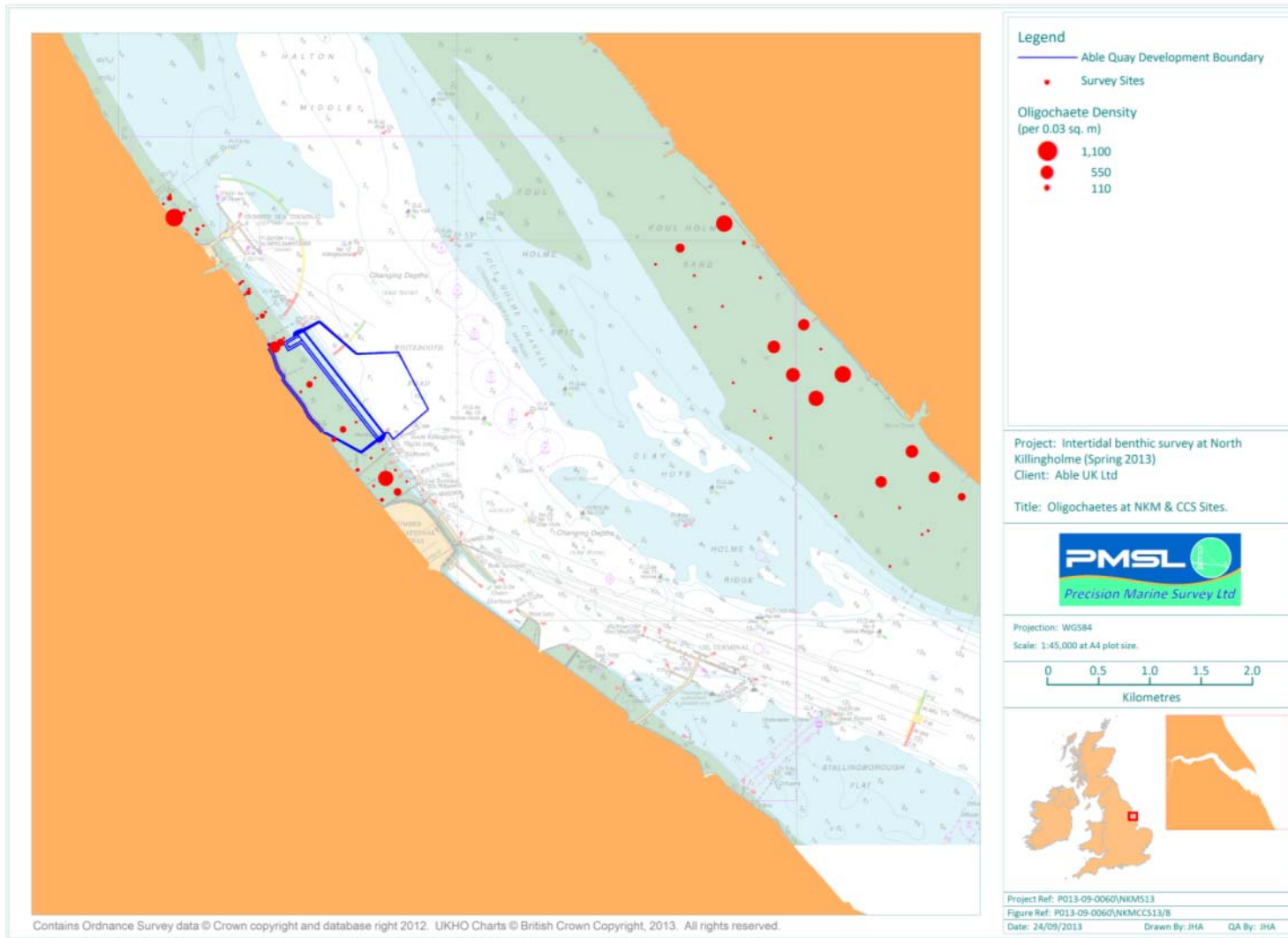
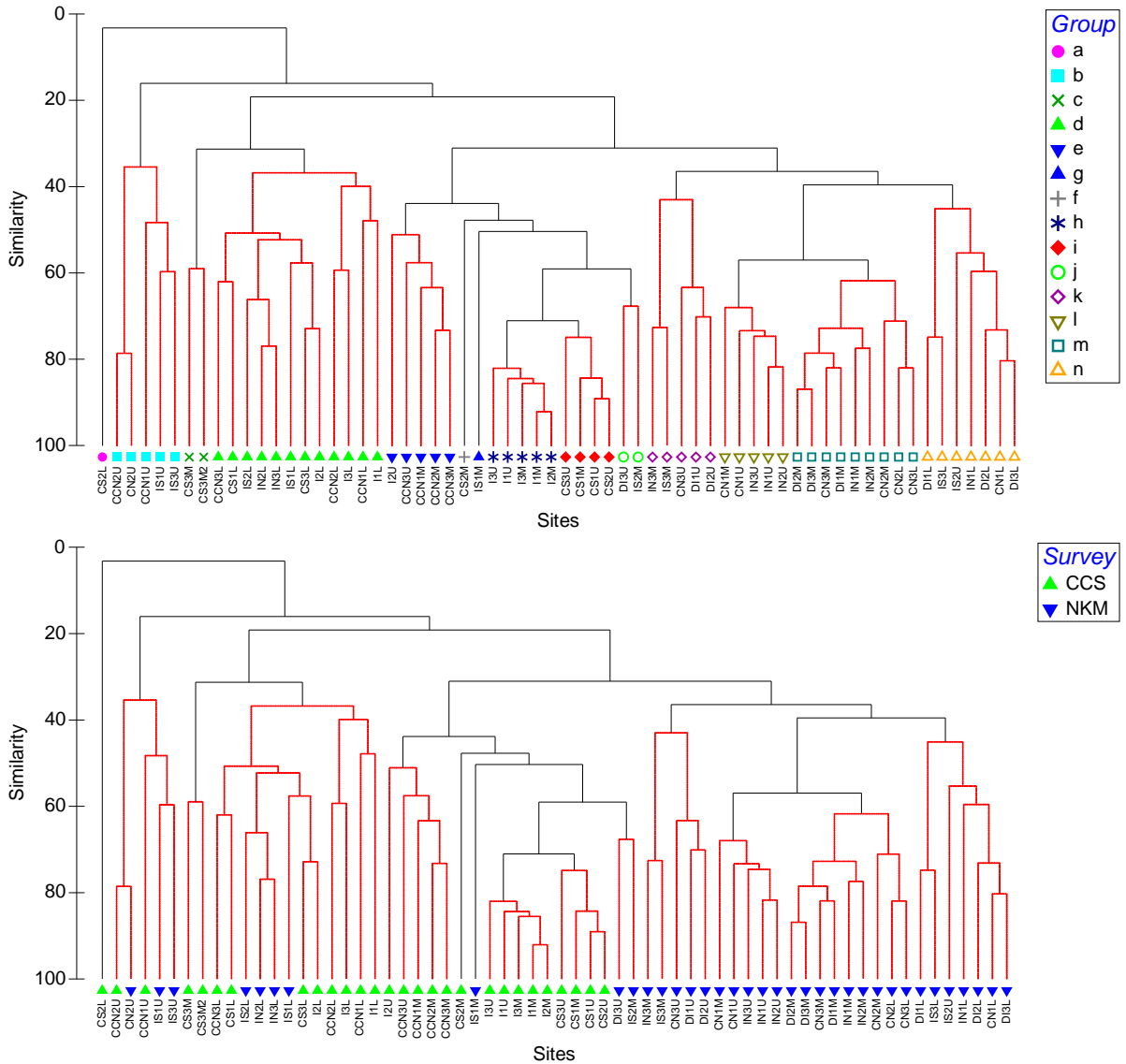**Figure 42.   Distribution of oligochaetes from spring NKM and CCS surveys.**

Figure 43. Results of cluster analysis on spring NKM and CCS data (samples highlighted by cluster group and area).
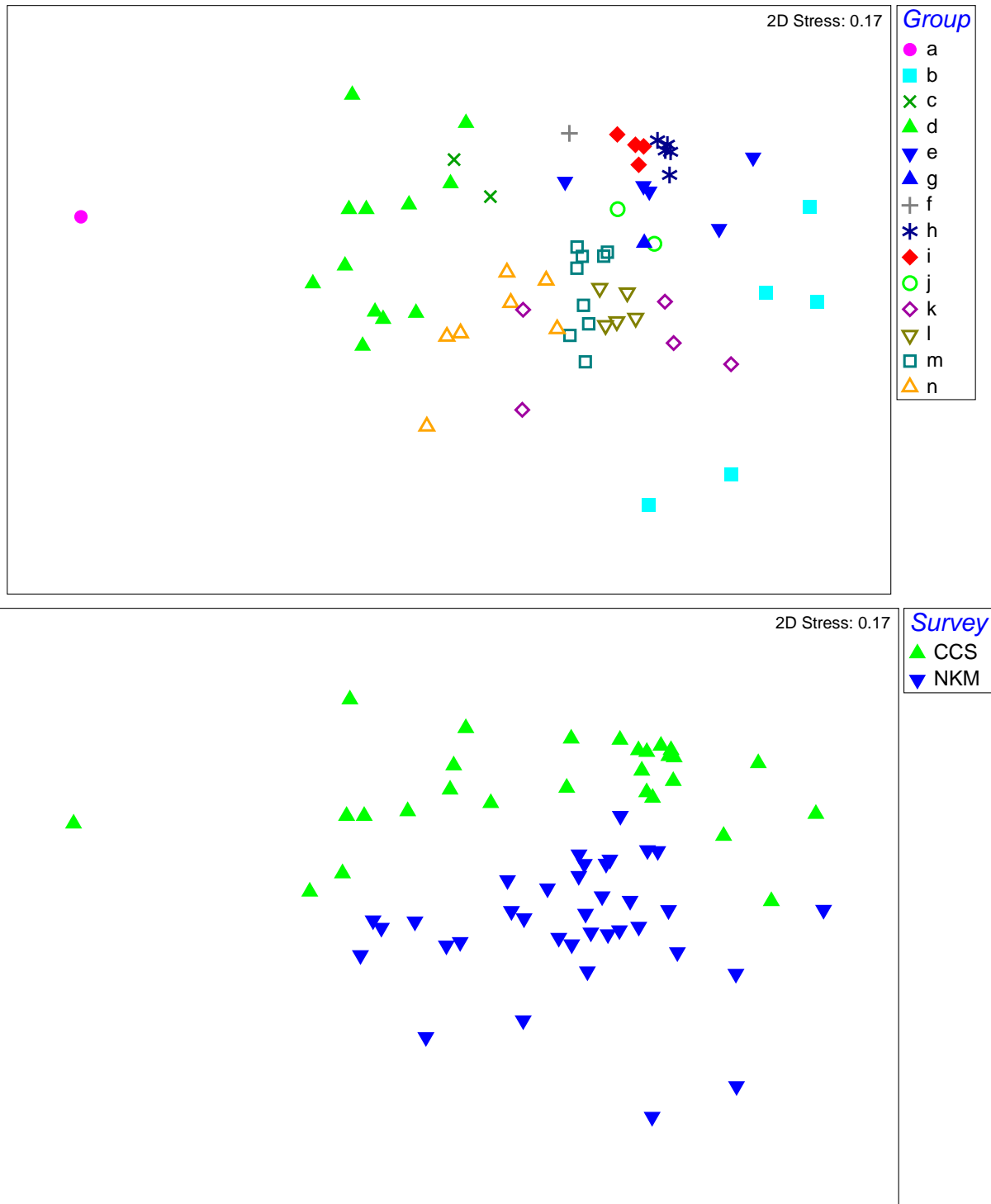
Figure 44.   Results of nMDS on spring NKM and CCS data (samples highlighted by cluster group and area).

Table 18. **Summary of characteristic taxa from site groups derived from cluster analysis on NKM and CCS data.**

SIMPROF Cluster	Area	Site	Species	Abundance	% of Sites	Contrib%	Cum.%
a	CCS	CS2L	Nephtys hombergii	2.00	-	-	-

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	CCS	CCN1U	Tubificoides agg. (pseudogaster)	337.40	100.00	52.47	52.47
	CCS	CCN2U	Collembola sp.	38.20	100.00	12.4	64.86
	NKM	CN2U	Diptera sp.	9.40	100.00	10.2	75.06
	NKM	IS1U	Nematoda	31.00	80.00	9.43	84.5
	NKM	IS3U	Hediste diversicolor	25.60	60.00	7.99	92.49
b			Enchytraeidae	82.40	60.00	5.36	97.84
Average similarity: 44.71			Tubificoides benedii	1.20	40.00	1.19	99.03
			Pygospio elegans	1.40	40.00	0.65	99.68
			Manayunkia aestuarina	2.40	40.00	0.32	100
			Corophium volutator	0.80	20.00	0	100
			Lekanesphaera hookeri	0.20	20.00	0	100
			Hydrobia ulvae	1.80	20.00	0	100
			Acarina sp.	0.20	20.00	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	CCS	CS3M	Macoma balthica	28.50	100.00	47.13	47.13
	CCS	CS3M2	Pygospio elegans	8.00	100.00	18.14	65.27
			Nephtys hombergii	3.50	100.00	12.83	78.1
			Corophium volutator	5.50	100.00	12.83	90.93
			Tubificoides benedii	2.00	100.00	9.07	100
c			Nematoda	1.50	50.00	0	100
Average similarity: 58.96			Eteone longa/flava agg.	0.50	50.00	0	100
			Hediste diversicolor	1.50	50.00	0	100
			Scoloplos armiger	0.50	50.00	0	100
			Bathyporeia sarsi	8.00	50.00	0	100
			Hydrobia ulvae	0.50	50.00	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	CCS	CCN1L	Macoma balthica	3.50	100.00	54.82	54.82
	CCS	CCN2L	Tubificoides benedii	1.75	83.33	34.51	89.33
	CCS	CCN3L	Nephtys hombergii	0.67	33.33	3.71	93.04
	CCS	CS1L	Streblospio shrubsolii	0.42	25.00	1.79	94.83
	CCS	CS3L	Hydrobia ulvae	0.42	25.00	1.56	96.39
d	CCS	I1L	Nematoda	0.67	25.00	1.51	97.9
Average similarity: 45.16	CCS	I2L	Mytilidae juv.	0.25	16.67	0.54	98.44
	CCS	I3L	Eteone longa/flava agg.	0.17	16.67	0.46	98.9
	NKM	IN2L	Pygospio elegans	0.25	16.67	0.4	99.31
	NKM	IN3L	Manayunkia aestuarina	0.17	16.67	0.35	99.65
	NKM	IS1L	Enchytraeidae	0.25	16.67	0.35	100
	NKM	IS2L	Hediste diversicolor	0.08	8.33	0	100
			Corophium volutator	0.08	8.33	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	CCS	CCN1M	Nematoda	110.00	100.00	39.85	39.85
	CCS	CCN2M	Hediste diversicolor	16.80	100.00	20.2	60.05
	CCS	CCN3M	Manayunkia aestuarina	17.00	100.00	11.59	71.65
	CCS	CCN3U	Tubificoides benedii	61.60	80.00	8.09	79.73
	CCS	I2U	Pygospio elegans	5.40	80.00	6.44	86.17
			Hydrobia ulvae	6.20	80.00	6.42	92.59
e			Enchytraeidae	11.40	80.00	5.24	97.83
Average similarity: 57.69			Macoma balthica	2.00	60.00	1.7	99.52
			Streblospio shrubsolii	2.00	40.00	0.48	100
			Alderia modesta	0.20	20.00	0	100
			Abra tenuis	0.20	20.00	0	100
			Collembola sp.	1.40	20.00	0	100
			Diptera sp.	0.20	20.00	0	100

Table 18 (cont.). Summary of characteristic taxa from site groups derived from cluster analysis on NKM and CCS data.

SIMPROF Cluster	Area	Site	Species	Abundance	% of Sites	Contrib%	Cum.%
	CCS	CS2M	Macoma balthica	199.00	-	-	-
			Pygospio elegans	37.00	-	-	-
			Tubificoides benedii	34.00	-	-	-
			Nematoda	18.00	-	-	-
			Nephtys hombergii	6.00	-	-	-
			Eteone longa/flava agg.	5.00	-	-	-
			Tharyx sp.	5.00	-	-	-
f			Hediste diversicolor	4.00	-	-	-
			Hydrobia ulvae	3.00	-	-	-
			Caulleriella killariensis	2.00	-	-	-
			Streblospio shrubsolii	1.00	-	-	-
			Enchytraeidae	1.00	-	-	-
			Sphaerodoropsis baltica	1.00	-	-	-
			Retusa obtusa	1.00	-	-	-
			Mytilidae juv.	1.00	-	-	-

SIMPROF Cluster	Area	Site	Species	Abundance	% of Sites	Contrib%	Cum.%
	NKM	IS1M	Tubificoides benedii	247.00	-	-	-
			Hediste diversicolor	14.00	-	-	-
			Manayunkia aestuarina	12.00	-	-	-
g			Corophium volutator	8.00	-	-	-
			Tubificoides agg. (pseudogaster)	2.00	-	-	-
			Nematoda	1.00	-	-	-
			Macoma balthica	1.00	-	-	-

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	CCS	I1M	Tubificoides benedii	609.60	100.00	38.68	38.68
	CCS	I1U	Nematoda	106.20	100.00	15.66	54.34
	CCS	I2M	Hediste diversicolor	49.60	100.00	10.54	64.88
	CCS	I3M	Hydrobia ulvae	55.40	100.00	10.12	75
	CCS	I3U	Pygospio elegans	43.40	100.00	9.1	84.1
			Macoma balthica	40.80	100.00	7.97	92.07
			Enchytraeidae	21.20	100.00	6.42	98.49
h			Eteone longa/flava agg.	0.60	60.00	0.5	99
Average similarity: 84.45			Streblospio shrubsolii	0.80	60.00	0.48	99.48
			Manayunkia aestuarina	1.00	40.00	0.19	99.66
			Diptera sp.	0.40	40.00	0.18	99.84
			Cyathura carinata	0.40	40.00	0.16	100
			Abra sp.	0.20	20.00	0	100
			Acarina sp.	0.20	20.00	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	CCS	CS1M	Tubificoides benedii	419.25	100.00	41.93	41.93
	CCS	CS1U	Macoma balthica	115.50	100.00	22.17	64.09
	CCS	CS2U	Pygospio elegans	42.75	100.00	12.39	76.48
	CCS	CS3U	Nematoda	28.25	100.00	9.66	86.14
			Hediste diversicolor	17.75	100.00	8.85	94.99
			Eteone longa/flava agg.	3.00	75.00	2.09	97.08
			Hydrobia ulvae	3.25	75.00	1.43	98.51
			Tubificoides agg. (pseudogaster)	2.25	50.00	0.74	99.26
i			Cyathura carinata	0.50	50.00	0.37	99.63
Average similarity: 80.38			Abra tenuis	1.00	50.00	0.37	100
			Dalyelliidae sp.	0.50	25.00	0	100
			Nemertea	0.25	25.00	0	100
			Streblospio shrubsolii	0.25	25.00	0	100
			Manayunkia aestuarina	0.25	25.00	0	100
			Enchytraeidae	1.00	25.00	0	100
			Alderia modesta	0.25	25.00	0	100
			Scrobicularia plana	0.25	25.00	0	100
			Diptera sp.	0.25	25.00	0	100

Table 18 (cont.). Summary of characteristic taxa from site groups derived from cluster analysis on NKM and CCS data.

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	NKM	DI3U	Tubificoides benedii	617.50	100.00	57.65	57.65
	NKM	IS2M	Streblospio shrubsolii	33.50	100.00	14.65	72.3
			Nematoda	28.50	100.00	9.81	82.11
			Hediste diversicolor	36.00	100.00	8.6	90.71
j			Macoma balthica	2.50	100.00	3.85	94.56
Average similarity: 67.65			Pygospio elegans	1.50	100.00	2.72	97.28
			Corophium volutator	146.00	100.00	2.72	100
			Manayunkia aestuarina	0.50	50.00	0	100
			Enchytraeidae	0.50	50.00	0	100
			Collembola sp.	0.50	50.00	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	NKM	CN3U	Hediste diversicolor	68.60	100.00	42.8	42.8
	NKM	DI1U	Corophium volutator	10.00	100.00	29.44	72.24
	NKM	DI2U	Tubificoides benedii	26.80	80.00	22.08	94.32
	NKM	IN3M	Tubificoides agg. (pseudogaster)	9.80	40.00	3.14	97.46
	NKM	IS3M	Nematoda	2.40	40.00	1.46	98.92
k			Streblospio shrubsolii	3.60	40.00	1.08	100
Average similarity: 52.72			Eteone longa/flava agg.	0.20	20.00	0	100
			Pygospio elegans	0.20	20.00	0	100
			Manayunkia aestuarina	0.40	20.00	0	100
			Macoma balthica	0.20	20.00	0	100
			Collembola sp.	0.20	20.00	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	NKM	CN1M	Corophium volutator	94.80	100.00	35.67	35.67
	NKM	CN1U	Hediste diversicolor	29.80	100.00	16.56	52.22
	NKM	IN1U	Enchytraeidae	12.80	100.00	12.98	65.21
	NKM	IN2U	Tubificoides benedii	14.60	100.00	10.47	75.67
	NKM	IN3U	Streblospio shrubsolii	12.80	100.00	9.88	85.55
			Nematoda	4.80	100.00	6.43	91.98
l			Macoma balthica	1.20	100.00	4.47	96.45
Average similarity: 72.28			Tubificoides agg. (pseudogaster)	7.40	60.00	2.63	99.08
			Pygospio elegans	0.60	40.00	0.46	99.54
			Manayunkia aestuarina	0.40	40.00	0.46	100
			Nemertea	0.20	20.00	0	100
			Coleoptera sp.	0.20	20.00	0	100

SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	NKM	CN2L	Corophium volutator	150.00	100.00	38.49	38.49
	NKM	CN2M	Tubificoides benedii	99.33	100.00	28.27	66.76
	NKM	CN3L	Streblospio shrubsolii	30.78	88.89	11.44	78.2
	NKM	CN3M	Nematoda	14.67	100.00	11.24	89.44
	NKM	DI1M	Macoma balthica	5.78	100.00	7.16	96.6
	NKM	DI2M	Pygospio elegans	2.11	55.56	1.28	97.88
m	NKM	DI3M	Hediste diversicolor	0.78	55.56	1.1	98.98
Average similarity: 68.83	NKM	IN1M	Tubificoides agg. (pseudogaster)	0.56	33.33	0.41	99.39
	NKM	IN2M	Enchytraeidae	0.67	33.33	0.32	99.71
			Tharyx sp.	0.89	22.22	0.16	99.87
			Diptera sp.	0.67	22.22	0.13	100
			Naididae	0.11	11.11	0	100
			Dipolydora coeca	0.11	11.11	0	100
			Coleoptera sp.	0.22	11.11	0	100

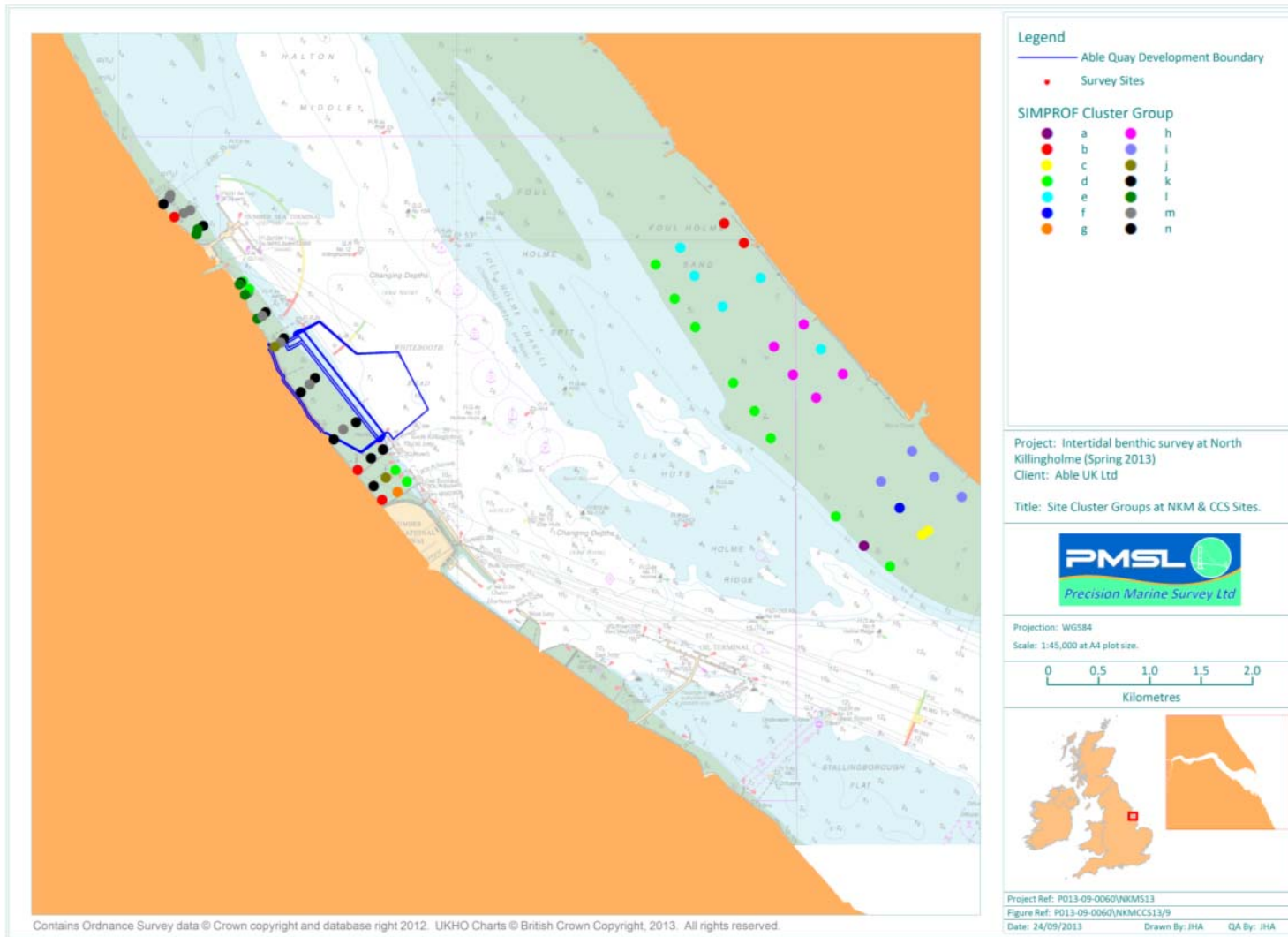| SIMPROF Cluster	Area	Site	Species	Av. Abundance	% of Sites	Contrib%	Cum.%
	NKM	CN1L	Streblospio shrubsolii	21.14	100.00	42.66	42.66
	NKM	DI1L	Tubificoides benedii	10.14	100.00	22.52	65.18
	NKM	DI2L	Corophium volutator	1.86	85.71	9.75	74.93
	NKM	DI3L	Macoma balthica	2.00	85.71	9.22	84.15
	NKM	IN1L	Nematoda	9.86	57.14	9.09	93.25
n	NKM	IS2U	Tubificoides swirencoides	4.86	42.86	4.33	97.57
Average similarity: 54.87	NKM	IS3L	Pygospio elegans	0.57	42.86	1.44	99.02
			Nephtys hombergii	0.43	28.57	0.54	99.55
			Diptera sp.	0.57	28.57	0.45	100
			Hediste diversicolor	0.14	14.29	0	100
			Tharyx sp.	0.29	14.29	0	100
			Tubificoides agg. (pseudogaster)	1.14	14.29	0	100
			Tellinacea juv.	0.14	14.29	0	100
			Collembola sp.	0.14	14.29	0	100

Figure 45.   Distribution of site groups derived from cluster analysis on NKM and CCS data.

6.   Conclusions

The results of the spring (May) intertidal benthic survey and preliminary results from the autumn survey indicate that the North Killingholme mudflats maintain a variety of infaunal invertebrates including good examples of mid estuary mud assemblages characterised by species such as *Corophium volutator*, *Tubificoides benedii*, *Streblospio shrubsolii*, *Hediste diversicolor*, Nematoda and *Macoma balthica* along with a number of other polychaete and oligochaete taxa which are typical residents of this section of the Humber. Numbers of species are relatively low as might be expected in a dynamic estuarine environment. Numbers of individuals and biomass tends to be quite variable across the survey area with values ranging from relatively low to moderately high but generally in the expected range for this area of the Humber and comparable to values recorded in other intertidal areas of the mid to outer Humber.

Some spatial variation is evident in terms of biological parameters and community structure but this is primarily in relation to shore position (and presumably subtle variations in sediment type/stability) with lower shore communities or those on the upper shore adjacent to saltmarsh (with greater elevation) exhibiting more impoverished communities. Sites on the remaining upper and mid shore or lower mid shore tend to be more diverse/productive although differences between the communities recorded tend to be rather subtle as opposed to significant shifts in community structure. Relatively few clear trends are evident (on the basis of the data processed so far) in terms any observable differences between the NKM mudflats inside and outside the proposed development area with sites from the control area to the north (for example) generally similar to those within the development area. There is however some indication of reduced diversity/productivity to the downstream side of the development area and also a slight increase in biomass or density of *Hediste diversicolor* and *Macoma balthica* on the upper and mid shore within the development area although such differences are relatively slight. Numbers of *Corophium volutator* also tend to reduce towards the southern end of the survey area.

The NKM intertidal area exhibits a degree of variability but is primarily characterised by typical estuarine mud biotopes although in many cases these are somewhat transitional forms and likely to be inherently variable as encountered during the 2010 Natural England biotope survey of the Humber. These include somewhat transitional middle estuary variants of LS.LMu.MEst.HedMac (*Hediste diversicolor* and *Macoma balthica* in littoral sandy mud) often with elements of LS.LMu.UEst.Hed.Cvol (*Hediste diversicolor* and *Corophium volutator* in littoral mud) reflecting the fact that the abundances of *Corophium volutator* were moderately high at the NKM area, particularly upstream of the development site in the spring survey. Densities of *Corophium* volutator appear to decline further downstream toward the outer Humber and this species was largely absent from the CCS area during the spring survey although populations of this species are known show high levels of temporal and spatial variability in the Humber with populations exhibiting periods of expansion and reduction in the middle estuary over time (Allen, 2009). However, *Corophium* aside the majority of taxa recorded were found in both survey areas albeit with varying levels of dominance/abundance. A range of other estuarine biotopes are present at NKM and CCS including transitional variants of LS.LMu.MEst.NhomMacStr (*Nephtys hombergii*, *Macoma balthica* and *Streblospio*

shrubsolii in littoral sandy mud), LS.LMu.UEst.NhomStr (*Nephtys hombergii* and *Streblospio shrubsolii* in littoral mud) or LS.LMu.UEst.Hed.Str (*Hediste diversicolor* and *Streblospio shrubsolii* in littoral sandy mud). Oligochaete dominated biotopes are also present in both areas such as LS.LMu.UEst.Hed.Ol (*Hediste diversicolor* and oligochaetes in littoral mud) and LS.LMu.UEst.Tben (*Tubificoides benedii* and other oligochaetes in littoral mud). The CCS area also appears to include sand or muddy sand biotopes on the lower shore and also some areas of LS.LSa.MuSa.MacAre (*Macoma balthica* and *Arenicola marina* in littoral muddy sand). Full maps of biotope type will be compiled in the final report but it is considered that in general terms the biotopes (and associated infaunal densities and biomass) recorded during the current surveys appear to be typical for muddy intertidal areas in the mid to outer Humber and generally correspond to those recorded in previous surveys (ABPmer & PMSL, 2010; Allen, 2007; Allen, 2008; Allen, 2009).

Appendix 1. ABC Curves.