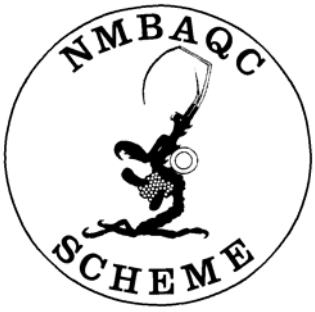

The National Marine Biological Analytical Quality Control Scheme

Benthic Invertebrate, Particle Size and Fish Components Report from the Contractor Scheme Operation – Year 13 2006/07

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INVERTEBRATE, PARTICLE SIZE AND FISH COMPONENTS
REPORT FROM THE CONTRACTOR

SCHEME OPERATION – YEAR 13 – 2006/07

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Summary of Performance

This report presents the findings of the Invertebrate, Particle Size, and Fish components for the thirteenth year of operation of the National Marine Biological Analytical Quality Control (NMBAQC) Scheme.

These components consisted of six modules (each with one or more exercises):

- Analysis of a single marine macrobenthic sample (Macrobenthic Sample module).
- Re-analysis by Unicomarine Ltd. of three own samples supplied by each of the participating laboratories (Own Sample module).
- Analysis of two sediment samples for physical description (Particle Size module).
- Identification of two sets of twenty-five invertebrate specimens (Invertebrate Ring Test module).
- Identification of one set of twenty-five fish specimens (Fish Ring Test module).
- Re-identification of a set of twenty-five specimens supplied by each of the participating laboratories (Laboratory Reference module).

The analytical procedures of the various modules were the same as for the twelfth year of the Scheme. The results for each of the Scheme exercises are presented and discussed. Comments are provided on the performance for each of the participating laboratories in each of the exercises.

Analysis of the **Macrobenthic sample (MB)** by the participating laboratories and subsequent re-analysis by Unicomarine Ltd. provided information on the efficiency of extraction of the fauna; accuracy of enumeration and identification and the reproducibility of biomass estimations. Agreement between the laboratories and Unicomarine Ltd. was variable with results generally lower than those achieved in previous MB exercises. The samples posed several problems associated with faunal extraction and identification of the taxa. Extraction efficiency, irrespective of sorting, was on average 88.8%; three laboratories extracted greater than 95% of the individuals from the residue; none of the laboratories extracted all fauna from the residue. Comparison of the results from the laboratories with those from analysis by Unicomarine Ltd. was made using the Bray-Curtis similarity index (untransformed). The value of the index varied between approximately 79.8% and 97% and was better than 95% in 33% of comparisons.

The Scheme year ten revised protocols for 'blind' **Own Sample (OS)** audits were continued in this Scheme year. Laboratories were to submit full completed data matrices from their previous year's UK National Marine Monitoring Programme (UK NMMP 2005) samples or alternative sampling programmes (if not responsible for UK NMMP samples). The OS 'pass/fail' flagging system, introduced in Scheme year eight, was continued (See Appendix 2: Description of the Scheme standards). The results for the Own Samples were generally better than those from the Macrobenthic sample. Agreement between the laboratories and Unicomarine Ltd. was generally very good. Extraction efficiency, irrespective of sorting, was better than 90% in 94% of comparisons and better than 95% in 88% of all comparisons. The Bray-Curtis similarity index ranged from 80% to 100% with an average figure of 96%. The Bray-Curtis similarity index was greater than 95% in 77% of comparisons and in most cases (91%) the value of the index was greater than 90%, these samples all achieved 'pass' flags. Eleven samples achieved 'excellent' pass flags with Bray-Curtis similarity scores of 100%.

The **Particle Size exercises (PS)** were conducted as in the previous Scheme year. 'Pass/fail' criteria were applied based upon z-scores from the major derived statistics with an acceptable range of ±2 standard deviations (See Appendix 2: Description of the Scheme standards). The influence of analytical technique on the results returned for the PS exercises was evident, as found in previous exercises. In most cases there was relatively good agreement between laboratories. The first particle size exercise of the Scheme year (PS28; mud sample) received ten data returns (including replicated data) that resulted in seven 'fail' and forty-three 'pass' flags. The second particle size exercise of the Scheme year (PS29; sand sample) received nine data returns (including replicated data) that resulted in four 'fail' and forty-one 'pass' flags.

Three **Ring Tests (RT)** of twenty-five animal specimens were distributed. One set contained twenty-five general invertebrate fauna (RT29), another set consisted of 'targeted' cirratulid specimens (RT30) and a third ring test was circulated that comprised fish taxa (RT31). For the

general set of fauna (RT29) there was fairly good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd. On average each participating laboratory recorded 4.1 generic errors and 6.0 specific errors. The majority of the generic errors can be attributed to four polychaete and four molluscan taxa. The 'targeted' ring test (RT30 – 'Cirratulidae taxa'), unexpectedly, posed very few problems for species identification. On average each participating laboratory recorded just 1.8 generic errors and 3.5 specific errors. Six specimens were responsible for 62% of all generic and 52% of specific errors recorded. The fish ring test (RT31) produced good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd. On average each participating laboratory recorded 3.4 generic errors and 4.9 specific errors. Six specimens were responsible for 62% of all generic and 69% of specific errors recorded.

Laboratory Reference (LR): The identification of a set of twenty-five species selected and supplied by the participating laboratories, from a list distributed by Unicomarine Ltd., was generally accurate. No clear problem areas were identified. However, there were differences in the approach to this exercise by the individual laboratories. For example, some laboratories used this as a test for confirming voucher specimens whilst others sought a means of having 'unknowns' identified.

Comments are provided on the individual performance of the participating laboratories in each of the above components. A summary of their performance with respect to standards determined for the UK NMMP is presented.

1. Introduction

The Scheme addresses three main areas relating to benthic biological data collection:

- The processing of macrobenthic samples.
- The identification of macrofauna.
- The determination of physical parameters of sediments.

The thirteenth year of the Scheme (2006/07) followed the format of the twelfth year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. Twenty-six laboratories participated in the Scheme. Sixteen laboratories were government laboratories; ten were private consultancies. Over half of the participants (14) were responsible for UK NMMP sample analysis (excluding subcontracted samples).

As in previous years, some laboratories elected to be involved in limited aspects of the Scheme. UK NMMP laboratories were required to participate in all components of the Scheme, although this was not strictly enforced.

In this report performance targets have been applied for the OS and PS components only (See Appendix 2: Description of the Scheme standards for each component). These targets have been applied to the results from laboratories (See Section 5: Application of NMBAQC Scheme standards) and "Pass" or "Fail" flags assigned accordingly. As these data have been deemed the basis for quality target assessment, where laboratories failed to fulfil these components through not returning the data, a "Fail" flag has been assigned. These flags are indicated in the Tables presenting the comparison of laboratory results with the standards (Tables 15 and 16).

2. Description of the Scheme Modules

There are six modules; Macrobenthic sample analysis (MB), Invertebrate and Fish Ring Test identification (RT) modules, Particle Size analysis (PS), Laboratory Reference voucher specimen identification (LR) and Own Sample (OS) reanalysis.

Each of the Scheme modules is described in more detail below. A brief outline of the information to be obtained from each module is given, together with a description of the preparation of the necessary materials and brief details of the processing instructions given to each of the participating laboratories.

2.1 General

2.1.1 Logistics

The labelling and distribution procedures employed previously have been maintained and specific details can be found in the Scheme's annual reports for 1994/95 and 1995/96 (Unicomarine, 1995 & 1996). Email has become the primary means of communication for all participating laboratories. This has considerably reduced the amount of paper required for the administration of the Scheme.

2.1.2 Data returns

Return of data to Unicomarine Ltd. followed the same process as in previous years. Spreadsheet based forms (tailored to the receiving laboratory) were distributed for each circulation via email, with additional hard copies where appropriate. All returned data have been converted to Excel 2003 format for storage and analysis. In this and previous Scheme years slow or missing returns for exercises lead to delays in processing the data and resulted in difficulties with reporting and rapid feedback of results to laboratories. Reminders were distributed shortly before each exercise deadline.

2.1.3 Confidentiality

To preserve the confidentiality of participating laboratories, each are identified by a four-digit Laboratory Code. Each Scheme year thirteen participant was given a confidential LabCode in September 2006, these codes were randomly assigned. These new codes are prefixed with the Scheme

year to reduce the possibility of obsolete codes being used inadvertently by laboratories, *e.g.* Laboratory number four in Scheme year thirteen will be recorded as LB1304.

In the present report all references to Laboratory Codes are the post-August 2006 codes (Scheme year thirteen), unless otherwise stated.

Participating laboratories were also provided with unique passwords for unlocking confidential PDF interim reports distributed throughout the year.

2.2 Macrobenthic Samples (MB)

A single unsorted grab sample from coastal waters was distributed to each participating laboratory. This part of the Scheme examined differences in sample processing efficiency and identification plus their combined influence on the results of multivariate analysis. In addition, an examination of the estimates of biomass made by each of the participating laboratories was undertaken.

2.2.1 Preparation of the Samples

Sample MB14 was collected from Sheerness, Isle of Sheppey; in an area of compacting mixed sediment. A set of samples was collected using a 0.1m² Day Grab. Sampling was carried out while at anchor and samples for distribution were collected within a five hour period. All grabs taken were equal in size. Sieving was carried out on-board using a mesh of 0.5mm, followed by fixing in buffered formaldehyde solution. Samples were mixed after a week in the fixative. Prior to distribution to the participating laboratories the samples were washed over a 0.5mm sieve and transferred to 70% IMS (Industrial Methylated Spirits).

2.2.2 Analysis required

Each participating laboratory was required to carry out sorting, identification, enumeration and biomass estimations of the macrobenthic fauna contained in the sample. Precise protocols were not provided, other than the use of a 0.5 mm sieve mesh; participating laboratories were instructed to employ their normal methods. The participating laboratories were required to complete a Macrobenthic Sample Details Form, which specified their processing methodology (for example, stating whether nematodes are extracted). The extracted fauna were to be separated, identified and stored in individually labelled vials. Labels were provided and cross-referenced to the recording sheets.

In addition, measurements of the biomass of the recorded taxa were requested. Detailed instructions were provided for this exercise; measurements were to be blotted wet weights to 0.0001g for each of the enumerated taxa.

Eight weeks were allowed for completion of the sample analysis. All sorted and unsorted sediments and extracted fauna were to be returned to Unicomarine Ltd., together with the data on counts and biomass determinations.

2.2.3 Post-return analysis

Upon return to Unicomarine Ltd. the various components of the MB samples were re-examined. All extracted fauna was re-identified and re-counted for comparison with the participating laboratory's own counts. The sample residues were re-sorted and any missed fauna removed, identified and counted. All fauna weighed by the participating laboratories were re-weighed to 0.0001g by the same member of Unicomarine Ltd. staff using the same technique.

2.3 Own Sample (OS)

This exercise examined laboratory analytical performance on material from each participating laboratory's 'home' area. Following a review of the Own Sample exercise (Unicomarine, 2001) several changes to sample selection and scoring were implemented in Scheme year eight. All participants must meet the new Own Sample requirements. Own Sample participants must supply their previous year's UK NMMP data matrices, where relevant, for Own Sample selection, *i.e.* 2005 NMMP data. This is to ensure that all processing is completed, preventing reworking of the selected Own Samples and enabling samples to be audited earlier in the Scheme year. Each participating laboratory was requested to send a data matrices from which three samples were selected. The selection was in turn notified to the laboratories. UK NMMP laboratories were advised to use UK NMMP samples if possible, otherwise

there was free choice providing a minimum of twelve samples were included in the submitted data matrix.

2.3.1 *Analysis required*

Participating laboratories were instructed to have conducted macrobenthic analysis of the samples using their normal procedures. Samples requiring sub-sampling were to be avoided where possible. All procedures were to be documented and details returned with the sample components. All material from the sample was to be sent to Unicomarine Ltd. broken down as follows:

- Sorted residue - material from which all animals had been removed and counted.
- Separated taxa - individually labelled vials containing the identified fauna.
- Other fractions - *e.g.* material containing fauna which had been counted *in situ*.

Identification was to be to the normal taxonomic level employed by the laboratory (usually species). The names and counts of specimens were to be recorded on a matrix and linked to the vials through a specimen code number. Biomass analysis was to be carried out in the same manner as for the MB exercise.

Ten weeks were allowed for the submission of data and preparation of the Own Samples selected for reanalysis. Upon receipt at Unicomarine Ltd. all OS samples were re-analysed by the same operator. The sorted residue was re-examined and any countable material extracted. Identified fauna was checked for the accuracy of enumeration and identification and all specimens were re-weighed using the same procedure as for the MB exercise.

2.4 Particle Size Analysis (PS)

This component examined the production of derived statistics from the particle size analysis of replicate sediment samples. Two samples of sediment, one coarse the other much finer, were distributed in 2006/07. Both of the samples were derived from natural marine sediments, both were prepared as described below. In each case a random subsample of the prepared replicates were divided for laser diffraction analysis using either a Malvern laser (Mastersizer X) or a Coulter laser (LS230) to ensure sample replicate consistency and illustrate any potential variations between these two laser instruments.

2.4.1 *Preparation of the Samples*

The sediments circulated were collected from two separate natural marine environments. A minimum of 30 litres of visually similar sediment was collected for each circulation. This material was returned to the laboratory and coarse sieved (1 mm) to remove gravel, shell and large faunal content. Following sieving, the sediment for each PS circulation was well mixed in a large tray and allowed to settle for a week. Each sediment was sub-sampled by coring in pairs. One core of a pair was stored as the 'A' component, the other as the 'B'. To ensure sufficient weight for analysis, and to further reduce variation between distributed PS samples, this process was repeated three times for each sample replicate, *i.e.* each distributed sample was a composite of three cores.

The numbering of the replicate samples was random. All of the odd-numbered 'B' components (a total of 14) were sent for particle size analysis to assess the degree of inter-sample variation. Half the replicates were analysed using Malvern laser and half by a Coulter laser. The 'A' components were assigned to participating laboratories randomly and distributed according to the Scheme timetable.

2.4.2 *Analysis required*

The participating laboratories were required to conduct particle size analysis on the samples using their normal technique (either in-house or using a subcontractor) and to return basic statistics on the sample including %< 63µm, mean, median, sorting and skewness. A written description of the sediment characteristics was to be recorded (pre-processing and post-processing using the Folk Triangle) along with an indication of any peroxide treatment. Also requested was a breakdown of the particle size distribution of the sediment, to be expressed as a weight of sediment in half-phi (ϕ) intervals. **Eight weeks** were allowed for the analysis of the first PS sample (PS28) and a shorter analysis period of **four weeks** was tested for the second PS sample (PS29).

2.5 Ring Test Specimens (RT) – (Invertebrates and Fish)

These modules of the Scheme examined inter-laboratory variation in the participants' ability to identify fauna and attempted to determine whether any errors were the result of inadequate keys, lack of reference material (*e.g.* growth series), or the incorrect use of satisfactory keys.

Three sets of twenty-five specimens were distributed in 2006/07. The first of the year's RT circulations (RT29) was a general invertebrate ring test. The specimens included representatives of the major phyla and approximately 36% of the taxa were annelids, 28% were crustaceans and 36% were molluscs. The second circulation (RT30) comprised 'targeted' cirratulid specimens. The third circulation (RT31) 'targeted' specimens of fish and was circulated to fewer laboratories that routinely identify fish. Details of substratum, salinity, depth and geographical location were provided for all ring test specimens to assist identification.

2.5.1 Preparation of the Samples

The specimens distributed were obtained from a range of surveys from around the UK. Specimens were also donated by Scheme participants and other organisations. Every attempt was made to provide animals in good condition and of similar size for each laboratory. Each specimen sent was uniquely identifiable by means of a coded label and all material has been retained for subsequent checking. Where relevant, every effort was made to ensure all specimens of a given species were of the same sex.

For the standard RT (RT29) and the 'targeted' RTs (RT30 & RT31), all specimens were taken from replicate trawls, grabs or cores within a single survey and in most cases they were replicates from a single sampling station.

2.5.2 Analysis required

The participating laboratories were required to identify each of the RT specimens to species and provide the Species Directory code (Howson & Picton, 1997) for the specimen (where available). If a laboratory would not routinely have identified the specimen to the level of species then this should be detailed in the 'confidence level' field. Laboratories can also add brief notes and information on the keys or other literature used to determine their identifications. Specimens from RT29 were to be returned to Unicomarine Ltd. for verification and resolution of any disputed identifications. This was the same procedure as for earlier circulations. Specimens from RT30 (cirratulids) and RT31 (fish) were retained by the participant laboratories for incorporation into their in-house reference collections or training material. **Eight weeks** were allowed for the analysis of the first RT exercise (RT29), a shorter analysis period of **four weeks** was tested for the second RT sample (RT30) and **ten weeks** were allowed for the third RT exercise (RT31 – fish taxa).

2.6 Laboratory Reference (LR)

This component encourages laboratories to build extensive, verified reference collections to improve identification consistency. The creation and use of reference collections are viewed as best practice. The participants were required to submit a reference collection of twenty-five specimens for re-examination by Unicomarine Ltd. Laboratories are also permitted to use this exercise to verify identifications of taxa including difficult or problematic taxa about which they are unsure.

2.6.1 Selection of fauna

The different geographical distributions of species meant that a request for a uniform set of species from all laboratories was unlikely to be successful. Accordingly a list of instructions was distributed to participating laboratories (Appendix 1). The specimens were to broadly represent the faunal groups circulated in the general Ring Tests, *i.e.* mixed phyla. However, each laboratory was permitted to include any number of unidentified or problematic taxa. Specimens wherever possible were to be representatives from UK NMMP reference collections.

2.6.2 Analysis

A prepared results sheet was distributed with the exercise's instructions and attached labels for the laboratories to identify each of the specimens. Participating laboratories were permitted **ten weeks** to prepare and submit their reference specimens. All specimens were re-identified and the identification made by Unicomarine Ltd. compared with that made by the participating laboratories. All specimens

were returned to the laboratories after analysis. Results for the exercise were recorded separately at the generic and specific level, in the same manner as for the Ring Test exercise.

3. Results

The exercises in 2006/07 were undertaken, in varying numbers, by twenty-six laboratories. Differences in the number of exercises in which laboratories participated meant that some exercises had more data returned than others. There were, as in previous years, large differences between laboratories in their ability to meet the target deadlines. Sub-contracting by participating laboratories of certain sample analyses also contributed to delays.

Some laboratories did not submit returns for a number of the exercises, or the returns were not in the format requested; this is indicated in the tables by a dash (-). In some instances, laboratories had elected not to participate in a particular module of the Scheme despite originally subscribing to the module.

To avoid unnecessary detail in the Tables described below the reasons for the dashes are explained in each case under the appropriate heading in Section 6: Comments on Individual Laboratories.

3.1 Macrobenthic Samples (MB)

3.1.1 General comments

The distributed macrobenthic sample (MB14) was from an estuarine location near Sheerness, Isle of Sheppey. The distributed samples comprised approximately two litres of compacting mixed sediment, predominantly sands, collected from a depth of approximately five metres. The samples contained on average thirty species and three-hundred and sixteen individuals, covering a variety of phyla (excluding nematodes and sessile taxa). The composite list from all samples was one-hundred and three species. Four of the six samples returned had been stained in some or all parts with Rose Bengal during sample processing. None of the laboratories subsampled their residues. Six of the nine laboratories participating in this exercise returned samples and data; two laboratories communicated their intention to abstain; one laboratory did not supply data or communicate their abstention. Detailed results have been reported to the participating laboratories (Hall, 2007b) and are available on the Scheme's website (www.nmbaqcs.org); additional comments are added below.

3.1.2 Efficiency of sample sorting

Table 1 presents a summary of the estimate of numbers of taxa and individuals made by each of the participating laboratories for sample MB14, together with the corresponding count made by Unicomarine Ltd upon reanalysis. Comparison of the number of taxa and number of individuals between the participating laboratory and Unicomarine Ltd. is given as a percentage in Table 1. Prior to analyses of these data some minor adjustments (combination of juvenile taxa, spelling errors, removal of spaces, etc.) were made to allow direct comparisons to be made and remove artificial differences in these data. Table 2 shows the composition of fauna missed by each participating laboratory.

3.1.2.1 Number of Taxa

Table 1 (column 5) shows variation between laboratories in the percentage of taxa identified in the samples. At most eight taxa (and 25% of the total taxa in the sample) were either not extracted or not recognised within the picked material. Unicomarine Ltd. recorded the same number of taxa as the participating laboratory in just one of the six returned samples.

The values presented for the number of taxa not extracted (column 10) represent taxa not recorded or extracted (even if misidentified) elsewhere in the results, *i.e.* these were taxa completely missed by the laboratory. Two laboratories (33%) extracted representatives of all the species present in their samples. On average laboratories missed approximately two taxa in their residues and in the worst instance six new taxa were missed during the picking stage of this exercise.

3.1.2.2 Number of Individuals

Re-sorting of the sample residues by Unicomarine Ltd. retrieved additional individuals from all samples; these data are presented in columns 11 and 12 of Table 1. The number of individuals not extracted from the sample (column 11) is given as a percentage of the total number in the sample (including those missed) in column 12 (*i.e.* column 12 = column 11 / column 7 %). The proportion of missed individuals in half of the samples was less than 5% of the true total number in the sample. In the worst instances fifty-seven individuals and 24.8% of the total number of individuals were not extracted during the initial sample processing. The average number of missed individuals found upon re-sorting the residue was approximately thirty-one. A breakdown of the missed individuals by taxonomic group is presented in Table 2.

3.1.2.3 Uniformity of identification

Most of the species in the distributed sample were identified correctly by the participating laboratories. All of the participating laboratories produced taxonomic differences, *i.e.* disagreement with the AQC identification (Table 1, column 15). In the worst instances twelve taxonomic differences were recorded. On average over five taxonomic differences were encountered per sample; these showed no particular correlations across the data set.

3.1.3 Comparison of Similarity Indices (Bray-Curtis)

The fauna list for each sample obtained by the participating laboratory was compared with the list obtained for the same sample following its re-examination by Unicomarine Ltd. The comparison was made by calculating the Bray-Curtis similarity index for the pair of samples using non-transformed data. The results of this calculation are presented in Table 1 (column 14). There was variation among laboratories in the values calculated for the index, from 79.8% to 97%, with an average value of 89.9%. The index for the majority of laboratories (4 of 6) was below 95% and three of the participating laboratories would have achieved 'fail' sample flags if the NMBAQC / UK NMMP standards were applied. Further details of each participating laboratory's performance are given in Section 6: Comments on Individual Laboratories.

3.1.4 Biomass determinations

A comparison of the estimates of the biomass made by the participating laboratories and Unicomarine Ltd. broken down by major taxonomic group for the MB14 circulation is presented in Table 3. Two laboratories did not supply biomass data. The average difference between the two weight values was -2.3% (*i.e.* lighter than that made by Unicomarine Ltd.), however the measurements by major faunal groups made by Unicomarine Ltd. were typically less (*i.e.* lighter) than that made by the participating laboratory. There was great variation in biomass estimations between participating laboratories and between taxonomic groups. The range of overall biomass percentage difference results, between participating laboratories and Unicomarine Ltd., was from –8.4% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +0.3% (measurements by laboratory were greater than those made by Unicomarine Ltd.). The average difference between estimations varied greatly between faunal groups, ranging from –296.6% to +65.5% (from Chelicerata to Nemertea, respectively). Several anomalous biomass records were supplied; these are likely to be the result of transcription errors.

3.1.5 Uniformity of samples

The faunal content of the samples distributed as MB14 is shown in Table 4. Data received from the participating laboratories were fairly similar showing natural variation often encountered in estuarine samples.

3.2 Own Sample (OS)

3.2.1 General comments

Following the request to participating laboratories to submit data of suitable samples for re-analysis, sixty-nine selected samples were received from twenty-three laboratories, together with descriptions of their origin and the collection and analysis procedures employed. An additional laboratory supplied samples without the associated residues; these samples have been excluded from this report. Samples were identified as OS32, OS33 and OS34 and labelled with LabCodes. The nature of the samples varied

considerably. Samples were received from estuarine and marine locations, both intertidal and subtidal. The sediment varied from mud to gravel and from 15 ml to 7 L of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 2 to 151, with the number of countable individuals from 1 to 6590. All of the twenty-four laboratories participating in this exercise returned three Own Samples; twelve of these Own Samples have been audited externally by Aquatic Environments due to Unicomarine Ltd. being responsible for the initial sample processing; one laboratory (LB1312) supplied three Own Samples without sorted residues, details of these samples are not included in this report and their summary statistics have been excluded.

3.2.2 *Efficiency of sample sorting*

Table 5 displays a summary of the data obtained from the analysis of the Own Sample exercise. All taxa identified and enumerated by the participating laboratory were included in the analysis, except in instances where the fauna had been damaged and rendered unidentifiable and uncountable. In forty samples (58% of all samples) the number of taxa recorded by the participating laboratories was identical to that obtained by Unicomarine Ltd. (column 4). In the twenty-nine exceptions, the difference was at most six taxa and the average difference was less than two taxa.

Data for the numbers of individuals recorded (columns 6 and 7) shows a range of differences from re-analysis of between 0% and 31%. The average difference was 2.7% (seventeen samples exceeded this average). Thirty of the sixty-nine samples reported showed 100% extraction of fauna from the residue (column 12), and in nineteen samples various numbers of individuals (but no new taxa) were missed during sorting (column 11). The remaining twenty samples contained taxa in the residue which were not previously extracted, the worst example being five new taxa found in the residue (column 10). In the worst instance residue was found to contain one hundred and twenty-nine individuals. A breakdown of the missed individuals by taxonomic group is presented in Table 6. The average number of missed individuals found upon re-sorting the residue was six, and the average number of missed taxa was less than one (0.46).

3.2.3 *Uniformity of identification*

Taxonomic differences between Unicomarine Ltd. and participating laboratories' results were found in thirty-six (52%) of the sixty-nine samples re-analysed. An average of 1.6 taxonomic differences per laboratory were recorded; in the worst instance fifteen differences in identification occurred. A great variety of samples (and hence fauna) was received and no particular faunal group was found to cause problems.

3.2.4 *Comparison of Similarity Indices (Bray-Curtis)*

The procedure for the calculation of the similarity index was as used for the MB exercise. The Bray-Curtis similarity index figures (Table 5, column 14) ranged from 80% to 100%, with an average figure of 96%. Six samples from six different laboratories achieved a similarity figure of less than 90% (excluding samples supplied without residue). Eleven samples produced a similarity figure of 100%; these were submitted by nine different laboratories (LB1301, LB1302, LB1307, LB1311, LB1314, LB1317, LB1320, LB1323 and LB1325). The best overall results were achieved by laboratory LB1314 (results comprised 99.73%, 99.59% and 100%), which averaged 99.77% similarity. The worst overall results were achieved by laboratory LB1305, whose results comprised 90.13%, 85.99% and 90.11%. It should be noted that a small number of differences between samples can result in a large difference in the Bray-Curtis index. This difference does not necessarily reflect the laboratory's interpretative ability.

3.2.5 *Biomass determinations*

It was not possible to make an accurate comparison of the biomass determination in all cases; twenty-one samples were not supplied with species blotted wet weight biomass data; four samples were reported to five decimal places and six to three decimal places (4 decimal places is required). Consequently, only forty-eight of the sixty-nine samples received have been used for comparative analysis. Table 7 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. The total biomass values obtained by the participating laboratories varied greatly with those obtained by Unicomarine Ltd. The average was a +6.5% difference between the two sets of results (*i.e.* heavier than Unicomarine Ltd.); the range was from –72.6% to +44.4%. The reason for these large differences is presumably a combination of variations in apparatus (*e.g.* calibration) and operator technique (*e.g.* period of, and effort applied to, drying). Further analysis of

biomass results by major taxonomic groups indicated an average difference of +3.5% for polychaetes, +14.1% for oligochaetes, -18.2% for nemerteans, -47.9% for Chelicerata, -8.5% for crustaceans, +4.4% for echinoderms, -7.0% for molluscs and +11.0% for all remaining faunal groups. These figures are different to those produced by this same exercise in each of the previous years. This emphasises the variability caused by not only duration and method of drying but also the consistency of results within each major taxonomic group. The Unicomarine Ltd. biomass data was achieved using a non-pressure drying procedure as specified in the Green Book.

3.3 Particle Size Analysis (PS)

3.3.1 General comments

Most participating laboratories now provide data in the requested format, though some variations remain. As previously reported, it should be remembered that the results presented are for a more limited number of analytical laboratories than is immediately apparent since this component of the Scheme is often sub-contracted by participants to one of a limited number of specialist laboratories. For PS28, ten out of eleven participating laboratories returned data (including laboratories with grouped results); one laboratory did not provide data or provide notification of abstention. For PS29, nine out of the eleven participating laboratories returned data; two laboratories did not provide data, one of which provided notification of abstention. Detailed results for each exercise have been reported to the participating laboratories (Hall, 2006 & 2007a) and are available on the Scheme's website (www.nmbaqcs.org); additional comments are added below.

3.3.2 Analysis of sample replicates

Replicate samples of the sediment used for the two PS distributions were analysed using two different laser diffraction instruments. *Replicates* have previously been examined by both laser and sieve/ pipette methods, however as the majority of laboratories are conducting analyses by laser diffraction the testing of different lasers is of more use. Half of the *replicates* were analysed using the Malvern Mastersizer X laser and half by the Coulter LS230 laser. *Replicate* analyses were performed by Plymouth University, Geography Department (Malvern) and Partrac (Coulter).

Some differences were noted between the two laser instruments, however the seven PS28 *replicate* samples analysed by each instrument showed very good agreement. There was very good agreement between the *replicate* samples analysed using the Malvern Mastersizer X laser; the Coulter LS230 laser results showed some variability. Both instruments produced data to classify the PS28 *replicate* samples as silt samples. The shape of the cumulative distribution curves were generally similar for the two laser instruments, however the Coulter LS230 laser did not record any material coarser than 4 phi and produced zero or significantly lower values than the Malvern for the coarse and very coarse silt fractions. This sample had a high percentage of sediment in the fine fraction (average of 97.42% <63µm). The figures for %<63µm varied significantly between the two instruments with the Malvern instrument producing an average figure of 94.83% and the Coulter 100%. Consequently, the derived statistics were slightly different between the two instruments. Results for the individual *replicates* are provided in Table 8 and are displayed in Figure 1.

Sample PS29 was of a sandy sediment (average of 0.95% <63µm) and the cumulative distribution curves were very similar between the two instruments (Malvern Mastersizer X and Coulter LS230). The Coulter results showed slight variation between the PS29 *replicate* samples; the Malvern showed practically no variation between *replicate* samples. The Malvern instrument produced an average silt/clay content figure of 1.14%; this figure was just 0.77% for the Coulter data. Results for the individual *replicates* are provided in Table 9 and are displayed in Figure 2.

3.3.3 Results from participating laboratories

Summary statistics for the two PS circulations are presented in Tables 10 and 11. After resolution of the differences in data format, the size distribution curves for each of the sediment samples were plotted and are presented in Figures 3 and 4. Included on each of these Figures for comparison are the mean distribution curves for the *replicate* samples as obtained by Unicomarine Ltd. (using Malvern and Coulter instruments), Figures 5 and 6 show the z-scores for each of the derived statistics. The z-scores were calculated with outliers and replicated data (see below) removed from the mean estimations of each of the major derived statistics.

One laboratory, which normally sub-contract their particle size analysis to another laboratory (also participating), elected to utilise the results from this laboratory for PS28 and PS29; this laboratory's data are regarded as replicated data and are not included in the calculation of z-scores. This laboratory is indicated in Tables 10 and 11 by an asterisk against their LabCode. Accordingly the results from the sub-contracting laboratory have been used in the Figures and Tables as appropriate. In Figures 3, 4, 5 and 6 only data from the sub-contracting laboratory are displayed, although it also applies to the contracting laboratory. In Tables 10 and 11, which present the summary statistics for PS28 and PS29 respectively, although the results are displayed for all participating laboratories the replicated data supplied by the centralised laboratory (sub-contractor) have been included only once in the calculation of mean values for each exercise. Performance flags (as discussed in Section 5: Application of NMBAQC Scheme standards) have been assigned to laboratories using replicated data in the same manner as for other laboratories.

3.3.3.1 Twenty-eighth distribution – PS28

There was generally good agreement for PS28 between the results from the analysis of *replicates* and those from the majority of participating laboratories. The results for two laboratories (LB1307 and LB1320) were notably atypical due to higher records of coarse material (18% and 61% material <4 phi, respectively). All except one of the participants used the laser diffraction technique to analyse the sample; LB1320 was the only laboratory to provide sieve method derived data. Table 10 shows the variation in data received from the participating laboratories. The derived statistic for %silt/clay ranged from 38.6% to 96.1%, with all laboratories producing figures lower than the combined *replicate* analyses produced by Unicomarine Ltd.

3.3.3.2 Twenty-ninth distribution – PS29

There was generally good agreement for PS29 between the results from the analysis of *replicates* and those from the majority of participating laboratories. The results from LB1307 were notable atypical due to relatively high records of silt/clay material (4.7%). LB1307 was the only participant that pre-treated the replicate sample with hydrogen peroxide. All except two of the participants used the laser diffraction technique to analyse the sample; LB1302 and LB1320 provided sieve method derived data. Table 11 shows the variation in data received from the participating laboratories. The derived statistic for %silt/clay ranged from 0% to 4.7%, with the majority of laboratories producing figures slightly lower than the *replicate* analyses produced by Unicomarine Ltd.

3.4 Ring Test Circulations (RT) -– (Invertebrates and Fish)

3.4.1 General comments

The implementation of this part of the Scheme was the same as previous years and included an additional exercise to specifically address the identification of fish from transitional waters. All three RT circulations were accompanied by details of each specimen's habitat details (depth, salinity, substratum, and geographical location). A number of laboratories use these modules of the Scheme for training purposes and have selected them preferentially over other modules. UK NMMP laboratories are required to participate in this component though it is not used when assigning 'pass' or 'fail' flags. Three circulations of twenty-five specimens were made. For RT29 twenty-five specimens from a variety of invertebrate Phyla were circulated. For RT30 the species were 'targeted' upon the family Cirratulidae (Polychaeta). RT31 'targeted' fish species for circulation to slightly fewer laboratories that routinely identify fish; however the introduction of multiple data entries for each participating laboratory was tested for this exercise. Other aspects of the three circulations, in particular the method of scoring results, were the same as for previous circulations. Participating laboratories were permitted to retain the RT30 cirratulid and RT31 fish specimens as part of their in-house reference collections. In total eighteen laboratories were distributed with RT29 specimens; eighteen laboratories received RT30 specimens; fifteen laboratories received RT31 fish specimens. For RT29, fourteen laboratories returned data; two laboratories specified non-participation for this exercise; two did not supply data or indicate non-participation. For RT30, twelve laboratories returned data; four laboratories specified non-participation for this exercise; two did not supply data or indicate non-participation. For RT31, fourteen laboratories returned data; one did not supply data or indicate non-participation. Multiple data

submissions were introduced for RT31 to combat the difficulty in preparing fish ring tests and the high number of interested fish monitoring teams; thirty-two RT31 data sets were received from the fourteen participating laboratories.

3.4.2 Returns from participating laboratories

Each laboratory returned a list of their identifications of the taxa. The identifications made by the participating laboratories were then compared with the AQC identifications to determine the number of differences. A simple character-for-character comparison of the text of the two names (the AQC identification and the laboratory identification) was the starting point for this determination and provided a pointer to all those instances where (for whatever reason) the names differed. Each of these instances was examined to determine the reason for the difference.

As previously found, the main cause of an identification being different from the AQC identification was through differences in spelling of what was clearly intended to be the same species or the use of a valid synonym. There were several examples of these differences:

- Use of a different synonym for a taxon, *e.g. Tharyx vivipara* for *Chaetozone vivipara*.
- Simple mis-spelling of a name, *e.g. Polyphysa crassa* for *Polyphysia crassa*.

NB. For the purposes of calculating the total number of differences in identification made by each laboratory a difference was ignored if it was clearly a result of one of the above.

Tables 12, 13 and 14, respectively, present the identifications made by each of the participating laboratories for each of the twenty-five specimens in RT circulations RT29, RT30 and RT31. For clarity the name is given only in those instances where the generic or specific name given by the laboratory differed from the AQC identification. Where it was considered that the name referred to the same species as the AQC identification but differed for one of the reasons indicated above, then the name is presented in brackets "[name]". Errors of spelling or the use of a different synonym are not bracketed in this way if the species to which the laboratory was referring was not the same as the AQC identification. A dash, "-", in the Tables indicates that the name of the genus (and / or species) given by the laboratory was considered to be the same as the AQC identification. A pair of zeros, "0 0", in the Tables indicates that the subscribing laboratory did not return data.

3.4.2.1 Scoring of RT results

The method of scoring was to increase a laboratory's score by one for each difference between their identification and the AQC identification, *i.e.* for each instance where text other than a dash or a bracketed name appears in the appropriate column in Tables 12, 13 and 14. Two separate scores were maintained; for differences at the level of genus and species. These are not independent values, if the generic level identification was incorrect then the specific identification would normally also be incorrect, though the reverse is not necessarily the case.

3.4.3 Ring Test distribution results

The RT component of the Scheme mirrored that of 2005/06 as there was only a single 'standard' exercise (RT29). RT30 was targeted on cirratulids. RT31 was targeted on fish from transitional waters. The RT circulations are designed as a learning exercise to discover where particular difficulties lie within specific common taxa. Results were forwarded to the participating laboratories as soon as practicable. Each participant also received a ring test bulletin (RTB29, RTB30 and RTB31), outlining the reasons for each individual identification discrepancy. These bulletins contained images of the test material. Participating laboratories were instructed to retain their ring test specimens, for approximately three weeks after the arrival of their results, to facilitate an improved learning dimension via the essential 'second look'. The cirratulid specimens circulated as RT30 and fish specimens circulated as RT31 were donated for inclusion in each participant laboratories in-house reference collection or for future in-house training.

3.4.3.1 Twenty-ninth distribution – RT29

Table 12 presents the results for the RT29. One of the specimens was donated by Carol Milner (SEPA, Dingwall) and one was donated by Myles O'Reilly (SEPA, East Kilbride). Nine of the twenty-five

specimens circulated were polychaetes; seven were crustaceans; and nine were molluscs. The agreement at the generic level was relatively good; fifty-seven errors (from a potential three hundred and fifty) were recorded from the fourteen participating laboratories. Agreement at the specific level was also relatively good; eighty-four errors were recorded. Four of the specimens circulated were incorrectly identified by at least half of the participants. These taxa, responsible for the majority of differences, are described briefly below.

The bulk of the errors recorded could be attributed to eight specimens. *Facelina annulicornis* (large, fair specimen), *Polyphysia crassa* (juvenile, fair specimen), *Paraonis fulgens* (medium, good, complete specimen), *Lumbrineris gracilis* (medium, fair specimen), *Abyssoninoe hibernica* (medium, good specimen), *Fabulina fabula* (juvenile, fair specimen), *Gari tellinella* (juvenile, 2-3mm, good specimen) and *Limatula subauriculata* (medium, good specimen) accounted for a total of 70% of all generic and 67% of all the specific differences recorded. Two of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Corophium multisetosum* and *Chelura terebrans*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB29 – Hall & Worsfold, 2006) which was circulated to each laboratory that supplied results for this exercise and is available on the Scheme's website (www.nmbaqcs.org).

3.4.3.2 Thirtieth distribution – RT30

RT30 contained twenty-five cirratulids. Two specimens were donated by Shelagh Wilson (Environment Agency, West Malling). The results from the circulation are presented in Table 13 in the same manner as for all previous RT circulations. The agreement at the generic level was very good; twenty-one errors (from a potential three hundred) were recorded from the twelve participating laboratories. Agreement at the specific level was also good; forty-two errors were recorded. Six of the specimens circulated were incorrectly identified by several of the participants. These taxa, responsible for the majority of differences, are described briefly below.

Six of the ring test specimens caused problems at the species level for three to five laboratories; specifically *Chaetozone vivipara* (medium, complete specimen), *Aphelochaeta marioni* (large, anterior only specimen), *Cirratulus cirratus* (medium, complete specimen), *Tharyx killariensis* (medium, anterior only specimen) and *Tharyx* 'A' x 2 (medium, complete specimens). These taxa accounted for 62% of the generic and 52% of the specific differences recorded. Seven of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Caulleriella alata*, *Chaetozone gibber* x 2, *Cirriformia tentaculata* x 2, *Cirratulus caudatus*, and *Tharyx killariensis* (complete specimen)). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB30 - Hall & Worsfold, 2007a) which was circulated to each laboratory that supplied results for this exercise and is available on the Scheme's website (www.nmbaqcs.org).

3.4.3.3 Thirty-first distribution – RT31

RT31 contained twenty-five fish specimens. Two of the specimens were donated by Myles O'Reilly (SEPA, East Kilbride); one specimen was donated by Tim Mackie (NIEA, formerly EHS, Lisburn). The results from the circulation are presented in Table 14 in the same manner as for the other circulations. The agreement at the generic level was very good; just one hundred and eight errors (from a potential eight hundred) were recorded from the thirty-two data sets received via the fourteen participating laboratories. Agreement at the specific level was also very good; one hundred and fifty-seven errors were recorded. The majority of participating laboratories correctly identified each of the specimens. Only a few of the taxa were responsible for the majority of differences and these are described briefly below.

The bulk of the errors recorded could be attributed to six specimens. *Gaidropsarus mediterraneus* (3cm specimen), *Trisopterus minutus* (15-18cm specimen), *Raja montagui* (25-30cm specimen), *Ammodytes marinus* (9-11cm specimen), *Arnoglossus laterna* (11-13cm specimen) and *Ammodytes tobianus* (13-14cm specimen) accounted for a total of 62% of all generic and 69% of all the specific differences recorded. Four of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Zeus faber*, *Scyliorhinus canicula*, *Scomber acombrus* and *Merlangius merlangus*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB31 – Hall & Worsfold, 2007b) which was circulated to all RT31 participants and is available on the Scheme's website (www.nmbaqcs.org).

3.4.4 *Differences between participating laboratories*

Figures 7, 8 and 9 present the number of differences recorded at the level of genus and species for each of the participating laboratories, for RT circulations RT29, RT30 and RT31 respectively. The laboratories are ordered by increasing number of differences at the level of species. The division of laboratories into three bands (Low, Medium and High) on the basis of the number of differences at the level of species is also shown. These bands are discussed further in Section 6: Comments on Individual Laboratories.

3.4.5 *Differences by taxonomic group*

Most of the differences of identification in the general RT29 were of polychaetes. Polychaete specimens (nine specimens in total) were responsible for 58% of generic differences and 48% of the total number of specific differences. Nine of the total twenty-five specimens circulated were molluscs and these produced 37% of the generic and 46% of the specific differences recorded. Seven crustacean specimens completed the ring test circulation and were responsible for 5% of generic differences and 6% of the total number of specific differences.

3.5 Laboratory Reference (LR)

3.5.1 *General comments*

The value of reference material in assisting the process of identification cannot be over-emphasised. Accordingly the Laboratory Reference (LR) component of the Scheme was introduced in Scheme year three (1996/97). This component assesses the ability of participating laboratories to identify material from their own area, or with which they are familiar. The component can also be used to have unidentified or problematic specimens reviewed. Of the fifteen laboratories participating in this exercise, ten laboratories supplied specimens for verification; one laboratory decided not to participate; four laboratories did not submit specimens or provide notification of abstention from this exercise.

3.5.2 *Returns from participating laboratories*

The identification of the specimens received from the participating laboratories was checked and the number of differences at the level of genus and species calculated, in the same manner as for the RT exercises. Due to this component's emphasis upon training and the diversity of submissions, comparisons of results are not applicable and as such no summary statistics are provided in this report.

4. Discussion of Results

The results presented in the Tables and the discussions below should be read in conjunction with Section 6: Comments on Individual Laboratories.

4.1 Macrobenthic Analyses

The sample distributed as MB14 comprised a diverse and relatively well populated estuarine compacted sand and stone sample. The extraction of fauna from the sediment was difficult, due to the volume of sediment and quantities of infaunal and epifauna taxa and individuals present. There were also preservation problems, due to the compacting nature of the residue, which resulted in some taxa being poorly preserved. The dominant taxa present in the majority of samples were *Crepidula fornicata, Tubificoides pseudogaster* agg., *Elminius modestus, Balanus crenatus and* Nematoda; the latter three taxa were excluded from the analysis by some of the participating laboratories on the basis of their in-house processing policies. None of the participating laboratories extracted all the countable material from the residue; in the best instances LB1302 missed two individuals and LB1305 missed six individuals. In the worst instances fifty-seven individuals and 24.8% of the individuals were not extracted from the residue. Identification of the extracted fauna also caused several problems for participants. None of the laboratories correctly identified all their extracted fauna. There were a total of thirty-two taxonomic mistakes from all six participants, these included misidentifications of *Molgula manhattensis, Balanus crenatus, Anoplodactylus pygmaeus, Eumida bahusiensis, Noemiamea dolioliformis* and several cirratulid taxa. Only half of the six returning laboratories attained a Bray-Curtis similarity higher than 90%. The highest Bray-Curtis similarity index achieved was 97%

(LB1305). The average Bray-Curtis figure achieved was 89.9%. This figure is relatively consistent for an estuarine sample in the MB module; the average for MB13 (coastal) was 97%, MB12 (estuarine) was 77%, MB11 (an artificial coastal sample) was 93%, MB10 (estuarine) was 88%, MB09 (coastal) was 93%, MB08 (estuarine) was 95%, MB07 (coastal) was 88%, MB06 (estuarine) was 91%, MB05 (coastal) was 85% and MB04 (estuarine) was 82%.

Table 4 shows the variation, by major Phyla, between those samples circulated for the macrobenthic exercise (MB14). The area sampled was well uniformed in its faunal composition. The samples were typical of the area and showed only slight natural variation. All samples were of relatively equal volume and sediment characteristics.

The 'blot-drying' procedure employed by Unicomarine Ltd. for the determination of biomass was as specified in the Green Book, *i.e.* avoiding excessive pressure when blotting specimens dry. However, there remains a considerable variation between the estimates of total biomass made by the participating laboratories and Unicomarine Ltd. Four laboratories provided biomass data; three provided data that was lighter in total than Unicomarine Ltd.; one supplied data that was heavier than Unicomarine Ltd. estimations. The extremes recorded were 8.4% lighter (LB1303) and 0.3% heavier (LB1302) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories and Unicomarine Ltd. was -2.3% (*i.e.* laboratory measurements were lighter than those made by Unicomarine Ltd.). Previous Scheme years have not shown any particular pattern of variance for biomass estimations; the last two year's average biomass difference figures were 9.9% heavier (MB13) and 2.2% heavier (MB12). It seems likely that the main reasons for the observed differences between the measurements are more thorough, or less consistent, drying by participating laboratories prior to weighing. A similar observation was made in previous years of the Scheme. The average percentage difference between Unicomarine Ltd. and participating laboratories biomass figures for MB11 was -3.1%, MB10 was -13.3%, MB09 was –14.6%, MB08 it was +4.9%, MB07 it was –1.67%, MB06 it was +26%, MB05 it was +32% and for MB04 it was +20%. There are likely to be several reasons for the differences between years, though the nature of the fauna in the distributed samples is likely to be of particular importance.

Clearly, determination of biomass remains a problem area warranting further examination. Although all laboratories are following the same protocol it is apparent that different interpretations are being made of the degree of drying required. When single specimens of small species are being weighed (*e.g.* amphipods) very small differences in the effectiveness of drying will make large percentage differences in the overall weight recorded. It must be noted that the Green Book recommends that ash-free dry weights for biomass are derived from the blotted wet weights using published conversion factors. However the details of techniques used to determine initial wet weights for these conversion factors may vary from those specified in the green book. A series of trials should be commissioned to ascertain the best methods for accurate and consistent 'blotted' dry weight figures which can in turn be reliably applied to existing or new conversion factors.

4.2 Own Sample Analyses

Considering just the Bray-Curtis index, as a measure of similarity between the results obtained by the participating laboratories and those obtained from re-analysis, participating laboratories performed much better in the OS exercise compared to the MB14 exercise. The average value of the index was 96% for the OS, compared with 89.9% for MB14. Both modules have produced several good results and some instances of excellent sample processing.

There were sixty-nine samples submitted for this module, including twelve samples that have been processed by the Scheme's external auditor. One laboratory (LB1312) supplied three Own Samples without sorted residues (due to accidental disposal), fauna for these samples have been audited separately and the results and summary statistics are excluded from this report, however remedial action will still be required. Approximately 91% of the sixty-nine comparable samples reported exceeded the 90% Bray-Curtis pass mark and approximately 77% of the samples exceeded 95% Bray-Curtis similarity. The average Bray-Curtis similarity index achieved was 96%. These figures are consistent with the high quality results from previous OS exercises. In the 2005/06 Scheme year twelve (OS29, 30 and 31) the average Bray-Curtis figure was 96%, and 93% (of the fifty-four comparable samples received) achieved more than 90% Bray-Curtis results. In the 2004/05 Scheme year eleven (OS26, 27 and 28) the average Bray-Curtis figure was 96%, and 94% (of the fifty-four samples received) achieved more than 90% Bray-Curtis results. In the 2003/04 Scheme year ten (OS 23, 24 and 25) the average

Bray-Curtis figure was 94%, and 84% (of the fifty-one samples received) achieved more than 90% Bray-Curtis results. In the 2002/03 Scheme year nine (OS 20, 21 and 22) the average Bray-Curtis figure was 92%, and 75% (of the forty-four samples received) achieved more than 90% Bray-Curtis results. In the 2001/02 Scheme year eight (OS 17, 18 and 19) the average Bray-Curtis figure was 90.5% and 78% (of the forty-five samples received) achieved more than 90% Bray-Curtis results. In the 2000/01 Scheme year seven (OS 14, 15 and 16) the average Bray-Curtis figure was 90.8% and 67% (of the forty-five samples received) achieved more than 90% Bray-Curtis results. In the 1999/2000 Scheme year six (OS 11, 12 and 13) the average Bray-Curtis figure was 91.4% and 73% (of the fifty-one samples received) achieved more than 90% Bray-Curtis results. In the 1998/99 Scheme year five (OS 08, 09 and 10) the average Bray-Curtis figure was 89.3% and 71% (of the forty-two samples received) achieved more than 90%. In the 1997/98 Scheme year four (OS 05, 06 and 07) the average Bray-Curtis figure was 93.6% and 83% (of the forty samples received) achieved more than 90%.

Since the beginning of the OS component five hundred and forty-seven admissible samples have been received (OS01-34), with an average Bray-Curtis similarity figure of 93.31%. One hundred and one samples have fallen below the 90% pass mark (18%). Sixty-eight samples have achieved a similarity figure of 100% (12% of all returns). Extraction of fauna is an area in which several participating laboratories could review their efficiency. All countable fauna must be extracted to record a truly representative sample, although this is rarely the case due to time restraints or inefficient methods used. A sample that has been poorly picked stands a high possibility of being unrepresentative regardless of the quality of subsequent faunal identifications, and should the sorted residue be disposed, this cannot be rectified. Laboratories should study their detailed OS and MB reports and target the particular taxon or groups of taxa that are being commonly overlooked during the picking stages of sample analysis. It must be resolved whether the individuals are either not recognised as countable or not scanned using the extraction methods employed. If it is the former, then training is appropriate. If the latter is the case then a review of current extraction methods should be conducted. Some instances of repeated taxonomic errors in Own Samples from previous Scheme years have been noted. Taxonomic errors should be investigated by participating laboratories even if the 'whole sample' has achieved a 'pass' flag. If a participating laboratory disagrees with any recorded taxonomic errors they should contact Unicomarine Ltd for further information (as they are invited to do so upon receipt of their Own Sample Interim Report).

4.3 Particle Size Analyses

The difference between the two main techniques employed for particle size analysis (laser and sieve) was again evident when comparing the results from the few remaining sieve technique laboratories. Previous PS exercises have proven that laser and sieve/pipette techniques can produce vastly differing data, with the PS module now dominated by laser analysts, the sieve analyst's data is far more likely to 'failed' based upon the 'majority rule' z-score pass/fail criteria. LB1320 submitted the only sieve technique derived dataset for PS28 and failed four of the five derived statistic criteria, however on this occasion it appears that this failure is likely to be the result of a more fundamental error associated with the disaggregation of dried particles. LB1302 and LB1320 submitted the only sieve derived data for PS29, resulting in a single fail from the combined ten pass/fail measures.

The sample distributed as PS28 appeared from an analysis of *replicates* (Figure 1) to be very uniform and the results from participating laboratories (Figure 3) were relatively closely grouped, with the exception of two data sets. Figure 5 shows the z-scores for each of the major statistics supplied by the participating laboratories. Data received from two laboratories (LB1307 and LB1320) indicated much higher proportions of coarse particles than the other data returns for PS28, hence these two sets of results are clearly atypical in the cumulative curve figure (Figure 3).

The sample distributed as PS29 appeared from an analysis of *replicates* (Figure 2) to be very uniform, with the results from both laser instruments (Malvern and Coulter) closely grouped. Results from participating laboratories were also relatively well grouped, with the notable exception of LB1307 data (Figure 4). LB1307 was the only laboratory that pre-treated the replicate sample with hydrogen peroxide, which has resulted in an increase in fine particles. Figure 6 shows the z-scores for each of the major statistics supplied by the participating laboratories.

Additional experiments were conducted upon the sandy PS29 *replicate* samples to investigate the effect of hydrogen peroxide pre-treatment. It was confirmed that the pre-treatment resulted in an average

increase of silt/clay fraction from 1.14% to 4.30%. The reverse effect (decreased fine particles) is often evident when pre-treating muddy samples with hydrogen peroxide.

Participating laboratories were asked to provide a visual description of the PS28 and PS29 samples prior to analysis. The results varied considerably and some were extremely descriptive (Table 16, final column). Participating laboratories were also instructed to describe the sediment using the Folk triangle after analysis. Data were provided by nine laboratories for PS28 and eight laboratories for PS29. Six of the nine laboratories, that submitted data using the Folk triangle, described PS28 as 'Mud'; one recorded '(g) M' (slightly gravelly mud); one recorded 'medium silt'; and one described 'Muddy sand'. PS28 was pre-sieved at 1mm prior to the creation of replicates; therefore the record of gravel content (LB1305) can only be attributed to a maximum axial measurement of either broken shell fragments or hydrobiid snails. Seven of the eight laboratories, that submitted data using the Folk triangle, described PS29 as 'Sand'; and one laboratory recorded 'Medium sand'.

It is essential that analytical methods, including pre-treatment, are stated when reporting or attempting to compare results. The situation is complicated further by the fact that the difference between the techniques and the effects of the pre-treatment also varies with the nature of the sediment sample. As demonstrated in these and previous PS exercises, possible variations in equipment and methods can result in highly variable data. In order to eliminate as much variation as possible a detailed and prescriptive method for particle size analysis must be devised for the UK NMMP sample analysis.

4.4 Ring Test Distributions

The results were in general comparable with those from all previous exercises, with a high level of agreement between participating laboratories for the majority of distributed species. The RT component is considered to provide a valuable training mechanism and be an indicator of problem groups and possible areas for further 'targeted' exercises or inclusion at taxonomic workshops. The ring test bulletins (RTB), which detail specifically the reasons for any identification errors, have further emphasised the learning aspect of this component. RT29 identified discrepancies with literature used by some participating laboratories for their identification of the *Lumbrineris gracilis* and *Abyssoninoe hibernica* specimens. RT30 identified discrepancies with literature used by some participating laboratories for their identification of cirratulid specimens. One Laboratory (LB1306) identified all twenty-five RT30 specimens correctly. RT31 identified discrepancies with literature for the taxon, *Osmerus eperlanus*. One participating laboratory incorrectly identified *Lophius piscatorius* as *Squatina squatina*, presumably due to an incorrect translation from the common name, Monk Fish. One laboratory (LB1302a) correctly identified all twenty-five RT31 fish specimens. All participating laboratories have been made aware of the variety of problems encountered for these ring tests via the ring test bulletins (RTB29, RTB30 and RTB31).

4.5 Laboratory Reference

In view of the different species that were sent by laboratories for identification it is inappropriate to make detailed inter-lab comparisons. In the majority of instances identifications made by Unicomarine Ltd. were in agreement with those made by the participating laboratories. Due to the range of species submitted it was not possible to identify a single taxon causing the majority of problems.

The results for this exercise should be viewed giving consideration to the different approaches by participant laboratories. Some laboratories appear to be sending well known species while others elect to obtain a 'second opinion' on more difficult species. Thus the scores are not comparable and it is not considered appropriate to assign any rank to the laboratories. Each participant should deliberate upon the aims of this component in terms of data quality assessment.

5. Application of NMBAQC Scheme Standards

One of the key roles of the Invertebrate and Particle Size components of the NMBAQC Scheme is to assess the reliability of data collected as part of the UK National Marine Monitoring Programme (UK NMMP). With this aim performance target standards were defined for certain Scheme exercises and applied in Scheme year three (1996/97). These standards were the subject of a review in 2001 (Unicomarine, 2001) and were altered in Scheme year eight; each performance standard is described in detail in Appendix 2: Description of the Scheme Standards. Laboratories meeting or exceeding the required standard for a given exercise would be considered to have performed satisfactorily for that

particular exercise. A flag indicating a 'Pass' or 'Fail' would be assigned to each laboratory for each of the exercises concerned. It should be noted that, as in previous years, only the OS and PS exercise have been used in 'flagging' for the purposes of assessing data for the UK NMMP.

As the Scheme progresses, additional exercises may be included. In the meantime, the other exercises of the Scheme as presented above are considered of value as more general indicators of laboratory performance, or as training exercises.

As mentioned in the Introduction, non-return of samples or results for the PS and OS modules resulted in the assignment of a "Fail" flag to the laboratory (see Section 3: Results). The only exception to this approach has been in those instances where laboratories elected not to participate in a particular module of the Scheme.

5.1 Laboratory Performance

The target values for each exercise and the corresponding laboratory results are presented in Table 15 (OS) and Table 16 (PS). The assigned flags for each laboratory for each component are also given. An assessment is performed separately for each of the three OS samples. The tables should be read in conjunction with the comments on individual laboratories' results made in Section 6: Comments on Individual Laboratories.

Where no returns were made for an exercise this is indicated in Tables 15 and 16 with a "-". The reason for not participating, if given, will be stated in Section 6: Comments on Individual Laboratories.

It can be seen from Table 15 (columns 4, 13 and 22) that for the OS exercise the majority of laboratories are considered to have met or exceeded the required standard for three of the OS targets - the enumeration of taxa and individuals and the Bray-Curtis comparison. Overall 97% of the comparisons were considered to have passed the enumeration of taxa standard; 93% exceeded the enumeration of individuals standard and 91% passed the Bray-Curtis comparison standard. NMBAQC Scheme / UK NMMP sample flags have been applied to each of the Own Samples in accordance with the performance flagging criteria introduced in Scheme year eight (Table 15, column 23); three of the sixty-nine applicable samples are flagged as 'Fail - Bad'; three are flagged as 'Fail - Poor'; ten are flagged as 'Pass - Acceptable'; forty-two are flagged as 'Pass - Good'; and eleven are flagged as 'Pass - Excellent' for achieving 100% Bray-Curtis similarity indices. All the laboratories with 'Poor' or 'Bad' sample flags have already addressed their 'failing' samples by undertaking remedial action (see 5.4.3 Remedial Action below).

Performance with respect to the biomass standard was slightly poorer (Table 15, column 19) with only 74% of the eligible samples meeting the required standard. It should be noted that there were laboratories for which the results from the biomass exercise should be considered unsuitable for comparison with the standard (expressed as five decimal places instead of the requested four, and fauna rendered dry or damaged by initial biomass procedures).

Application of the new PS exercise standards, introduced in Scheme year nine, (See Appendix 2: Description of the Scheme Standards) is shown in Table 16. The upper section of Table 16 shows the results for the PS28 exercise. One laboratory (LB1301) is deemed to have failed all criteria due to non-submission of data. Two laboratories (LB1307 and LB1320) failed to meet the standard for %< 63µm; one laboratory (LB1320) failed to meet the standard for median (ϕ); one laboratory (LB1320) failed to meet the standard for mean (ϕ); one laboratory (LB1307) failed to meet the standard for sorting; and two laboratories (LB1307 and LB1320) failed to meet the standard for IGS (SKi). Eight of the participating laboratories passed all standards. The lower section of Table 16 shows the results for the PS29 exercise. One laboratory (LB1301) is deemed to have failed all criteria due to non-submission of data. One laboratory (LB1307) failed to meet the standard for %< 63µm; all laboratories passed the standard for median (ϕ); all laboratories passed the standard for mean (ϕ); two laboratories (LB1302 and LB1307) failed to meet the standard for sorting; one laboratory (LB1307) failed to meet the standard for IGS (SKi). Seven laboratories passed all standards.

5.2 Statement of Performance

Each participating laboratory has received a 'Statement of Performance', which includes a summary of results for each of the Schemes modules and details the resulting flags where appropriate. These statements were first circulated with the 1998/1999 annual report, for the purpose of providing proof of Scheme participation and for ease of comparing year on year progress.

5.3 Comparison with Results from Previous Years

A comparison of the overall results for recent years is presented in Table 17. The Table shows the number of laboratories assigned 'Pass' and 'Fail' flags for the OS exercises over the past twelve years based upon the current NMBAQC Scheme standards (See Appendix 2: Description of the Scheme standards for each component). This year's sixty-nine comparable Own Samples resulted in fourth highest percentage pass rate, 91% (the highest being 100% achieved in exercise OS01 that involved just fourteen samples), since the beginning of the Own Sample component and matches that of the previous Scheme year. The number of non-returned results, 'Deemed Fails', have been significantly reduced in recent years of the Scheme. This can be attributed to the 'deadline reminders' dispatched throughout the Scheme year. Table 18 shows the trend of OS results for each participating laboratory over the past twelve years. There appears to be a fairly high level of consistency within each laboratory with an overall increase in data quality, *i.e.* fewer failing samples and a higher average Bray-Curtis similarity score. Monitoring the situation over a longer period is required before a firm statement about changes in laboratory standards could be made. However, the introduction of 'blind' audits in Scheme year eight have not caused an increase in the number of failures, as initially expected.

5.4 Remedial Action

It is imperative that failing UK NMMP samples, audited through the Own Sample exercise, are addressed. Remedial action should be conducted upon the remaining UK NMMP station replicates to improve upon the flagged data. The revised NMBAQC Scheme OS standards, introduced in Scheme year eight, give clear methods for discerning the level of remedial action required (See Appendix 2: Description of the Scheme Standards). A failing Own Sample is categorised by the achievement of a Bray-Curtis similarity indices of <90%. The performance indicators used to determine the level of remedial action required are %taxa in residue, %taxonomic errors, %individuals in residue (see Table 15, columns 7, 10 and 16) and %count variance. Own Samples not achieving the required standards are monitored by the NMBAQC committee. The participating laboratories are expected to initiate remedial action and notify the NMBAQC Scheme Contract Manager when this has been completed. Any remedial action undertaken should be audited externally where required. The NMBAQC Contract Manager and Scheme's contractor, Unicomarine Ltd., will provide clarification on specific details of remedial action or consider appeals relating to the remedial action process.

Below is a summary of the samples that have been flagged with 'fail' flags in Scheme year 13. Also 'failing' samples with outstanding remedial action from Scheme years 11 and 12 are listed.

5.4.1 Scheme Year 11 (OS26, 27 & 28) – 2004/05

Three samples 'failed' in Scheme year 11 (including two UK NMMP samples). Remedial action, outlined below, is still outstanding for the associated replicates of the following Own Samples:

NMMP samples

LB1110 OS26- Review *Fabricia stellaris / Manayunkia aestuarina* identifications;
Re-sort residue for remaining replicates and re-audit.
Remedial Action - status unknown.

LB1110 OS28- Review *Tubificoides* cf. *galiciensis* identifications.
Remedial Action - status unknown.

Non-NMMP samples

LB1120 OS28- Review policy for recording *in-situ* records;
Review identification of live versus dead *Hydrobia ulvae.*
Remedial Action - status unknown.

5.4.2 *Scheme Year 12 (OS29, 30 & 31) – 2005/06*

Seven samples 'failed' in Scheme year 12 (including five UK NMMP samples). Remedial action, outlined below, is still outstanding for the associated replicates of the following Own Samples:

NMMP samples

LB1226 OS31- Review *Bathyporeia elegans* / *B. pelagica* identifications;
Review methods for estimation of taxa and abundance.
Remedial Action - status unknown.

Non-NMMP samples

LB1201 OS29- Reprocess residues for remaining replicate samples;
Review identifications of *Pholoe inornata*, *Monocorophium sextonae*, *Eumida sanguinea* and *Malmgreniella arenicolae*.
Remedial Action - status unknown.

One participating laboratory responsible for NMMP samples, LB1218, supplied three Own Samples without their associated sorted residues. In this instance the samples (fauna only) have been processed, but excluded from the annual report. Remedial action was not possible due to the disposal of all residues from associated samples. These samples were processed by a subcontractor; a review of the provision of processing instructions for subcontractors has been undertaken.

5.4.3 *Scheme Year 13 (OS32, 33 & 34) – 2006/07*

For Year 13, remedial action, outlined below, was required for associated replicates of the following Own Samples:

NMMP samples

LB1303 OS34- Reprocess residues for remaining replicate samples.
Remedial Action - completed (22/08/2007).

LB1305 OS33- Review *Abra alba / A. nitida* identifications.
Remedial Action – completed (04/03/2008).

LB1324 OS34- Review enumeration / transcription procedures.
Remedial Action – completed (22/10/2007).

Non-NMMP samples

LB1307 OS34- Review *Mangelia nebula / M. brachystoma* identifications.
Remedial Action – completed (10/08/2007).

LB1309 OS33- Review *Pholoe baltica / P. inornata*,*Sige fusifera*? / *Eumida sanguinea*, *Trichobranchus roseus / T. glacialis*, *Phisidia aurea*? / *Lanassa vanusta*, *Balanus balanus / B. crenatus*, *Idotea* sp. / *Janira maculosa*, *Anapagarus hyndmanni / Pagurus alatus*, *Hanleyi hanleyi / Tonicella rubra*, *Rissoa interrupta / Pusillina inconspicua*, *Lucinoma borealis* juv. / *Dosinia exoleta*, *Tapes* sp. juv. / *Venerupis senegalensis*?, *Alcyonidium diaphanum* / Didemnidae, *Echarella immersa / Microporella ciliata*, *Phylactella labrosa*? / *Neolagenipora collaris* and *Molgula manhattensis / Molgula* sp. identifications. Remedial Action – completed (29/06/2007).

LB1321 OS34- Review *Ophelia limacina / O. borealis*, *Typhlotanais* #1 / *Tanaissus danica*, *Spisula elliptica* juv. / *S. solida* juv., *Retusa obtusata* / *R. umbilicata*, *Exogone hebes / Sphaerosyllis taylori*, *Ephesiella abyssorum* / *Sphaerodopsis minuta* and *Tubificoides* sp. / *Questa* sp. identifications.
Reprocess residues for associated replicate samples.
Remedial Action – completed (15/02/2008).

One participating laboratory responsible for NMMP samples, LB1312, supplied three Own Samples without their associated sorted residues. In this instance the samples (fauna only) have been processed, but excluded from this report. Remedial action was not possible due to the disposal of all residues from associated samples. These samples were processed by a subcontractor; a review of the provision of processing instructions for subcontractors has been undertaken.

6. Comments on Individual Laboratories

Brief comments on the results for individual laboratories are provided below. These are not intended to be detailed discussions of all aspects of the results but provide an indication of the main issues arising for each of the exercises. Clearly different laboratories have encountered different analytical problems. Broadly, these fell into the following areas:

- Incomplete sorting and extraction of individuals from whole samples.
- Particular taxonomic problems in RTs and whole samples
- Accuracy in biomass measurement
- Particle size procedures and calculation of statistics

Where possible these are noted for each laboratory listed below.

Also in the comments below, the results for RT29, RT30 and RT31 are expressed in terms of their position relative to the results from all laboratories. The overall range of differences at the level of genus and species was used to define three categories according to the number of differences: **Low**, **Mid** and **High** (based on the number of differences with the Unicomarine identifications, *i.e.* **Low** = relatively good agreement with Unicomarine identifications). Each laboratory has been placed into a group for information only, on this basis.

This year one laboratory which normally use a separate centralised sediment analysis laboratory (also participating in the Scheme) for the PS exercises, have decided to pool their data from this sub-contracting laboratory. Their data are indicated accordingly in all figures and tables. In the comments below these data are termed 'Data from centralised analysis'.

If an exercise contains the comment 'not participating in this module' then the laboratory has not subscribed to the module. If an exercise contains the comment 'not participating in this exercise' then the laboratory, despite subscribing to this exercise, has decided not to submit data for the exercise.

Laboratory – LB1301

Macrobenthos (Training Module)

MB14 – Estuarine sample. No data received.

Ring Test (Training Module)

RT29 (invertebrates) – No data received.
RT30 (invertebrates) – No data received.
RT31 (fish) – No data received.

Laboratory Reference (Training Module)

LR11 – No specimens received.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
All individuals correctly identified. Eleven individuals not extracted from the residue, including two previously unpicked taxa (*Polydora caulleryi* and Sabellidae indet.). Count variance of three individuals. Bray-Curtis similarity index of 96.07%. Biomass on average 3.43% heavier than Aquatic Environments.
OS33 – NMBAQCS sample flag – Pass, 'Excellent'. (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 5.76% lighter than Aquatic Environments.

OS34 – NMBAQCS sample flag – Pass, 'Excellent'. (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 6.58% heavier than Aquatic Environments.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – No data received. All NMBAQCS standards deemed failed.
PS29 – No data received. All NMBAQCS standards deemed failed.

Laboratory – LB1302

Macrobenthos (Training Module)

MB14 – Estuarine sample. Twelve taxonomic differences (*Anoplodactylus pygmaeus, Bodotria scorpioides, Noemiamea dolioliformis, Leptochiton asellus, Mysella bidentata, Balanus crenatus, Eumida bahusiensis, Exogone naidina, Chaetozone zetlandica, Capitella* sp., *Spiophanes bombyx, Tubificoides* cf. *galiciensis*). Eight additional taxa found within the extracted fauna (*Anoplodactylus pygmaeus, Monocorophium acherusicum / insidiosum, Balanus crenatus, Mya truncata* juv., *Thelepus setosus, Chaetozone zetlandica, Manayunkia aestuarina* and *Polydora caeca* agg.). Four individuals not extracted from the residue. Count variance of twenty-five individuals. Bray-Curtis similarity index of 89.53%. Biomass on average 0.30% heavier than Unicomarine Ltd. Residue/fauna partially stained. Laboratory policy stated as not extracting bryozoans, hydroids, copepods and tunicates.

Ring Test (Training Module)

RT29 (invertebrates) – Six generic and eight specific differences. Number of AQC identifications in Mid group.
RT30 (invertebrates) – Two generic and three specific differences. Number of AQC identifications in Mid group.
RT31 (fish) – One generic and one specific difference. Number of AQC identifications in Low group.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
One taxonomic difference/transcription error (*Amphiblestrum auritum*). Twenty-one individuals not extracted from the residue, including one previously unpicked taxon (*Timoclea ovata*). Count variance of thirty-six individuals. Bray-Curtis similarity index of 99.59%. Biomass on average 0.68% lighter than Aquatic Environments.
OS33 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
One taxonomic difference (*Heterosiphonia plumosa*). Nine individuals not extracted from the residue. Count variance of three individuals. Bray-Curtis similarity index of 99.28%. Biomass on average 0.60% lighter than Aquatic Environments.
OS34 – NMBAQCS sample flag – Pass, 'Excellent'. (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 6.39% heavier than Aquatic Environments.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'M' (mud) prior to analysis; described as 'M' (mud) using the Folk triangle.
PS29 – NMBAQCS standard for sorting failed. All remaining NMBAQCS standards passed.
Dry sieve analysis conducted (air dried). Size distribution curve slightly compressed compared with the other curves, primarily due to the analysis method (dry sieve data). Sediment described as 'Medium sand' prior to analysis; described as 'Sand' using the Folk triangle.

Laboratory – LB1303

Macrobenthos (Training Module)

MB14 – Estuarine sample. Three taxonomic differences (*Eumida bahusiensis*, *Aphelochaeta marioni* and *Molgula manhattensis*). One additional taxon found within the extracted fauna (*Eumida bahusiensis*). Fifty-seven individuals not extracted from the residue, including six previously unpicked taxa (*Mytilus edulis* juv., *Mysella bidentata*, *Tubificoides benedii*, *Grania* sp., *Abra alba* and *Cirriformia* sp. juv.). Count variance of eleven individuals. Bray-Curtis similarity index of 79.82%. Biomass on average 8.40% lighter than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated barnacles and nematodes <1cm not extracted.

Ring Test (Training Module)

RT29 (invertebrates) – Two generic and three specific differences. Number of AQC identifications in Low group.
RT30 (invertebrates) – Five generic and six specific differences. Number of AQC identifications in High group.
RT31 (fish) – Multi-data:
LB03a - One generic and two specific differences. Number of AQC identifications in Low group.
LB03b - Two generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. One individual not extracted from the residue. Bray-Curtis similarity index of 98.04%. Biomass on average 0.40% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Four individuals not extracted from the residue, including one previously unpicked taxon (*Mangelia brachystoma*). Bray-Curtis similarity index of 98.63%. Biomass on average 1.04% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, following Remedial Action ('Poor' original flag).
All individuals correctly identified. Three individuals not extracted from the residue, including one previously unpicked taxon (*Abra nitida*). Bray-Curtis similarity index of 88.89%. Biomass on average 4.71% lighter than Unicomarine Ltd. Remedial action (residue re-sort) audit completed 22/08/07.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed results for the clay fractions provided (>8 phi). Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.
PS29 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed results for the clay fractions provided (>4 phi). Sediment described as 'Coarse sand' prior to analysis; described as 'sand' using the Folk triangle.

Laboratory – LB1304

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this exercise.

Ring Test (Training Module)

RT29 (invertebrates) – One generic and five specific differences. Number of AQC identifications in Mid group.

RT30 (invertebrates) – One specific difference. Number of AQC identifications in Low group.
RT31 (fish) – Not participating in this exercise.

Laboratory Reference (Training Module)

LR11 – No specimens received.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Aphrodita aculeata* juv.). All individuals extracted from the residue. Count variance of three individuals. Bray-Curtis similarity index of 98.17%. Biomass on average 19.37% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
Eleven taxonomic differences (*Moerella pygmaea*, *Modiolus* sp. juv., *Mysella bidentata*, *Parvicardium scabrum*, *Obtusella intersecta*, *Diaphana minuta*, *Gouldia minima / Dosinia* sp. juv., *Alderina imbellis*, *Palliolum tigerinum*, *Pholoe baltica*, *Parvicardium scabrum*). Two additional taxa found within the extracted fauna (*Diaphana minuta* and *Cliona* sp.). Eight individuals not extracted from the residue, including one previously unpicked taxon (Animalia – unusual forms in white striped tubes). Count variance of thirty-four individuals. Bray-Curtis similarity index of 96.66%. Biomass on average 3.93% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Abra prismatica*). All individuals extracted from the residue, however no preservative apparent in residue. Bray-Curtis similarity index of 99.01%. Biomass on average 11.84% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'Mud (anoxic)' prior to analysis; described as 'Mud' using the Folk triangle.
PS29 – Not participating in this exercise.

Laboratory – LB1305

Macrobenthos (Training Module)

MB14 – Estuarine sample. Eight taxonomic differences (*Tharyx* sp. A, *Fabulina fabula*, *Abra alba*, *Noemiamea dolioliformis*, *Anoplodactylus pygmaeus*, *Carcinus maenas* juv., *Atylus guttatus* and *Cirriformia* sp. juv.). One additional taxon found within the extracted fauna (*Conopeum reticulatum*). Six individuals not extracted from the residue. Bray-Curtis similarity index of 97.01%. Biomass data supplied to 5 decimal places; not 4 as requested. Biomass on average 1.43% lighter than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Module)

RT29 (invertebrates) – Three generic and four specific differences. Number of AQC identifications in Low group.
RT30 (invertebrates) – One generic and four specific differences. Number of AQC identifications in Mid group.
RT31 (fish) – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference (Training Module)

LR11 - Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Acceptable'.
Eight taxonomic differences (*Abra nitida*, *Glycinde nordmanni*, *Amphictene auricoma*, *Circomphalus casina* juv., *Owenia fusiformis / Lanice concheliga* juv., *Nephtys assimilis*, *Thyasira polygona* and *Goniada maculata*). Three additional taxa found within the extracted fauna (*Glycinde nordmanni*, *Owenia fusiformis* and *Thyasira polygona*). One individual not

extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 90.13%. Biomass on average 9.49% heavier than Unicomarine Ltd. Biomass data supplied to 5 decimal places; not 4 as requested.

OS33 – NMBAQCS sample flag – Pass, following Remedial Action ('Poor' original flag).
Two taxonomic differences (*Scolelepis korsuni* and *Abra nitida*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 85.99%. Biomass on average 13.71% heavier than Unicomarine Ltd. Biomass data supplied to 5 decimal places; not 4 as requested. Remedial action (review *Abra nitida*) completed 04/03/08.

OS34 – NMBAQCS sample flag – Pass, 'Acceptable'.
Four taxonomic differences (*Nephtys hystricis, Golfingia elongata,Pharus legumen* and *Nephtys hombergii*). Seven individuals not extracted from the residue, including one previously unpicked taxon (*Phaxas pellucidus*). Count variance of one individual. Bray-Curtis similarity index of 90.11%. Biomass on average 10.55% heavier than Unicomarine Ltd. Biomass data supplied to 5 decimal places; not 4 as requested.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve displaced slightly to the left (coarser) of the majority of curves. Sediment described as 'thick dark brown mud + occasional shell fragments' prior to analysis; described as '(g)M' (slightly gravelly mud) using the Folk triangle.

PS29 – All NMBAQCS standards passed.
Laser diffraction analysis conducted (wet sieve, dry sieve, freeze dried, laser diffraction). No major differences in size distribution curve. Sediment described as 'Very slightly gravelly (shelly) sand' prior to analysis; described as 'Sand' using the Folk triangle.

Laboratory – LB1306

Macrobenthos (Training Module)

MB14 – Estuarine sample. One taxonomic difference (*Cirriformia* sp. juv.). Fifty-two individuals not extracted from the residue, including one previously unpicked taxon (*Balanus crenatus*). Bray-Curtis similarity index of 91.41%. Biomass data supplied to 5 decimal places; not 4 as requested. Biomass on average 1.39% lighter than Unicomarine Ltd. Residue/fauna partially stained. No sample processing details form received.

Ring Test (Training Module)

RT29 (invertebrates) – Two generic and five specific differences. Number of AQC identifications in Mid group.

RT30 (invertebrates) – All specimens correctly identified. Number of AQC identifications in Low group.

RT31 (fish) – Two generic and three specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Six taxonomic differences (*Anaitides groenlandica, Philine* sp., *Spisula subtruncata, Ophiura albida / O. ophiura, Modiolus* sp. juv. and *Aricidea minuta*). Three additional taxa found within the extracted fauna (*Ophiura ophiura, Modiolus* sp. juv. and *Aricidea minuta*). Thirteen individuals not extracted from the residue, including one previously unpicked taxon (*Obtusella interstincta*). Count variance of twelve individuals. Bray-Curtis similarity index of 96.11%. Biomass on average 7.81% lighter than Unicomarine Ltd.

OS33 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Nine individuals not extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 98.59%. Biomass on average 14.83% lighter than Unicomarine Ltd.

OS34 – NMBAQCS sample flag – Pass, 'Good'.
Four taxonomic differences (*Mysia undata*, *Ampelisca tenuicornis*, *Praxillella affinis* and *Nephtys kersivalensis*). Three individuals not extracted from the residue, including one previously unpicked taxon (*Pterygocythereis jonesi*). Count variance of three individuals. Bray-Curtis similarity index of 96.92%. Biomass on average 3.78% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Data from centralised analysis. Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.
PS29 – All NMBAQCS standards passed.
Data from centralised analysis. Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'Coarse sand' prior to analysis; described as 'sand' using the Folk triangle.

Laboratory – LB1307

Macrobenthos (Training Module)

MB14 – Estuarine sample. Three taxonomic differences (*Monocorophium acherusicum, Tharyx killariensis* and *Mytilus edulis* juv.). One additional taxon found within the extracted fauna (*Tharyx killariensis*). Fifty-five individuals not extracted from the residue, including four previously unpicked taxa (*Mysella bidentata, Pholoe inornata, Epitonium clathratulum* and *Tapes philippinarum* juv.). Count variance of one individual. Bray-Curtis similarity index of 85.13%. No biomass data supplied. Residue/fauna stained. Laboratory policy stated as not extracting nematodes, bryozoans, hydroids, copepods, tunicates, anthozoans, aquatic insects and barnacles.

Ring Test (Training Module)

RT29 (invertebrates) – Four generic and five specific differences. Number of AQC identifications in Mid group.
RT30 (invertebrates) – One specific difference. Number of AQC identifications in Low group.
RT31 (fish) – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Acceptable'.
Two taxonomic differences (*Thracia* sp. juv. and *Thracia phaseolina*). One additional taxon found within the extracted fauna (*Thracia* sp. juv.). All individuals extracted from the residue. Bray-Curtis similarity index of 90%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, following Remedial Action ('Bad' original flag).
One taxonomic difference (*Mangelia brachystoma*). All individuals extracted from the residue. Bray-Curtis similarity index of 80%. No biomass data supplied. Remedial action (review *Mangelia brachystoma*) completed 10/08/07.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – NMBAQCS standards for %silt/clay, sorting and IGS (SKi) failed; median and mean NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve showing slightly less silt/clay than the majority of curve data and an anomalous coarse sand fraction, which may be the result of poor disaggregation following drying or the presence of hydrobiid snails. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.

PS29 – NMBAQCS standards for %silt/clay, sorting and IGS (SKi) failed; median and mean NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve showing more fine particles than the majority of curve data, which is likely to have been caused by the hydrogen peroxide pre-treatment separating bound fine particles. Sediment described as 'Sand' prior to analysis; described as 'Sand' using the Folk triangle.

Laboratory – LB1308

Macrobenthos (Training Module)

MB14 - Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – One generic and two specific differences. Number of AQC identifications in Low group.
RT30 (invertebrates) – One generic and one specific difference. Number of AQC identifications in Low group.
RT31 (fish) – Not participating in this exercise.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Five taxonomic differences (*Malmgreniella arenicolae, Tharyx killariensis, Ondina obliqua, Parvicardium scabrum* and *Mya truncata*). All individuals extracted from the residue. Count variance of nine individuals. Bray-Curtis similarity index of 96.34%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Acceptable'.
Two taxonomic differences (*Pirakia punctifera* and *Epilepton clarkiae*). Three additional taxa found within the extracted fauna (*Epilepton clarkiae, Edwardsia claparedii* and *Commensodorum commensalis*). One individual not extracted from the residue. Count variance of three individuals. Bray-Curtis similarity index of 94.69%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, 'Acceptable'.
Three taxonomic differences (*Epilepton clarkiae, Parvicardium scabrum* and *Thracia villosiuscula*). One additional taxon found within the extracted fauna (*Epilepton clarkiae*). All individuals extracted from residue. Count variance of eighteen individuals. Bray-Curtis similarity index of 93.19%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed results for the clay fractions provided (>8.5 phi). Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.
PS29 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve displaced slightly to the right of the majority of curves, indicating less coarse to medium sand material. Sediment described as 'Sand' prior to analysis; described as 'Sand' using the Folk triangle.

Laboratory – LB1309

Macrobenthos (Training Module)

MB14 – Estuarine sample. Five taxonomic differences (*Balanus crenatus, Crepidula fornicate* juv., *Anoplodactylus pygmaeus, Nephtys hombergii* and *Glycera oxycephala*). One additional taxon found within the extracted fauna (*Nephtys hombergii*). Sixteen individuals not extracted from the residue, including two previously unpicked taxa (*Anguinella palmata* and *Vesicularia spinosa*). Bray-Curtis similarity index of 96.39%. No biomass data supplied. Residue/fauna not stained. Laboratory policy stated as nematodes <1cm, ostracods and foraminiferids not extracted.

Ring Test (Training Module)

RT29 (invertebrates) – Two generic and two specific differences. Number of AQC identifications in Low group.
RT30 (invertebrates) – Two generic and two specific differences. Number of AQC identifications in Mid group.
RT31 (fish) – Not participating in this exercise.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of fifteen individuals. Bray-Curtis similarity index of 99.37%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, following Remedial Action ('Bad' original flag).
Fifteen taxonomic differences (*Pholoe inornata, Eumida sanguinea, Trichobranchus glacialis, Lanassa venusta, Balanus crenatus, Janira maculosa, Pagurus alatus, Tonicella rubra, Pusillina inconspicua, Dosinia exoleta, Venerupis senegalensis*?, Didemnidae, *Microporella ciliata, Neolagenipora collaris* and *Eugyra arenosa*). Three additional taxa found within the extracted fauna (*Pholoe inornata, Eugyra arenosa* and Podocopida). Ten individuals not extracted from the residue, including three previously unpicked taxa (Polynoidae, *Sphaerosyllis taylori* and Arenicoliidae juv.). Count variance of one individual. Bray-Curtis similarity index of 84.04%. No biomass data supplied. Remedial action (review taxonomic errors) completed 29/06/07.
OS34 – NMBAQCS sample flag – Pass, 'Acceptable'.
Three taxonomic differences (*Parvicardium ovale, Moerella pygmaea* and *Chamelea striatula*). One individual not extracted from the residue. Bray-Curtis similarity index of 94.66%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1310

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this exercise.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this exercise.
RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – Not participating in this exercise.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
One taxonomic difference (*Harmothoe* cf. *ljungmani*). Eight individuals not extracted from the residue. Count variance of three individuals. Bray-Curtis similarity index of 99.49%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
All individuals correctly identified. Three individuals not extracted from the residue. Count variance of six individuals. Bray-Curtis similarity index of 99.88%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Count variance of ten individuals. Bray-Curtis similarity index of 98.91%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1311

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Five generic and seven specific differences. Number of AQC identifications in Mid group.
RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – Not participating in this exercise.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Acceptable'.
One taxonomic difference (*Scolelepis bonnieri*). All individuals extracted from the residue. Bray-Curtis similarity index of 92.86%. Biomass on average 0.96% lighter than Unicomarine.
OS33 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 9.19% lighter than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Scolelepis bonnieri*). All individuals extracted from the residue. Bray-Curtis similarity index of 97.98%. Biomass on average 2.17% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1312

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Seven generic and nine specific differences. Number of AQC identifications in High group.
RT30 (invertebrates) – Eight specific differences. Number of AQC identifications in High group.
RT31 (fish) – Multi-data:
LB12a - One generic and four specific differences. Number of AQC identifications in Mid group.
LB12b - Two generic and four specific differences. Number of AQC identifications in Mid group.
LB12c - Five generic and seven specific differences. Number of AQC identifications in High group.
LB12d - Eight generic and ten specific differences. Number of AQC identifications in High group.
LB12e - Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – No specimens received.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Fail, 'Deemed Fail'. Samples not provided in the correct format (sample residues unavailable).
OS33 – NMBAQCS sample flag – Fail, 'Deemed Fail'. Samples not provided in the correct format (sample residues unavailable).
OS34 – NMBAQCS sample flag – Fail, 'Deemed Fail'. Samples not provided in the correct format (sample residues unavailable).

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1313

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Nine generic and thirteen specific differences. Number of AQC identifications in High group.
RT30 (invertebrates) – No data received.
RT31 (fish) – Multi-data:
LB13a - Four generic and five specific differences. Number of AQC identifications in Mid group.
LB13b - Four generic and six specific differences. Number of AQC identifications in Mid group.
LB13c - Four generic and five specific differences. Number of AQC identifications in Mid group.
LB13d - Seven generic and eight specific differences. Number of AQC identifications in High group.
LB13e - Six generic and seven specific differences. Number of AQC identifications in High group.
LB13f - Five generic and six specific differences. Number of AQC identifications in Mid group.
LB13g - Six generic and eight specific differences. Number of AQC identifications in High group.
LB13h - Three generic and five specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – No specimens received.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Corophium arenarium*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 97.81%. Biomass on average 33.80% heavier than Unicomarine.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of twenty-one individuals. Bray-Curtis similarity index of 97.27%. Biomass on average 0.93% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.

One taxonomic difference (*Harpinia antennaria*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 98.25%. Biomass on average 20.82% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1314

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this exercise.
RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – Multi-data:
LB14a - One generic and three specific differences. Number of AQC identifications in Low group.
LB14b - Three generic and three specific differences. Number of AQC identifications in Low group.
LB14c - Three generic and four specific differences. Number of AQC identifications in Mid group.
LB14d - Six generic and eight specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
One vial contained a mixture of species (*Aphelochaeta marioni* and *Tharyx* sp. A). All individuals extracted from the residue. Bray-Curtis similarity index of 99.73%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Good'. (External audit by Aquatic Environments).
All individuals correctly identified. One individual not extracted from the residue. Bray-Curtis similarity index of 99.59%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, 'Excellent'. (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'mud' prior to analysis; no post-analysis Folk triangle description supplied.
PS29 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'Sandy' prior to analysis; no post-analysis Folk triangle description supplied.

Laboratory – LB1315

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this exercise.

RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – Three generic and six specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Two taxonomic differences (*Pholoe inornata* and Arenicoliidae juv.). One additional taxon found within the extracted fauna (Arenicoliidae juv.). Two individuals not extracted from the residue. Count variance of eight individuals. Bray-Curtis similarity index of 97.18%. Biomass on average 9.65% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
Five taxonomic differences (*Paradoneis lyra*, *Chaetozone gibber / Caulleriella alata*, *Harpinia crenulata*, *Nucula nitidosa* and *Mya arenaria* juv.). One additional taxon found within the extracted fauna (*Caulleriella alata*). Three individuals not extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 96.88%. Biomass on average 3.97% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.
Two taxonomic differences (*Eusarsiella zostericola* and a tentacle). Two individuals not extracted from residue. Count variance of twelve individuals. Bray-Curtis similarity index of 98.57%. Biomass on average 5.65% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1316

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Nine generic and ten specific differences. Number of AQC identifications in High group.
RT30 (invertebrates) – Five generic and nine specific differences. Number of AQC identifications in High group.
RT31 (fish) – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Three taxonomic differences (*Scrobicularia plana* juv., *Tubificoides benedii* (tail) and Arenicoliidae (fragments)). One additional taxon found within the extracted fauna (*Scrobicularia plana* juv.). Twenty-one individuals not extracted from the residue. Count variance of fourteen individuals. Bray-Curtis similarity index of 99.37%. Biomass on average 23.61% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
Two taxonomic differences (*Scrobicularia plana* juv. and *Electra crustulenta*). Two individuals not extracted from the residue. Count variance of three individuals. Bray-Curtis similarity index of 98.70%. Biomass on average 72.64% lighter than Unicomarine Ltd, due to a transcription error.
OS34 – NMBAQCS sample flag – Pass, 'Good'.

All individuals correctly identified. Fifteen individuals not extracted from the residue. Count variance of nine individuals. Bray-Curtis similarity index of 98.40%. Biomass on average 4.55% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1317

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this module.
RT30 (invertebrates) – Not participating in this module.
RT31 (fish) – Not participating in this module.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Two taxonomic differences (*Mangelia brachystoma* and *Abra nitida*). One individual not extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 97.51%. Biomass on average 18.05% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 4.45% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Corbula gibba*). One individual not extracted from residue, this was a previously unpicked taxon (*Polinices pallida*). Count variance of one individual. Bray-Curtis similarity index of 96.67%. Biomass on average 9.43% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'muddy silt' prior to analysis; described as 'medium silt' using the Folk triangle.
PS29 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'Muddy sand' prior to analysis; described as 'Medium sand' using the Folk triangle.

Laboratory – LB1318

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – One generic and two specific differences. Number of AQC identifications in Low group.
RT30 (invertebrates) – All specimens correctly identified. Number of AQC identifications in Low group.
RT31 (fish) – Not participating in this exercise.

Laboratory Reference (Training Module)

LR11 – Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Twenty-two individuals not extracted from the residue, including two previously unpicked taxa (*Mytilus edulis* juv. and *Jassa marmorata*). Count variance of one individual. Bray-Curtis similarity index of 97.88%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Acceptable'.
All individuals correctly identified. Sixteen individuals not extracted from the residue, including two previously unpicked taxa (*Pholoe baltica* and *Nuculoma tenuis*). Bray-Curtis similarity index of 93.44%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, 'Acceptable'.
One taxonomic difference (*Abra nitida*). One additional taxon found within the extracted fauna (*Abra nitida*). One hundred and twenty-nine individuals not extracted from the residue, including five previously unpicked taxa (*Bowerbankia* sp., *Fabulina fabula*, *Mya truncata* juv., *Hiatella arctica* and *Nuculoma tenuis*). Count variance of eight individuals. Bray-Curtis similarity index of 93.84%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1319

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Five generic and nine specific differences. Number of AQC identifications in High group.
RT30 (invertebrates) – Five generic and eight specific differences. Number of AQC identifications in High group.
RT31 (fish) – Not participating in this exercise.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – Not participating in this module.
OS33 – Not participating in this module.
OS34 – Not participating in this module.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1320

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this module.
RT30 (invertebrates) – Not participating in this module.
RT31 (fish) – Not participating in this module.

Laboratory Reference (Training Module)

LR11 - Specimens reviewed and returned.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Monocorophium sextonnae*). Seven individuals not extracted from the residue. Bray-Curtis similarity index of 97.49%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – NMBAQCS standard for sorting passed. All remaining NMBAQCS standards failed.
Dry sieve analysis conducted. Size distribution curve shows a significantly reduced silt/clay fraction, possibly due to inadequate disaggregation of compacted mud particles following drying. No detailed results provided above 4 phi. Sediment described as 'mud' prior to analysis; described as 'muddy sand' using the Folk triangle.
PS29 – All NMBAQCS standards passed.
Dry sieve analysis conducted. No major differences in size distribution curve. No detailed results provided above 4 phi. Sediment described as 'Sand' prior to analysis; described as 'Sand' using the Folk triangle.

Laboratory – LB1321

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this module.
RT30 (invertebrates) – Not participating in this module.
RT31 (fish) – Not participating in this module.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Four taxonomic differences (*Hesionura elongata, Lamellaria perspicua, Spisula solida* and *Pseudomystides limbata*). Four individuals not extracted from the residue, including one previously unpicked taxon (*Scalibregma inflatum*). Count variance of two individuals. Bray-Curtis similarity index of 98.12%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
Two taxonomic differences (*Syllis* sp. and *Pseudomystides limbata*). Two additional taxa found within the extracted fauna (*Pariambus typicus* and *Pseudomystides limbata*). Two individuals not extracted from the residue, including one previously unpicked taxon (*Syllis armillaris*). Count variance of one individual. Bray-Curtis similarity index of 97.92%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, following Remedial Action ('Poor' original flag).
Seven taxonomic differences (*Ophelia borealis, Tanaissus danica, Spisula solida* juv., *Retusa umbilicata, Sphaerosyllis taylori, Sphaerodoropsis minuta* and *Questa* sp.). Sixty individuals not extracted from the residue, including three previously unpicked taxa (*Nebalia* sp. *Exogone naidina* (epitoke) and *Brachystomia* sp.). Count variance of one individual. Bray-Curtis similarity index of 87.52%. No biomass data supplied. Remedial action (review taxonomic errors

and reprocess residues for associated samples; provide additional sample for audit) audit completed 15/02/08.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1322

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this module.
RT30 (invertebrates) – Not participating in this module.
RT31 (fish) – Not participating in this module.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Two individuals not extracted from the residue. Bray-Curtis similarity index of 96.97%. Biomass on average 18.46% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Paradoneis lyra*). Three individuals not extracted from the residue, including two previously unpicked taxa (*Tapes* sp. juv. and Arenicoliidae juv.). Count variance of four individuals. Bray-Curtis similarity index of 98.68%. Biomass on average 6.55% lighter than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Two individuals not extracted from the residue, including one previously unpicked taxon (*Mysella bidentata*). Two additional taxa found within the extracted fauna (*Sabellaria spinulosa* and *Autolytus* sp.). Count variance of one individual. Bray-Curtis similarity index of 97.46%. Biomass on average 4.83% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1323

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this exercise.
RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – Multi-data:
LB23a - Three specific differences. Number of AQC identifications in Low group.
LB23b - One generic and three specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of thirteen individuals. Bray-Curtis similarity index of 97.07%. No biomass data supplied.
OS33 – NMBAQCS sample flag – Pass, 'Good'.
One vial contained a mixture of species (*Tubificoides swirencoides* and *Tubificoides pseudogaster* agg.). All individuals extracted from the residue. Count variance of thirteen individuals. Bray-Curtis similarity index of 99.55%. No biomass data supplied.
OS34 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1324

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this module.
RT30 (invertebrates) – Not participating in this module.
RT31 (fish) – Not participating in this module.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
Fauna supplied not fully separated into taxon vials. One additional taxon found within the extracted fauna (*Tubificoides amplivasatus*). One individual not extracted from the residue (*Melinna palmata*). Count variance of four individuals. Bray-Curtis similarity index of 96.61%. Biomass data supplied to 3 decimal places, not 4 as requested. Biomass on average 21.39% heavier than Unicomarine Ltd.
OS33 – NMBAQCS sample flag – Pass, 'Acceptable'.
Two taxonomic differences (Enchytraeidae and *Cyathura carinata*). One additional taxon found within the extracted fauna (Enchytraeidae). All individuals extracted from the residue. Bray-Curtis similarity index of 90.20%. Biomass data supplied to 3 decimal places, not 4 as requested. Biomass on average 13.02% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, following Remedial Action ('Bad' original flag).
Three vials included mixtures of species. All individuals extracted from the residue. Count variance of sixty individuals, due to a transcription error. Bray-Curtis similarity index of 80.00%. Biomass data supplied to 3 decimal places, not 4 as requested. Biomass on average 34.47% heavier than Unicomarine Ltd. Remedial action (review enumeration/transcription procedures) completed 22/10/07.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1325

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this exercise.
RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – Multi-data:
LB25a - Nine generic and ten specific differences. Number of AQC identifications in High group.
LB25b - Four generic and five specific differences. Number of AQC identifications in Mid group.
LB25c - Seven generic and nine specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Seven individuals not extracted from the residue, including one previously unpicked taxon (*Sabellaria spinulosa*). Count variance of ten individuals. Bray-Curtis similarity index of 99.47%. Biomass on average 44.39% heavier than Unicomarine Ltd, primarily due to the differing weights for *Lagis koreni*.
OS33 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 12.50% heavier than Unicomarine Ltd.
OS34 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Edwardsia claparedii*). Eleven individuals not extracted from the residue, including one previously unpicked taxon (*Chamelea striatula* juv.). Bray-Curtis similarity index of 98.51%. Biomass on average 21.47% heavier than Unicomarine Ltd.

Particle Size (Quality Control Module with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

Laboratory – LB1326

Macrobenthos (Training Module)

MB14 – Estuarine sample. Not participating in this module.

Ring Test (Training Module)

RT29 (invertebrates) – Not participating in this exercise.
RT30 (invertebrates) – Not participating in this exercise.
RT31 (fish) – One generic and five specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Module)

LR11 – Not participating in this module.

Own Sample (Quality Control Module with Pass/Fail NMBAQC Standards)

OS32 – Not participating in this module.
OS33 – Not participating in this module.
OS34 – Not participating in this module.

Particle Size (Quality Control Exercise with Pass/Fail NMBAQC Standards)

PS28 – Not participating in this module.
PS29 – Not participating in this module.

7. Conclusions and Recommendations

A number of observations may be made from the results of the exercises described above. The following is a summary of the major points of importance.

1. Laboratories should endeavour to report their results within the requested time; this would greatly facilitate the analysis of results and effective feedback. Participating laboratories must give adequate priority to the NMBAQC Scheme components, ensure that they are aware of, and adhere to, the component deadlines circulated at the beginning of each Scheme year.
2. All Scheme participants now use e-mail as their primary means of communication. Many of the interim results are now provided as secure PDF documents. E-mail capabilities must be made a prerequisite for participation in the Scheme. All primary correspondence for Scheme year thirteen will continue to be conducted via e-mail; hard copies of data sheets will be provided only where appropriate or specifically requested. The Scheme website should be fully utilised for reporting Scheme components.
3. Laboratories involved in UK NMMP data submission should endeavour to return data on **ALL** necessary components of the Scheme in the format requested. This will be required to allow the setting of performance "flags". Non-return of data will result in assignment of a "Fail" flag. For NMMP laboratories this deemed "Fail" for no submitted data is to be perceived as far worse than a participatory "Fail" flag.
4. A minority of participating laboratories have received 'deemed fail' flags as a result of not informing Unicomarine Ltd. of their intentions to abstain from particular exercises. The RT exercises are directly influenced by the number of participants, *i.e.* fewer participants enable less abundantly encountered taxa to be circulated. Some laboratories receive RT material but do not return data. Participating laboratories must only subscribe to components for which they intend to provide data; participating laboratories should ensure that any changes to the level of their participation in the Scheme is communicated to Unicomarine Ltd as soon as possible.
5. There were continued problems associated with the measurement of biomass for individual species. In this and the previous Scheme year several laboratories, despite using blotted wet weight biomass techniques, rendered some of their specimens too damaged to be re-identified. Some laboratories are still presenting data to five decimal places with six used for nominal weights. This produces spurious errors due to nominal weights one hundred times smaller than those reported at four decimal places. The initial processing of an NMMP sample should in no way compromise the effectiveness of an audit. Biomass procedures should not render the specimens unidentifiable; trials should be commissioned to derive the best protocol for the blotted weighing technique. Biomass must be reported to four decimal places with nominal weights recorded as 0.0001g. A standardised protocol and reporting format for UK NMMP analysis is to be developed via the NMBAQC Scheme.
6. The particle size exercises (PS) once again show differences in the results obtained by different analytical methods (*e.g.* laser, sieve) and also difference between equipment (e.g. Malvern Mastersizer X and Coulter LS230 lasers). PS data indicates that the variance between laser and sieve results is further emphasised by certain sediments characteristics. The overall range of these variances needs to be determined if combining data sets derived from differing methods. It is essential that particle size data should be presented with a clear description of the method of analysis used. PS exercises have highlighted the need for a prescriptive method for laser analysis (including equipment specifications) for the analysis of UK NMMP samples. Replicate samples analysed using the same broad technique resulted in highly variable summary statistics. A particle size standard operating procedure is to be developed through the NMBAQC Scheme for UK NMMP. The final draft will accommodate consultation and feedback from all significant parties.
7. The maintenance of a comprehensive reference collection has numerous benefits for improving identification ability, maintaining consistency of identification between surveys and access to growth series material. The Laboratory Reference exercise (LR) can be used as a means of verifying reference specimens. Laboratories are strongly recommended to implement and expand in-house reference collections of fauna. The inclusion of growth series material is extremely useful for certain faunal groups, *e.g.* identifying certain molluscs. All surveys should have an associated reference collection to enable ease of cross-checking or adopting future taxonomic developments.
8. Differences in the literature used for identification of invertebrates have been highlighted by the RT, MB and OS exercises. Unpublished keys from Scheme workshops, *etc.* could be posted on the

Scheme's website. The Scheme has produced a UK Standard Taxonomic Literature List database. Laboratories are encouraged to review the content and give details of additions wherever possible.

9. The Own Sample component has shown repeated taxonomic errors for some laboratories from the same UK NMMP sites over several years. Participating laboratories are encouraged to redress or resolve disagreements for taxonomic errors reported in their Own Samples even if their 'whole samples' achieve a 'pass' flag.

10. There are still some problems of individuals and taxa missed at the sorting stage of Own Sample analysis. This is an area that is often the major contributing factor in samples with 'fail' flags or low Bray-Curtis similarity indices. In general the MB14 samples were poorly sorted and all participants missed individuals (up to a quarter of the total individuals), and in the majority of instances taxa, in the residues. The situation was generally better for the OS samples where up to a maximum of 5 taxa were not extracted. In the worst instances 129 individuals were not picked from the residue and up to 20% of the total individuals remained in the residue. On average for the OS exercise 0.46 taxa were not extracted compared with 0.7, 0.52, 0.84, 1.73, 1.98, 2.04, 1.25, 1.48, 0.45 and 1.39 taxa from the last ten years of data, respectively. Enumeration of sorted individuals is generally good. When taxa and individuals are missed during the extraction of fauna from the sediment, laboratories should determine why certain taxa have not been extracted. This could be due to the taxon not being recognised as countable or due to problems with the effect of stains upon the specimens. There may also be a problem within certain taxonomic groups (*e.g.* crustaceans floating within sample or molluscs settled within the coarser sediment fractions). Additional training may be required and a review of existing extraction techniques and internal quality control measures may be beneficial.

11. In Scheme year seven a NMBAQCS Sorting Methods Questionnaire was circulated to all laboratories participating in macrobenthic analysis components (OS & MB). The responses showed that little or no consistency in extraction or identification protocols existed between participating laboratories. The results of this questionnaire have been reported separately to the participating laboratories (Worsfold & Hall, 2001). The report concluded that there is a need for standardisation of extraction protocols, in terms of which fauna are extracted/not extracted. Also a consensus needs to be reached for what constitutes 'countable' individuals and at which taxonomic level specific taxa should be identified. Protocols are to be developed to standardise the approach towards headless and partial specimens. This also has implications for comparing biomass estimations; certain laboratories pick headless portions of specimens from residues and assign them to the relevant taxa for combined biomass measurements. In Scheme year eight RT19 targeted 'Oligochaeta and similar fauna' and was complimented by a questionnaire regarding oligochaete identification. The ring test and accompanying questionnaire were reported to the participating laboratories (Hall & Worsfold, 2002) and reiterated the need for a standard identification protocol for UK NMMP samples. A proposal for a standard NMMP approach to oligochaete identification was included in the report. In Scheme year ten MB11 (artificial macrobenthic sample) showed that identical samples processed by differing laboratories can result in sample data that are interpreted as having little similarity due to inconsistency of extraction, enumeration and identification policy.

    In this year's MB14 exercise the exclusion policies of several participants led to the loss of three dominant taxa (*Elminius modestus, Balanus crenatus* and Nematoda) from their data submissions and consequently their raw MB14 data showed very poor similarity with that of other participants that fully processed the sample.

    Standard UK NMMP protocols are being developed through the NMBAQC Scheme, to standardise the faunal groups to be extracted from NMMP samples and reasonable levels of identification for all taxa likely to be encountered. Participating laboratories will be required to provide comments prior to the production of the final draft. MB samples are currently audited according to policy and details sheets submitted by the individual participants; however NMBAQC standard methods, once devised, should be applied and tested in the MB training module.

12. An improved learning structure to the Scheme through detailed individual exercise reports has been successfully implemented and was continued in this Scheme year. For the PS, LR, OS and MB exercises, detailed results have been forwarded to each participating laboratory as soon after the exercise deadlines as practicable. After each RT exercise a bulletin was circulated, reviewing the literature used and detailing the correct identification of the taxa circulated. Participants are encouraged to review their exercise reports and provide feedback concerning content and format wherever appropriate.

13. This year's fish ring test exercise (RT31) introduced a mechanism for the submission of multiple data sets from each participating laboratory to maximise data collated from the specimens distributed. This proved very successful and the option of multiple data submissions per participant laboratory will be extended to all future RT exercises.
14. The fish ring test (RT31) highlighted at least one instance of error due to the incorrect translation of an ambiguous common name. Fish teams are to incorporate scientific names in field data records and/or ensure that common to scientific name translations are correct prior to database submission.
15. The NMMP database should be managed with a clear emphasis upon data quality. A facility for indicating audited samples and flags should be available. In the event of an NMMP Own Sample failing to attain a 'pass' flag all replicates from the NMMP site should be upheld as 'failing' until remedial action upon the remaining replicates has attained a 'pass' flag. A facility for tracking and evaluating the remedial action applied to failing samples must be devised.

8. References

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Tables

Table 1. Results from the analysis of Macrobenthic sample MB14 by the participating laboratories.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	Number of Taxa				Number of Individuals				Not extracted			Individuals	Similarity	Taxonomic
LabCode	PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	New Taxa	Ind	%ind	Count Error	index	errors
LB1301	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1302	48	56	-8	14.3	1696	1675	21	1.2	0	4	0.2	25	89.53	12
LB1303	21	28	-7	25.0	184	252	-68	27.0	6	57	22.6	-11	79.82	3
LB1305	38	37	1	2.6	1213	1219	-6	0.5	0	6	0.5	0	97.01	8
LB1306	29	29	0	0.0	296	345	-49	14.2	1	52	15.1	3	91.41	1
LB1307	24	29	-5	17.2	168	222	-54	24.3	4	55	24.8	1	85.13	3
LB1309	37	39	-2	5.1	397	415	-18	4.3	2	16	3.9	-2	96.39	5

Key: PL - participating laboratory.
UM - Unicomarine Ltd.
"-" - No data. See Section 6, for details.

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB14.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1301	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1302	UM count	5	129	212	26	456	2	235	610	1675
	PL missed	0	1	1	0	0	0	1	1	4
	%missed	0.0	0.8	0.5	0.0	0.0	0.0	0.4	0.2	0.2
LB1303	UM count	4	81	21	0	1	0	94	51	252
	PL missed	3	12	14	0	0	0	16	12	57
	%missed	75.0	14.8	66.7	-	0.0	-	17.0	23.5	22.6
LB1305	UM count	0	45	51	1	350	1	97	674	1219
	PL missed	0	1	0	0	0	0	1	4	6
	%missed	-	2.2	0.0	0.0	0.0	0.0	1.0	0.6	0.5
LB1306	UM count	0	52	55	1	2	0	147	88	345
	PL missed	0	3	3	0	0	0	9	37	52
	%missed	-	5.8	5.5	0.0	0.0	-	6.1	42.0	15.1
LB1307	UM count	0	58	53	0	3	0	108	0	222
	PL missed	0	17	14	0	0	0	24	0	55
	%missed	-	29.3	26.4	-	0.0	-	22.2	-	24.8
LB1309	UM count	0	73	99	1	1	0	194	47	415
	PL missed	0	4	1	0	0	0	3	8	16
	%missed	-	5.5	1.0	0.0	0.0	-	1.5	17.0	3.9

Key: PL - participating laboratory.
UM - Unicomarine Ltd.
"-" - No data. See Section 6, for details.

Table 3. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in sample MB14. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1301	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1302	PL	0.0007	0.3046	0.0015	0.0054	0.0107	7.0587	8.8881	0.1115	16.3812
	UM	0.0001	0.2197	0.0004	0.0072	0.0077	7.6622	8.3409	0.0939	16.3321
	%diff.	85.7	27.9	73.3	-33.3	28.0	-8.5	6.2	15.8	0.2997
LB1303	PL	0.0223	0.7564	0.0026	-	0.1494	-	10.7045	0.9392	12.5744
	UM	0.0122	0.4401	0.0013	-	0.1192	-	12.3501	0.7079	13.6308
	%diff.	45.3	41.8	50.0	-	20.2	-	-15.4	24.6	-8.401196
LB1305	PL	-	0.12355	0.00326	0.00071	0.03571	0.00141	2.94574	0.09591	3.20629
	UM	-	0.1037	0.004	0.0004	0.0347	0.001	3.0228	0.0856	3.2522
	%diff.	-	16.1	-22.7	43.7	2.8	29.1	-2.6	10.7	-1.431873
LB1306	PL	-	0.06670	0.00258	0.00001	0.00026	-	2.55654	0.33687	2.96296
	UM	-	0.0622	0.0024	0.0001	0.0001	-	2.6204	0.319	3.0042
	%diff.	-	6.7	7.0	-900.0	61.5	-	-2.5	5.3	-1.391851
LB1307	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1309	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Section 6, for details.

Table 4. Variation in the faunal content of samples distributed as MB14.

Taxa*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total taxa
LB1301	-	-	-	-	-	-	-	-	-
LB1302	1	24	3	3	8	2	11	1	53
LB1303	1	17	3	0	1	0	4	0	26
LB1305	0	15	1	1	4	1	5	0	27
LB1306	0	12	2	1	2	0	4	0	21
LB1307	0	16	2	0	3	0	8	0	29
LB1309	0	14	1	1	1	0	8	0	25
Mean	0	16	2	1	3	1	7	0	30
Max	1	24	3	3	8	2	11	1	53
Min	0	12	1	0	1	0	4	0	21

*UM data used for all faunal groups (excludes sessile taxa & nematoda).

Individuals*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total Ind.
LB1301	-	-	-	-	-	-	-	-	-
LB1302	5	129	212	26	41	2	235	1	651
LB1303	4	81	21	0	1	0	94	0	201
LB1305	0	45	51	1	4	1	97	0	199
LB1306	0	52	55	1	2	0	147	0	257
LB1307	0	58	53	0	3	0	108	0	222
LB1309	0	73	99	1	1	0	194	0	368
Mean	2	73	82	5	9	1	146	0	316
Max	5	129	212	26	41	2	235	1	651
Min	0	45	21	0	1	0	94	0	199

*UM data used for all faunal groups (excludes sessile taxa & nematoda).

Table 5. Results from the analysis of Own Samples (OS32 to OS34) supplied by the participating laboratories and re-analysis by Unicomarine Ltd.

1		2	3	4	5	6	7	8	9	10	11	12	13	14	15	
		Number of Taxa				Number of Individuals				Not extracted			Count	Similarity	Taxonomic	
LabCode		PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	NewTaxa	Ind	%ind	Error	index	Errors	Note
LB1301	OS32	66	68	-2	2.9	151	165	-14	8.5	2	11	6.7	-3	96.07	0	External audit (completed 16/05/08)
LB1301	OS33	7	7	0	0.0	22	22	0	0.0	0	0	0.0	0	100.00	0	External audit (completed 16/05/08)
LB1301	OS34	2	2	0	0.0	1	1	0	0.0	0	0	0.0	0	100.00	0	External audit (completed 16/05/08)
LB1302	OS32	150	151	-1	0.7	6605	6590	15	0.2	1	21	0.3	36	99.59	1	External audit (completed 16/05/08)
LB1302	OS33	77	77	0	0.0	962	968	-6	0.6	0	9	0.9	3	99.28	1	External audit (completed 16/05/08)
LB1302	OS34	41	41	0	0.0	121	121	0	0.0	0	0	0.0	0	100.00	0	External audit (completed 16/05/08)
LB1303	OS32	9	9	0	0.0	25	26	-1	3.8	0	1	3.8	0	98.04	0	-
LB1303	OS33	19	20	-1	5.0	144	148	-4	2.7	1	4	2.7	0	98.63	0	-
LB1303	OS34	6	7	-1	14.3	12	15	-3	20.0	1	3	20.0	0	88.89	0	Remedial Action completed 22/08/07.
LB1304	OS32	54	53	1	1.9	138	135	3	2.2	0	0	0.0	3	98.17	1	-
LB1304	OS33	133	136	-3	2.2	1732	1706	26	1.5	1	8	0.5	34	96.66	11	-
LB1304	OS34	42	41	1	2.4	100	100	0	0.0	0	0	0.0	0	99.01	1	0.5-1mm residue unpreserved; >1mm audit only
LB1305	OS32	36	37	-1	2.7	115	118	-3	2.5	0	1	0.8	-2	90.13	8	Biomass data to 5 dp
LB1305	OS33	40	39	1	2.5	260	261	-1	0.4	0	0	0.0	-1	85.99	2	Biomass data to 5 dp; Remedial action completed 04/03/08.
LB1305	OS34	25	26	-1	3.8	88	94	-6	6.4	1	7	7.4	1	90.11	4	Biomass data to 5 dp
LB1306	OS32	66	70	-4	5.7	1142	1143	-1	0.1	1	13	1.1	12	96.11	6	-
LB1306	OS33	39	39	0	0.0	345	355	-10	2.8	0	9	2.5	-1	98.59	0	Biomass to 5 dp
LB1306	OS34	68	69	-1	1.4	308	308	0	0.0	1	3	1.0	3	96.92	4	-
LB1307	OS32	13	13	0	0.0	34	34	0	0.0	0	0	0.0	0	100.00	0	No biomass data
LB1307	OS33	39	40	-1	2.5	80	80	0	0.0	0	0	0.0	0	90.00	2	No biomass data
LB1307	OS34	5	5	0	0.0	5	5	0	0.0	0	0	0.0	0	80.00	1	No biomass data; Remedial action completed 10/08/07.
LB1308	OS32	90	85	5	5.6	510	501	9	1.8	0	0	0.0	9	96.34	5	No biomass data; Taxa not split
LB1308	OS33	55	55	0	0.0	114	112	2	1.8	0	1	0.9	3	94.69	2	No biomass data; Taxa not split
LB1308	OS34	64	63	1	1.6	200	182	18	9.0	0	0	0.0	18	93.19	3	No biomass data; Taxa not split
LB1309	OS32	12	12	0	0.0	1175	1190	-15	1.3	0	0	0.0	-15	99.37	0	No biomass data
LB1309	OS33	82	87	-5	5.7	165	176	-11	6.3	3	10	5.7	-1	84.04	15	No biomass data; Remedial action completed 29/06/07.
LB1309	OS34	37	37	0	0.0	61	62	-1	1.6	0	1	1.6	0	94.66	3	No biomass data
LB1310	OS32	62	62	0	0.0	2233	2238	-5	0.2	0	8	0.4	3	99.49	1	External audit (completed 16/05/08)
LB1310	OS33	19	19	0	0.0	1246	1243	3	0.2	0	3	0.2	6	99.88	0	External audit (completed 16/05/08)
LB1310	OS34	52	52	0	0.0	726	716	10	1.4	0	0	0.0	10	98.91	0	External audit (completed 16/05/08)
LB1311	OS32	9	9	0	0.0	14	14	0	0.0	0	0	0.0	0	92.86	1	-
LB1311	OS33	28	28	0	0.0	141	141	0	0.0	0	0	0.0	0	100.00	0	-
LB1311	OS34	19	19	0	0.0	99	99	0	0.0	0	0	0.0	0	97.98	1	-
LB1312	OS32	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1312	OS33	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1312	OS34	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1313	OS32	4	4	0	0.0	69	68	1	1.4	0	0	0.0	1	97.81	1	Biomass data to 3 dp
LB1313	OS33	9	9	0	0.0	468	447	21	4.5	0	0	0.0	21	97.27	0	Biomass data to 3 dp
LB1313	OS34	8	8	0	0.0	142	143	-1	0.7	0	0	0.0	-1	98.25	1	Biomass data to 3 dp

Table 5. Results from the analysis of Own Samples (OS32 to OS34) supplied by the participating laboratories and re-analysis by Unicomarine Ltd.

1		2	3	4	5	6	7	8	9	10	11	12	13	14	15	
		Number of Taxa				Number of Individuals				Not extracted			Count	Similarity	Taxonomic	
LabCode		PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	NewTaxa	Ind	%ind	Error	index	Errors	Note
LB1314	OS32	23	23	0	0.0	747	747	0	0.0	0	0	0.0	0	99.73	0	External audit (completed 16/05/08)
LB1314	OS33	13	13	0	0.0	117	118	-1	0.8	0	1	0.8	0	99.59	0	External audit (completed 16/05/08)
LB1314	OS34	92	92	0	0.0	206	206	0	0.0	0	0	0.0	0	100.00	0	External audit (completed 16/05/08)
LB1315	OS32	32	32	0	0.0	464	458	6	1.3	0	2	0.4	8	97.18	2	-
LB1315	OS33	65	65	0	0.0	816	817	-1	0.1	0	3	0.4	2	96.88	5	-
LB1315	OS34	15	15	0	0.0	424	414	10	2.4	0	2	0.5	12	98.57	2	-
LB1316	OS32	19	19	0	0.0	1574	1581	-7	0.4	0	21	1.3	14	99.37	3	-
LB1316	OS33	20	20	0	0.0	653	652	1	0.2	0	2	0.3	3	98.70	2	-
LB1316	OS34	12	12	0	0.0	371	377	-6	1.6	0	15	4.0	9	98.40	0	-
LB1317	OS32	54	53	1	1.9	141	140	1	0.7	0	1	0.7	2	97.51	2	-
LB1317	OS33	20	20	0	0.0	42	42	0	0.0	0	0	0.0	0	100.00	0	-
LB1317	OS34	25	26	-1	3.8	60	60	0	0.0	1	1	1.7	1	96.67	0	-
LB1318	OS32	3	5	-2	40.0	507	528	-21	4.0	2	22	4.2	1	97.88	0	No biomass data
LB1318	OS33	31	33	-2	6.1	114	130	-16	12.3	2	16	12.3	0	93.44	0	No biomass data
LB1318	OS34	23	29	-6	20.7	1043	1164	-121	10.4	5	129	11.1	8	93.84	1	No biomass data
LB1320	OS32	52	52	0	0.0	166	173	-7	4.0	0	7	4.0	0	97.49	1	No biomass data; some bivalves used for AFDW
LB1320	OS33	3	3	0	0.0	10	10	0	0.0	0	0	0.0	0	100.00	0	No biomass data
LB1320	OS34	18	18	0	0.0	74	74	0	0.0	0	0	0.0	0	100.00	0	No biomass data; some bivalves used for AFDW
LB1321	OS32	73	73	0	0.0	425	427	-2	0.5	1	4	0.9	2	98.12	4	No biomass data
LB1321	OS33	52	55	-3	5.5	167	170	-3	1.8	1	2	1.2	-1	97.92	2	No biomass data
LB1321	OS34	64	67	-3	4.5	327	386	-59	15.3	3	60	15.5	1	87.52	7	No biomass data; Remedial action completed 15/02/08.
LB1322	OS32	12	12	0	0.0	31	33	-2	6.1	0	2	6.1	0	96.97	0	-
LB1322	OS33	47	49	-2	4.1	341	340	1	0.3	2	3	0.9	4	98.68	1	-
LB1322	OS34	22	25	-3	12.0	97	100	-3	3.0	1	2	2.0	-1	97.46	0	-
LB1323	OS32	12	12	0	0.0	215	228	-13	5.7	0	0	0.0	-13	97.07	0	No biomass data
LB1323	OS33	20	20	0	0.0	2549	2536	13	0.5	0	0	0.0	13	99.55	0	No biomass data
LB1323	OS34	6	6	0	0.0	9	9	0	0.0	0	0	0.0	0	100.00	0	No biomass data
LB1324	OS32	18	17	1	5.6	189	194	-5	2.6	0	1	0.5	-4	96.61	0	Biomass data to 3 dp; no data sheets; fauna not fully split
LB1324	OS33	9	10	-1	10.0	102	102	0	0.0	0	0	0.0	0	90.20	2	Biomass data to 3 dp; no data sheets
LB1324	OS34	12	12	0	0.0	135	195	-60	30.8	0	0	0.0	-60	80.00	0	Biomass data to 3 dp; no data sheets; Remedial action completed 22/10/07.
LB1325	OS32	21	22	-1	4.5	1403	1400	3	0.2	1	7	0.5	10	99.47	0	-
LB1325	OS33	5	5	0	0.0	15	15	0	0.0	0	0	0.0	0	100.00	0	-
LB1325	OS34	34	35	-1	2.9	564	575	-11	1.9	1	11	1.9	0	98.51	1	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See section 6, for details.

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS32-34).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1301	AE count	2	65	-	-	18	7	31	42	165
OS32	UM missed	0	11	-	-	0	0	0	0	11
	%missed	0.0	16.9	-	-	0.0	0.0	0.0	0.0	6.7
LB1301	AE count	-	6	-	-	1	-	-	-	7
OS33	UM missed	-	0	-	-	0	-	-	-	0
	%missed	-	0.0	-	-	0.0	-	-	-	0.0
LB1301	AE count	-	-	-	-	1	-	-	-	1
OS34	UM missed	-	-	-	-	0	-	-	-	0
	%missed	-	-	-	-	0.0	-	-	-	0.0
LB1302	AE count	5	828	1010	13	3656	64	472	542	6590
OS32	UM missed	0	8	4	0	2	0	4	3	21
	%missed	0.0	1.0	0.4	0.0	0.1	0.0	0.8	0.6	0.3
LB1302	AE count	6	529	5	1	216	-	162	49	968
OS33	UM missed	0	1	0	0	0	-	8	0	9
	%missed	0.0	0.2	0.0	0.0	0.0	-	4.9	0.0	0.9
LB1302	AE count	-	25	1	-	24	43	28	-	121
OS34	UM missed	-	0	0	-	0	0	0	-	0
	%missed	-	0.0	0.0	-	0.0	0.0	0.0	-	0.0
LB1303	UM count	-	10	-	-	-	-	16	-	26
OS32	PL missed	-	0	-	-	-	-	1	-	1
	%missed	-	0.0	-	-	-	-	6.3	-	3.8
LB1303	UM count	-	16	-	-	-	106	23	3	148
OS33	PL missed	-	0	-	-	-	2	2	0	4
	%missed	-	0.0	-	-	-	1.9	8.7	0.0	2.7
LB1303	UM count	-	4	-	-	8	1	1	1	15
OS34	PL missed	-	1	-	-	1	0	1	0	3
	%missed	-	25.0	-	-	12.5	0.0	100.0	0.0	20.0
LB1304	UM count	6	63	-	-	17	13	34	2	135
OS32	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1304	UM count	53	396	4	19	158	65	847	164	1706
OS33	PL missed	1	0	0	1	0	0	0	6	8
	%missed	1.9	0.0	0.0	5.3	0.0	0.0	0.0	3.7	0.5
LB1304	UM count	-	73	-	-	15	3	6	3	100
OS34	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1305	UM count	5	47	-	-	19	18	28	1	118
OS32	PL missed	0	0	-	-	1	0	0	0	1
	%missed	0.0	0.0	-	-	5.3	0.0	0.0	0.0	0.8
LB1305	UM count	6	126	-	-	36	1	89	3	261
OS33	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1305	UM count	-	10	-	-	13	40	29	2	94
OS34	PL missed	-	1	-	-	0	1	5	0	7
	%missed	-	10.0	-	-	0.0	2.5	17.2	0.0	7.4
LB1306	UM count	7	361	-	-	61	32	674	8	1143
OS32	PL missed	0	0	-	-	1	0	11	1	13
	%missed	0.0	0.0	-	-	1.6	0.0	1.6	12.5	1.1
LB1306	UM count	4	92	24	-	1	1	215	18	355
OS33	PL missed	0	0	0	-	0	0	9	0	9
	%missed	0.0	0.0	0.0	-	0.0	0.0	4.2	0.0	2.5
LB1306	UM count	7	159	-	-	60	18	54	9	307
OS34	PL missed	0	1	-	-	2	0	0	0	3
	%missed	0.0	0.6	-	-	3.3	0.0	0.0	0.0	1.0

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS32-34).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1307	UM count	-	12	-	-	14	2	6	-	34
OS32	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1307	UM count	5	16	-	-	34	8	16	1	80
OS33	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1307	UM count	-	-	-	-	-	-	-	-	0
OS34	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1308	UM count	-	-	-	-	-	-	-	-	0
OS32	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1308	UM count	-	-	-	-	-	-	-	-	0
OS33	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1308	UM count	-	-	-	-	-	-	-	-	0
OS34	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1309	UM count	-	1183	-	-	4	-	1	2	1190
OS32	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1309	UM count	2	62	-	2	16	9	72	13	176
OS33	PL missed	0	3	-	0	1	1	5	0	10
	%missed	0.0	4.8	-	0.0	6.3	11.1	6.9	0.0	5.7
LB1309	UM count	1	22	-	-	9	3	23	4	62
OS34	PL missed	0	1	-	-	0	0	0	0	1
	%missed	0.0	4.5	-	-	0.0	0.0	0.0	0.0	1.6
LB1310	AE count	20	1720	115	1	190	-	10	182	2238
OS32	UM missed	0	3	0	0	2	-	0	3	8
	%missed	0.0	0.2	0.0	0.0	1.1	-	0.0	1.6	0.4
LB1310	AE count	-	314	825	-	77	-	9	18	1243
OS33	UM missed	-	0	3	-	0	-	0	0	3
	%missed	-	0.0	0.4	-	0.0	-	0.0	0.0	0.2
LB1310	AE count	1	362	125	-	8	-	11	209	716
OS34	UM missed	0	0	0	-	0	-	0	0	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1311	UM count	-	7	-	-	1	2	4	-	14
OS32	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1311	UM count	-	41	-	-	21	5	71	3	141
OS33	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1311	UM count	-	27	-	-	18	3	51	-	99
OS34	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1312	UM count	-	-	-	-	-	-	-	-	0
OS32	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1312	UM count	-	-	-	-	-	-	-	-	0
OS33	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1312	UM count	-	-	-	-	-	-	-	-	0
OS34	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS32-34).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1313	UM count	-	-	1	-	68	-	-	-	69
OS32	PL missed	-	-	0	-	0	-	-	-	0
	%missed	-	-	0.0	-	0.0	-	-	-	0.0
LB1313	UM count	-	100	-	-	5	-	342	-	447
OS33	PL missed	-	0	-	-	0	-	0	-	0
	%missed	-	0.0	-	-	0.0	-	0.0	-	0.0
LB1313	UM count	-	24	117	-	2	-	-	-	143
OS34	PL missed	-	0	0	-	0	-	-	-	0
	%missed	-	0.0	0.0	-	0.0	-	-	-	0.0
LB1314	AE count	-	677	26	-	19	-	23	2	747
OS32	UM missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1314	AE count	-	43	6	-	2	-	1	66	118
OS33	UM missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1314	AE count	5	105	-	-	18	18	41	19	206
OS34	UM missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1315	UM count	-	335	23	-	29	2	69	-	458
OS32	PL missed	-	0	0	-	0	0	2	-	2
	%missed	-	0.0	0.0	-	0.0	0.0	2.9	-	0.4
LB1315	UM count	-	564	25	1	62	1	54	110	817
OS33	PL missed	-	1	0	0	0	0	2	0	3
	%missed	-	0.2	0.0	0.0	0.0	0.0	3.7	0.0	0.4
LB1315	UM count	-	239	86	-	27	-	60	2	414
OS34	PL missed	-	0	1	-	0	-	1	0	2
	%missed	-	0.0	1.2	-	0.0	-	1.7	0.0	0.5
LB1316	UM count	-	1326	45	-	202	-	5	3	1581
OS32	PL missed	-	20	1	-	0	-	0	0	21
	%missed	-	1.5	2.2	-	0.0	-	0.0	0.0	1.3
LB1316	UM count	-	504	76	-	41	-	12	17	650
OS33	PL missed	-	2	0	-	0	-	0	0	2
	%missed	-	0.4	0.0	-	0.0	-	0.0	0.0	0.3
LB1316	UM count	-	126	60	-	135	-	56	-	377
OS34	PL missed	-	8	1	-	6	-	0	-	15
	%missed	-	6.3	1.7	-	4.4	-	0.0	-	4.0
LB1317	UM count	-	88	-	-	3	8	32	9	140
OS32	PL missed	-	0	-	-	0	1	0	0	1
	%missed	-	0.0	-	-	0.0	12.5	0.0	0.0	0.7
LB1317	UM count	1	13	-	-	5	3	20	-	42
OS33	PL missed	0	0	-	-	0	0	0	-	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1317	UM count	-	34	-	-	6	13	4	3	60
OS34	PL missed	-	0	-	-	0	0	1	0	1
	%missed	-	0.0	-	-	0.0	0.0	25.0	0.0	1.7
LB1318	UM count	-	267	-	-	1	-	5	255	528
OS32	PL missed	-	3	-	-	1	-	5	13	22
	%missed	-	1.1	-	-	100.0	-	100.0	5.1	4.2
LB1318	UM count	1	72	-	-	1	10	37	9	130
OS33	PL missed	0	5	-	-	0	0	11	0	16
	%missed	0.0	6.9	-	-	0.0	0.0	29.7	0.0	12.3
LB1318	UM count	9	749	-	-	75	-	275	56	1164
OS34	PL missed	0	23	-	-	29	-	66	11	129
	%missed	0.0	3.1	-	-	38.7	-	24.0	19.6	11.1

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS32-34).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1320	UM count	16	53	-	-	69	7	20	8	173
OS32	PL missed	0	0	-	-	0	0	7	0	7
	%missed	0.0	0.0	-	-	0.0	0.0	35.0	0.0	4.0
LB1320	UM count	-	10	-	-	-	-	-	-	10
OS33	PL missed	-	0	-	-	-	-	-	-	0
	%missed	-	0.0	-	-	-	-	-	-	0.0
LB1320	UM count	1	60	-	-	-	8	5	-	74
OS34	PL missed	0	0	-	-	-	0	0	-	0
	%missed	0.0	0.0	-	-	-	0.0	0.0	-	0.0
LB1321	UM count	4	168	24	-	41	44	46	100	427
OS32	PL missed	0	1	0	-	0	0	3	0	4
	%missed	0.0	0.6	0.0	-	0.0	0.0	6.5	0.0	0.9
LB1321	UM count	9	102	8	-	21	7	13	10	170
OS33	PL missed	0	2	0	-	0	0	0	0	2
	%missed	0.0	2.0	0.0	-	0.0	0.0	0.0	0.0	1.2
LB1321	UM count	14	118	2	-	24	82	129	17	386
OS34	PL missed	3	7	0	-	1	4	37	8	60
	%missed	21.4	5.9	0.0	-	4.2	4.9	28.7	47.1	15.5
LB1322	UM count	-	16	-	-	10	-	7	-	33
OS32	PL missed	-	0	-	-	0	-	2	-	2
	%missed	-	0.0	-	-	0.0	-	28.6	-	6.1
LB1322	UM count	3	118	-	-	208	5	5	1	340
OS33	PL missed	0	2	-	-	0	0	1	0	3
	%missed	0.0	1.7	-	-	0.0	0.0	20.0	0.0	0.9
LB1322	UM count	-	24	-	-	60	4	10	2	100
OS34	PL missed	-	0	-	-	0	0	2	0	2
	%missed	-	0.0	-	-	0.0	0.0	20.0	0.0	2.0
LB1323	UM count	-	91	132	-	3	-	2	-	228
OS32	PL missed	-	0	0	-	0	-	0	-	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1323	UM count	-	2183	315	-	-	-	3	35	2536
OS33	PL missed	-	0	0	-	-	-	0	0	0
	%missed	-	0.0	0.0	-	-	-	0.0	0.0	0.0
LB1323	UM count	-	8	-	-	1	-	-	-	9
OS34	PL missed	-	0	-	-	0	-	-	-	0
	%missed	-	0.0	-	-	0.0	-	-	-	0.0
LB1324	UM count	-	175	12	-	5	-	1	1	194
OS32	PL missed	-	1	0	-	0	-	0	0	1
	%missed	-	0.6	0.0	-	0.0	-	0.0	0.0	0.5
LB1324	UM count	1	44	4	-	9	-	44	-	102
OS33	PL missed	0	0	0	-	0	-	0	-	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1324	UM count	2	47	117	-	17	-	12	-	195
OS34	PL missed	0	0	0	-	0	-	0	-	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1325	UM count	-	975	1	-	2	1	421	-	1400
OS32	PL missed	-	6	0	-	0	0	1	-	7
	%missed	-	0.6	0.0	-	0.0	0.0	0.2	-	0.5
LB1325	UM count	-	4	-	-	11	-	-	-	15
OS33	PL missed	-	0	-	-	0	-	-	-	0
	%missed	-	0.0	-	-	0.0	-	-	-	0.0
LB1325	UM count	6	109	-	-	4	208	208	40	575
OS34	PL missed	0	0	-	-	0	0	10	1	11
	%missed	0.0	0.0	-	-	0.0	0.0	4.8	2.5	1.9

Key: PL - participating laboratory
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AE- Aquatic Environments (External Auditor)
"-" - No data. See Section 6, for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS32-OS34.

Sample OS32

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1301	UM	0.0261	0.2871	-	-	0.0444	0.3426	0.3591	0.0017	1.0610
	AE	0.0240	0.2637	-	-	0.0406	0.3536	0.3412	0.0015	1.0246
	%diff.	8.0	8.2	-	-	8.6	-3.2	5.0	11.8	3.4
LB1302	UM	0.0054	4.6361	0.2504	0.0047	0.9131	51.0528	6.8827	3.3810	67.1262
	AE	0.0052	4.5422	0.2342	0.0043	0.8389	51.6419	6.8277	3.4911	67.5855
	%diff.	3.7	2.0	6.5	8.5	8.1	-1.2	0.8	-3.3	-0.7
LB1303	PL	-	0.3559	-	-	-	-	1.6562	-	2.0121
	UM	-	0.4193	-	-	-	-	1.5847	-	2.0040
	%diff.	-	-17.8	-	-	-	-	4.3	-	0.4
LB1304	PL	0.2513	0.3268	-	-	0.1679	0.2857	0.4112	0.0009	1.4438
	UM	0.2126	0.2363	-	-	0.1328	0.1792	0.4026	0.0007	1.1642
	%diff.	15.4	27.7	-	-	20.9	37.3	2.1	22.2	19.4
LB1305	PL	0.01874	0.33304	-	-	0.01920	0.29600	0.93530	0.00213	1.60441
	UM	0.0159	0.2646	-	-	0.0149	0.2771	0.8779	0.0018	1.4522
	%diff.	15.2	20.6	-	-	22.4	6.4	6.1	15.5	9.5
LB1306	PL	0.0022	0.5251	-	-	0.0220	0.0783	3.1521	0.0003	3.7800
	UM	0.0036	0.7200	-	-	0.0152	0.1009	3.2353	0.0004	4.0754
	%diff.	-63.6	-37.1	-	-	30.9	-28.9	-2.6	-33.3	-7.8
LB1307	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1308	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1309	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1310	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1311	PL	-	0.0672	-	-	0.1348	0.0026	0.0037	-	0.2083
	UM	-	0.0674	-	-	0.1367	0.0023	0.0039	-	0.2103
	%diff.	-	-0.3	-	-	-1.4	11.5	-5.4	-	-1.0
LB1312	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1313	PL	-	-	0.000	-	0.050	-	-	-	0.050
	UM	-	-	0.0001	-	0.0330	-	-	-	0.0331
	%diff.	-	-	-	-	34.0	-	-	-	33.8
LB1314	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1315	PL	-	5.1124	0.0065	-	0.5828	0.0001	37.3258	-	43.0276
	UM	-	4.9374	0.0033	-	0.5836	0.0001	33.3523	-	38.8767
	%diff.	-	3.4	49.2	-	-0.1	0.0	10.6	-	9.6
LB1316	PL	-	1.3055	0.0107	-	1.0136	-	0.0020	0.0001	2.33190
	UM	-	1.0905	0.0067	-	0.6826	-	0.0014	0.0001	1.7813
	%diff.	-	16.5	37.4	-	32.7	-	30.0	0.0	23.6
LB1317	PL	-	0.4908	-	-	0.0014	0.0912	0.2374	0.3623	1.1831
	UM	-	0.3481	-	-	0.0009	0.0808	0.1984	0.3413	0.9695
	%diff.	-	29.1	-	-	35.7	11.4	16.4	5.8	18.1
LB1318	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1320	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1321	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1322	PL	-	0.2797	-	-	0.0136	-	0.0188	-	0.3121
	UM	-	0.2323	-	-	0.0086	-	0.0136	-	0.2545
	%diff.	-	16.9	-	-	36.8	-	27.7	-	18.5
LB1323	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1324	PL	-	1.076	0.002	-	0.026	-	0.007	0.000	1.111
	UM	-	0.8461	0.0016	-	0.0185	-	0.0071	0.0001	0.8734
	%diff.	-	21.4	20.0	-	28.8	-	-1.4	-	21.4
LB1325	PL	-	86.2874	0.0001	-	0.0021	0.0477	3.3536	-	89.6909
	UM	-	46.9774	0.0003	-	0.0024	0.0717	2.8280	-	49.8798
	%diff.	-	45.6	-200.0	-	-14.3	-50.3	15.7	-	44.4

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"-" - No data. See Section 6, for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS32-OS34.

Sample OS33

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1301	UM	-	0.0163	-	-	0.4334	-	-	-	0.4497
	AE	-	0.0146	-	-	0.4610	-	-	-	0.4756
	%diff.	-	10.4	-	-	-6.4	-	-	-	-5.8
LB1302	UM	0.0633	4.7546	0.0004	0.0001	0.0702	-	14.2145	0.7189	19.8220
	AE	0.0583	4.4856	0.0004	0.0001	0.0672	-	14.6468	0.6831	19.9415
	%diff.	7.9	5.7	0.0	0.0	4.3	-	-3.0	5.0	-0.6
LB1303	PL	-	0.3966	-	-	-	3.8237	1.7629	0.6882	6.6714
	UM	-	0.3568	-	-	-	3.7903	1.7842	0.6707	6.6020
	%diff.	-	10.0	-	-	-	0.9	-1.2	2.5	1.0
LB1304	PL	0.1821	0.4149	0.0002	0.0001	0.1487	0.3706	172.0352	0.0503	173.2021
	UM	0.1442	0.3577	0.0001	0.0001	0.1354	0.3403	165.3776	0.0370	166.3924
	%diff.	20.8	13.8	50.0	0.0	8.9	8.2	3.9	26.4	3.9
LB1305	PL	0.00341	0.33981	-	-	0.01605	0.00326	0.10814	0.00017	0.47084
	UM	0.0030	0.2886	-	-	0.0118	0.0032	0.0996	0.0001	0.4063
	%diff.	12.0	15.1	-	-	26.5	1.8	7.9	41.2	13.7
LB1306	PL	0.00476	0.42578	0.00181	-	0.00001	0.00015	0.04026	0.01658	0.48935
	UM	0.0031	0.3263	0.0012	-	0.0001	0.0001	0.2150	0.0161	0.5619
	%diff.	34.9	23.4	33.7	-	-900.0	33.3	-434.0	2.9	-14.8
LB1307	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1308	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1309	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1310	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1311	PL	-	0.0787	-	-	0.0065	0.0064	0.3929	0.0030	0.4875
	UM	-	0.0907	-	-	0.0094	0.0076	0.4198	0.0048	0.5323
	%diff.	-	-15.2	-	-	-44.6	-18.8	-6.8	-60.0	-9.2
LB1312	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1313	PL	-	0.423	-	-	0.035	-	1.776	-	2.234
	UM	-	0.3045	-	-	0.0255	-	1.8833	-	2.2133
	%diff.	-	28.0	-	-	27.1	-	-6.0	-	0.9
LB1314	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1315	PL	-	1.6140	0.0037	0.0001	0.1275	0.0001	12.6581	0.1357	14.5392
	UM	-	1.3121	0.0021	0.0003	0.1258	0.0001	12.4328	0.0881	13.9613
	%diff.	-	18.7	43.2	-200.0	1.3	0.0	1.8	35.1	4.0
LB1316	PL	-	0.1852	0.0167	-	0.3257	-	0.0116	0.0007	0.53990
	UM	-	0.8041	0.0110	-	0.1066	-	0.0100	0.0004	0.9321
	%diff.	-	-334.2	34.1	-	67.3	-	13.8	42.9	-72.6
LB1317	PL	0.0001	0.6980	-	-	0.0104	0.5087	2.4501	-	3.6673
	UM	0.0001	0.5526	-	-	0.0050	0.4177	2.5286	-	3.5040
	%diff.	0.0	20.8	-	-	51.9	17.9	-3.2	-	4.5
LB1318	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1320	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1321	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1322	PL	0.0247	0.4607	-	-	8.1541	0.0063	1.2885	0.0015	9.9358
	UM	0.0231	0.3943	-	-	8.9042	0.0052	1.2595	0.0001	10.5864
	%diff.	6.5	14.4	-	-	-9.2	17.5	2.3	93.3	-6.5
LB1323	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1324	PL	0.000	0.619	0.000	-	0.018	-	15.620	-	16.257
	UM	0.0001	0.4674	0.0002	-	0.0146	-	13.6573	-	14.1396
	%diff.	-	24.5	-	-	18.9	-	12.6	-	13.0
LB1325	PL	-	0.0018	-	-	0.0102	-	-	-	0.0120
	UM	-	0.0016	-	-	0.0089	-	-	-	0.0105
	%diff.	-	11.1	-	-	12.7	-	-	-	12.5

Key: PL - participating laboratory
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"-" - No data. See Section 6, for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS32-OS34.

		Sample OS34								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1301	UM	-	-	-	-	0.7373	-	-	-	0.7373
	AE	-	-	-	-	0.6888	-	-	-	0.6888
	%diff.	-	-	-	-	6.6	-	-	-	6.6
LB1302	UM	-	0.4890	0.0001	-	0.0044	0.3441	0.0288	-	0.8664
	AE	-	0.4568	0.0001	-	0.0043	0.3199	0.0299	-	0.8110
	%diff.	-	6.6	0.0	-	2.3	7.0	-3.8	-	6.4
LB1303	PL	-	0.3108	-	-	0.0418	0.3296	-	65.6581	66.3403
	UM	-	0.3140	-	-	0.0327	0.3273	-	68.7900	69.4640
	%diff.	-	-1.0	-	-	21.8	0.7	-	-4.8	-4.7
LB1304	PL	-	0.8891	-	-	0.0352	0.0239	0.2293	0.0008	1.1783
	UM	-	0.7678	-	-	0.0241	0.0233	0.2232	0.0004	1.0388
	%diff.	-	13.6	-	-	31.5	2.5	2.7	50.0	11.8
LB1305	PL	-	0.54620	-	-	0.17835	3.27305	4.67661	0.24874	8.92295
	UM	-	0.5128	-	-	0.1447	2.6148	4.4981	0.2113	7.9817
	%diff.	-	6.1	-	-	18.9	20.1	3.8	15.1	10.5
LB1306	PL	0.0017	0.9096	-	-	0.0365	0.1055	9.6704	0.22958	10.95328
	UM	0.0064	0.8557	-	-	0.0251	0.0899	9.3567	0.2058	10.5396
	%diff.	-276.5	5.9	-	-	31.2	14.8	3.2	10.4	3.8
LB1307	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1308	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1309	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1310	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1311	PL	-	0.0569	-	-	0.0223	0.0061	0.7246	-	0.8099
	UM	-	0.0587	-	-	0.0268	0.0060	0.7008	-	0.7923
	%diff.	-	-3.2	-	-	-20.2	1.6	3.3	-	2.2
LB1312	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1313	PL	-	0.084	0.014	-	0.000	-	-	-	0.098
	UM	-	0.0687	0.0084	-	0.0005	-	-	-	0.0776
	%diff.	-	18.2	40.0	-	-	-	-	-	20.8
LB1314	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1315	PL	-	0.4070	0.0065	-	0.0032	-	0.0502	0.0001	0.4670
	UM	-	0.3836	0.0040	-	0.0026	-	0.0503	0.0001	0.4406
	%diff.	-	5.7	38.5	-	18.8	-	-0.2	0.0	5.7
LB1316	PL	-	0.0580	0.0041	-	3.7072	-	-	-	3.76930
	UM	-	0.0301	0.0019	-	3.5659	-	-	-	3.5979
	%diff.	-	48.1	53.7	-	3.8	-	-	-	4.5
LB1317	PL	-	0.0852	-	-	0.0073	0.0693	0.1371	-	0.2989
	UM	-	0.0673	-	-	0.0030	0.0711	0.1293	-	0.2707
	%diff.	-	21.0	-	-	58.9	-2.6	5.7	-	9.4
LB1318	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1320	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1321	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1322	PL	-	0.7195	-	-	4.3059	0.2351	12.2123	0.0897	17.5625
	UM	-	0.6490	-	-	4.2956	0.2288	11.4552	0.0859	16.7145
	%diff.	-	9.8	-	-	0.2	2.7	6.2	4.2	4.8
LB1323	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1324	PL	0.000	1.043	0.023	-	0.041	-	1.907	-	3.014
	UM	0.0002	0.7765	0.0219	-	0.0326	-	1.1439	-	1.9751
	%diff.	-	25.6	4.8	-	20.5	-	40.0	-	34.5
LB1325	PL	0.0153	0.5812	-	-	0.0015	15.6613	0.5435	0.0668	16.8696
	UM	0.0184	0.5817	-	-	0.0019	11.9933	0.5643	0.0874	13.2470
	%diff.	-20.3	-0.1	-	-	-26.7	23.4	-3.8	-30.8	21.5

Key: PL - participating laboratory
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"-" - No data. See Section 6, for details.

Table 8. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS28.

PS28	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS28 - 42 - laser¹	94.12	6.91	6.96	1.99	0.03
PS28 - 43 - laser¹	94.25	6.91	6.97	1.99	0.04
PS28 - 44 - laser¹	95.17	6.88	6.95	1.94	0.06
PS28 - 45 - laser¹	95.00	6.90	6.96	1.96	0.05
PS28 - 46 - laser¹	94.86	6.90	6.96	1.96	0.05
PS28 - 47 - laser¹	95.65	6.92	6.99	1.94	0.06
PS28 - 48 - laser¹	94.76	6.89	6.96	1.96	0.05
PS28 - 35 - laser²	100	7.200	7.400	1.417	-0.562
PS28 - 36 - laser²	100	7.010	7.210	1.429	-0.616
PS28 - 37 - laser²	100	7.129	7.320	1.395	-0.614
PS28 - 38 - laser²	100	7.118	7.307	1.424	-0.588
PS28 - 39 - laser²	100	7.075	7.268	1.424	-0.598
PS28 - 40 - laser²	100	6.999	7.147	1.543	-0.441
PS28 - 41 - laser²	100	7.128	7.316	1.431	-0.583

Key: laser¹ = Malvern Mastersizer X (School of Geography, Plymouth University)
laser² = Coulter LS230 (Partrac)

Table 9. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS29.

PS29	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS29 - 42 - laser¹	1.40	1.77	1.75	0.62	-0.040
PS29 - 43 - laser¹	1.16	1.77	1.75	0.62	-0.060
PS29 - 44 - laser¹	1.22	1.77	1.76	0.62	-0.050
PS29 - 45 - laser¹	1.05	1.75	1.74	0.63	-0.050
PS29 - 46 - laser¹	1.15	1.76	1.74	0.63	-0.040
PS29 - 47 - laser¹	0.98	1.76	1.74	0.62	-0.040
PS29 - 48 - laser¹	1.02	1.75	1.73	0.63	-0.050
PS29 - 35 - laser²	0.054	1.65	1.61	0.70	0.191
PS29 - 36 - laser²	0.049	1.63	1.58	0.73	0.319
PS29 - 37 - laser²	0.961	1.63	1.62	0.75	-0.517
PS29 - 38 - laser²	0.045	1.66	1.64	0.67	0.075
PS29 - 39 - laser²	1.982	1.67	1.71	0.65	-1.618
PS29 - 40 - laser²	1.226	1.64	1.65	0.76	-0.701
PS29 - 41 - laser²	1.048	1.65	1.65	0.73	-0.693

Key: laser¹ = Malvern Mastersizer X (School of Geography, Plymouth University)
laser² = Coulter LS230 (Partrac)

Table 10. Summary of the particle size information received from participating laboratories and replicate analysis laboratories for the twenty-eighth particle size distribution - PS28.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB1301	-	-	-	-	-	-
LB1302	L	90.89	6.74	6.65	1.96	0.050
LB1303	L	89.58	6.44	6.11	1.70	-0.260
LB1304	L	95.17	7.02	6.91	1.73	0.070
LB1305	L	89.98	5.81	5.95	1.74	0.220
LB1306*	L*	89.58	6.44	6.11	1.70	-0.260
LB1307	L	82.03	6.07	6.16	3.13	-0.62
LB1308	L	96.12	7.00	6.82	1.4	-0.26
LB1314	L	88.57	6.58	5.20	1.91	0.120
LB1317	L	91.94	5.96	4.97	1.71	0.170
LB1320	DS	38.61	3.624	4.54	2.31	0.565

Key to metho L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette

L* - replicated data - not included in calculations
"-" - No data. See Section 6, for details.
Shaded cells - maximum and minimum values for each derived statistic.

Table 11. Summary of the particle size information received from participating laboratories and replicate analysis laboratories for the twenty-ninth particle size distribution - PS29.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB1301	-	-	-	-	-	-
LB1302	Air dry, DS	0	2.05	2.00	0.54	-0.180
LB1303	L	0.69	1.4	1.42	0.71	0.030
LB1305	WS, DS, FD, L	0.87	1.65	1.67	0.74	0.020
LB1306*	L	0.69	1.4	1.42	0.71	0.030
LB1307	L	4.72	1.99	1.26	0.81	0.16
LB1308	L	0.89	2.13	2.11	0.57	-0.09
LB1314	L	0.00	1.63	1.47	0.69	0.010
LB1317	L	1.76	1.61	1.62	0.73	0.030
LB1320	DS	0.20	2.08	2.03	0.65	-0.102

Key to metho L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette

L* - replicated data - not included in calculations
"-" - No data. See Section 6, for details.
Shaded cells - maximum and minimum values for each derived statistic.

Table 12. The identifications of the fauna made by participating laboratories for RT29. Names are given only where different from the AQC identification.

RT29	Taxon	LB1302	LB1303	LB1304	LB1305	LB1306	LB1307
RT2901	Ditrupa arietina	- -	[Diptrupa] -	- -	- -	- -	- -
RT2902	Leucon nasica	Iphinoe serrata	- -	- -	- -	- -	- -
RT2903	Facelina annulicornis	Ancula sp.	- auriculata	- bostoniensis	- -	Ancula gibbosa	Okenia elegans
RT2904	Corophium multisetosum	- -	- -	- -	- -	- -	- -
RT2905	Polyphysia crassa	- -	Lipobranchius jeffreysii	Lipobranchius jeffreysii	Lipobranchius jeffreysii	- -	Asclerocheilus intermedius
RT2906	Bittium reticulatum	- -	[Bitium] -	- -	- -	- -	Cerithiopsis barleii
RT2907	Paraonis fulgens	Levinsenia gracilis	- -	- -	- -	- -	- -
RT2908	Pariambus typicus	- -	- -	- -	- -	- -	- -
RT2909	Lumbrineris gracilis	- -	- -	- -	- -	[Lumbrinereis] -	Augeneria sp.
RT2910	Echinogammarus marinus	- -	[Chaetogammarus] -	- -	- -	[Chaetogammarus] -	[Chaetogammarus] -
RT2911	Littorina obtusata	- -	- -	- mariae	- -	- -	- -
RT2912	Abra tenuis	Scrobicularia plana	- -	- -	- -	- -	- -
RT2913	Chelura terebrans	- -	- [tenebrans]	- -	- -	[Chelurus] -	- -
RT2914	Prionospio dubia	- ehlersi	- -	- -	- -	- -	- -
RT2915	Rissoa guerinii	- [guerini]	- [guerini]	- [guerini]	- -	- membranacea	- -
RT2916	Abyssoninoe hibernica	Scolotoma impatients	- -	- -	- -	- -	- -
RT2917	Leptocheirus pilosus	- -	- -	- -	- -	- -	- -
RT2918	Fabulina fabula	- -	- -	- -	Moerella pygmaea	Angulus tenuis	- -
RT2919	Armandia cirrhosa	- -	Ophelina modesta	- -	- -	- -	- -
RT2920	Emarginula rosea	- -	- [conica]	- -	- -	- fissura	- fissura
RT2921	Gari tellinella	Abra sp. juv.	- -	- costulata	Mya truncata	- -	- -
RT2922	Aonides paucibranchiata	- -	- -	- -	- -	- -	- -
RT2923	Lumbrineriopsis paradoxa	- -	- -	- -	- -	- -	- -
RT2924	Limatula subauriculata	- sulcata	[Lima] -	- sulcata	- sulcata	- sulcata	- -
RT2925	Dexamine thea	- -	- -	- -	- -	- -	- -

RT29	Taxon	LB1309	LB1311	LB1312	LB1313	LB1316	LB1318
RT2901	Ditrupa arietina	- -	Pulsellum lofotense	- -	- -	Antalis entalis	- -
RT2902	Leucon nasica	- -	- -	- -	- -	- -	- -
RT2903	Facelina annulicornis	- -	Flabellina pedata	Polycera quadrilineata	- coronata	0 0	- -
RT2904	Corophium multisetosum	- -	- -	- -	- -	- -	- -
RT2905	Polyphysia crassa	Lipobranchius jeffreysii	[Polyphysa] -	Lipobranchius jeffreysi	Travisia forbesii	Commensodorum commensalis	- -
RT2906	Bittium reticulatum	- -	- -	- -	- -	[Bithium] -	- -
RT2907	Paraonis fulgens	- -	Levinsenia gracilis	Levinsenia gracilis	- -	Aricidea minuta	Aricidea catherinae
RT2908	Pariambus typicus	- -	- -	[Paraiambus] -	Parvipalpus capillaceous	- -	- -
RT2909	Lumbrineris gracilis	- -	[Lumbrinereis] latreilli	[Lumbrineries] -	- tetraura	Dasybranchus -	- -
RT2910	Echinogammarus marinus	- -	- -	[Chaetogammarus] -	[Chaetogammarus] -	Eulimnogammarus obtusatus	- -
RT2911	Littorina obtusata	- -	- -	- -	- -	- -	- -
RT2912	Abra tenuis	- -	- -	- -	Scrobicularia plana	- -	- -
RT2913	Chelura terebrans	- -	- -	- -	- [telebrans]	- -	- -
RT2914	Prionospio dubia	- -	[Prinospio] ehlersi	- steenstrupi	Minuspio multibranchiata	- -	- -
RT2915	Rissoa guerinii	- -	- -	- [guerini]	- [guerini]	- [guerini]	- -
RT2916	Abyssoninoe hibernica	- -	- -	Lumbrineries latreilli	Lumbrineris latreilli	Scolotema impatiens	- -
RT2917	Leptocheirus pilosus	- -	- -	- pectinatus	- -	- -	- -
RT2918	Fabulina fabula	- -	- -	Tellina pygmaea	Abra longicallus	Abra prismatica (juv.)	- -
RT2919	Armandia cirrhosa	- -	Ophelina acuminata	- -	Aricidea sp.	- -	- -
RT2920	Emarginula rosea	- -	- -	- [conica]	- fissura	- -	- -
RT2921	Gari tellinella	- -	- -	Donax vittatus	Abra prismatica	Abra nitida (juv.)	- -
RT2922	Aonides paucibranchiata	- -	Aricidea cerrutii	- -	Levensinia gracilis	- -	- -
RT2923	Lumbrineriopsis paradoxa	Drilonereis filum	- -	Lumbrineries latreilli	- -	- -	- -
RT2924	Limatula subauriculata	- -	- -	[Lima] -	- sulcata	[Lima (Limatula)] sulcata	- sulcata
RT2925	Dexamine thea	- -	- -	- -	- -	- -	- -

Table 13. The identifications of the fauna made by participating laboratories for RT30. Names are given only where different from the AQC identification.

RT30	Taxon	LB1302	LB1303	LB1304	LB1305	LB1306
RT3001	Chaetozone setosa	- [setosa agg.]	- -	- -	- -	- [setosa agg.]
RT3002	Chaetozone vivipara	Tharyx acutus (Type A)	- -	- -	- -	[Tharyx] -
RT3003	Aphelochaeta marioni	- -	- "A"	- A	- -	- -
RT3004	Monticellina sp.	- [heterochaeta]	- [dorsobranchialis]	- -	- [heterochaeta]	- [dorsobranchialis / heterochaeta]
RT3005	Caulleriella alata	- -	- -	- -	- -	- -
RT3006	Cirratulus cirratus	- -	- -	- -	- sp. juv.	- -
RT3007	Chaetozone zetlandica	- -	[Caulleriella] -	- -	- -	[Caulleriella] -
RT3008	Chaetozone christiei	- [christiei (Type C)]	- -	- -	- -	- [christei]
RT3009	Chaetozone gibber	- -	- -	- -	- -	- -
RT3010	Cirriformia tentaculata	- -	- -	- -	- -	- -
RT3011	Protocirrineris chrysoderma	- -	- -	- -	- -	- -
RT3012	Tharyx killariensis	- Type A	Aphelochaeta marioni	- -	- -	- -
RT3013	Chaetozone christiei	- [christiei (Type C)]	- -	- -	- -	- [christei]
RT3014	Aphelochaeta marioni	- [monilaris]	- -	- -	- A	- -
RT3015	Tharyx A	- -	Aphelochaeta "A"	- -	Chaetozone C	- -
RT3016	Chaetozone vivipara	- -	- -	- -	- christiei	[Tharyx] -
RT3017	Cirratulus caudatus	- -	- -	- -	- -	- -
RT3018	Tharyx A	Aphelochaeta Type A	Aphelochaeta "A"?	- -	- -	- -
RT3019	Protocirrineris chrysoderma	- -	- -	- -	- -	- -
RT3020	Cirriformia tentaculata	- -	- -	- -	- -	- -
RT3021	Monticellina sp.	- [annulosa]	Aphelochaeta marioni	- -	- [heterochaeta]	- [dorsodranchialis / heterochaeta]
RT3022	Chaetozone setosa	- [Type A]	- -	- -	- -	- [setosa agg.]
RT3023	Caulleriella alata	- -	Chaetozone gibber?	- -	- -	- -
RT3024	Chaetozone gibber	- -	- -	- -	- -	- -
RT3025	Tharyx killariensis	- -	- -	- -	- -	- -

RT30	Taxon	LB1308	LB1309	LB1312	LB1316	LB1318
RT3001	Chaetozone setosa	- -	- -	[Caulleriella] zetlandica	- [setosa agg. Type A]	- -
RT3002	Chaetozone vivipara	- -	- -	- setosa	Tharyx A	- -
RT3003	Aphelochaeta marioni	- -	[Aphaelochaeta] -	- -	- -	- -
RT3004	Monticellina sp.	- [cf. heterochaeta]	- [(heterochaeta)]	- [dorsobranchialis]	Aphelochaeta A	- [cf. heterochaeta]
RT3005	Caulleriella alata	- -	- -	- -	- -	- -
RT3006	Cirratulus cirratus	- -	- -	- A	- sp. juv.	- -
RT3007	Chaetozone zetlandica	- -	- -	- gibba	- sp.	- -
RT3008	Chaetozone christiei	- -	- [christei]	[Caulleriella] zetlandica	- setosa agg. Type C	- -
RT3009	Chaetozone gibber	- -	- -	- [gibba]	- -	- -
RT3010	Cirriformia tentaculata	- -	- -	- [tentaculuata]	- -	- -
RT3011	Protocirrineris chrysoderma	- -	- -	- -	Aphelochaeta A	- -
RT3012	Tharyx killariensis	Aphelochaeta A	- -	- A	Aphelochaeta marioni Type B	- -
RT3013	Chaetozone christiei	- -	- [christei]	- setosa	- [setosa agg. Type B]	- -
RT3014	Aphelochaeta marioni	- -	[Aphaelochaeta] -	- [B]	- -	- -
RT3015	Tharyx A	- -	Chaetozone christei	- -	- -	- [A (cf. acutus)]
RT3016	Chaetozone vivipara	- -	- -	[Tharyx] -	- -	- -
RT3017	Cirratulus caudatus	- -	- -	- -	- [caudatus??]	- -
RT3018	Tharyx A	- -	Chaetozone christei	- -	- -	- [A (cf. acutus)]
RT3019	Protocirrineris chrysoderma	- -	- -	- -	Cirriformia tentaculata	- -
RT3020	Cirriformia tentaculata	- -	- -	- [tentaculuata]	- -	- -
RT3021	Monticellina sp.	- [cf. heterochaeta]	- [(heterochaeta)]	- [dorsobranchialis]	- [cf. dorsobranchialis]	- [cf. heterochaeta]
RT3022	Chaetozone setosa	- -	- -	- -	- christiei	- -
RT3023	Caulleriella alata	- -	- -	- -	- -	- -
RT3024	Chaetozone gibber	- -	- -	- [gibba]	- -	- -
RT3025	Tharyx killariensis	- -	- -	- -	- -	- -

Table 14. The identifications of the fauna made by participating laboratories for RT31. Names are given only where different from the AQC identification.

RT31	Taxon	LB1302a	LB1303a	LB1303b	LB1305a
RT3101	Echiichthys vipera	- -	- -	- -	- -
RT3102	Dicentrarchus labrax	- -	- -	- -	- -
RT3103	Platichthys flesus	- -	- -	- -	- -
RT3104	Sprattus sprattus	- -	- [spratus]	- [spratus]	- -
RT3105	Gaidropsarus mediterraneus	- -	- -	- -	- -
RT3106	Mullus surmuletus	- -	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -	- -
RT3108	Limanda limanda	- -	- -	- -	- -
RT3109	Scyliorhinus canicula	- -	- -	- -	- -
RT3110	Trachurus trachurus	- -	- [trachus]	- [trachus]	- -
RT3111	Scomber scombrus	- -	- -	- -	- -
RT3112	Callionymus lyra	- -	- -	- -	- -
RT3113	Agonus cataphractus	- -	- -	- -	- -
RT3114	Trisopterus minutus	- -	- -	- luscus	- -
RT3115	Merlangius merlangus	- -	- -	- -	- -
RT3116	Raja montagui	- -	- clavata	- radiata	- brachyura
RT3117	Aspitrigla cuculus	- -	- -	- -	- -
RT3118	Eutrigla gurnardus	- -	- -	- -	- -
RT3119	Syngnathus rostellatus	- -	- -	- -	- -
RT3120	Ammodytes marinus	- -	- -	Hyperoplus immaculatus	- -
RT3121	Clupea harengus	- -	- -	- -	- -
RT3122	Osmerus eperlanus	- -	- -	- -	- -
RT3123	Arnoglossus laterna	- -	- -	- -	- -
RT3124	Lophius piscatorius	- -	- -	- -	- -
RT3125	Ammodytes tobianus	- -	Hyperoplus lanceolatus	Hyperoplus lanceolatus	- -

RT31	Taxon	LB1306a	LB1307a	LB1310a	LB1312a
RT3101	Echiichthys vipera	- -	- -	[Echilchthys] -	- -
RT3102	Dicentrarchus labrax	[Dicentrachus] -	- -	- -	- -
RT3103	Platichthys flesus	[Platichtys] -	Pleuronectes platessa	- -	- -
RT3104	Sprattus sprattus	- -	- -	- -	- -
RT3105	Gaidropsarus mediterraneus	- -	Ciliata mustela	- -	Ciliata mustela
RT3106	Mullus surmuletus	- -	- -	- barbatus	- -
RT3107	Zeus faber	- -	- -	- -	- -
RT3108	Limanda limanda	Microstomus kitt	- -	- -	- -
RT3109	Scyliorhinus canicula	- [caniculus]	- -	- -	- [caniculus]
RT3110	Trachurus trachurus	- -	- -	Pollachius pollachius	- -
RT3111	Scomber scombrus	- -	- -	- -	- [scomber]
RT3112	Callionymus lyra	- -	- -	- -	- -
RT3113	Agonus cataphractus	- -	- -	- -	- -
RT3114	Trisopterus minutus	- luscus	- -	- -	- luscens
RT3115	Merlangius merlangus	- -	- -	- -	- -
RT3116	Raja montagui	- -	Raja [Rostroraja] alba	- -	- ?
RT3117	Aspitrigla cuculus	- -	- -	- -	- -
RT3118	Eutrigla gurnardus	- -	- -	- -	- -
RT3119	Syngnathus rostellatus	- [rostellus]	- -	- -	- -
RT3120	Ammodytes marinus	- -	Hyperoplus lanceolatus	Hyperoplus immaculatus	- ?
RT3121	Clupea harengus	- -	- -	- -	- -
RT3122	Osmerus eperlanus	- -	- -	- -	- -
RT3123	Arnoglossus laterna	Lepidorhombus whiffiagonis	- -	Lepidorhombus whiffiagonis	- -
RT3124	Lophius piscatorius	- -	- -	- -	- -
RT3125	Ammodytes tobianus	- -	- -	- -	- -

Table 14. The identifications of the fauna made by participating laboratories for RT31. Names are given only where different from the AQC identification.

RT31	Taxon	LB1312b	LB1312c	LB1312d	LB1312e	LB1313a
RT3101	Echiichthys vipera	- -	- -	[Trachinus] -	- -	- -
RT3102	Dicentrarchus labrax	- -	[Dicentrachus] -	- -	- -	[Dicentrachus] -
RT3103	Platichthys flesus	- -	[Platichtys] -	Pleuronectes platessa	- -	[Pleuronectes] -
RT3104	Sprattus sprattus	- -	- -	- -	- -	- -
RT3105	Gaidropsarus mediterraneus	Ciliata mustela	Hyperoplus immaculatus	Clupeid -	Rockling/burbot/ling? -	Enchelyopus cimbrus
RT3106	Mullus surmuletus	- -	- -	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -	- -	- -
RT3108	Limanda limanda	- -	Pleuronectes platessa	- -	- -	- -
RT3109	Scyliorhinus canicula	- [caniculus]	- [caninculus]	[Schliorhinus] -	- -	- -
RT3110	Trachurus trachurus	- -	Pollachius virens	- [tracurus]	- -	- -
RT3111	Scomber scombrus	[Scomer] -	- -	- [scomberus]	- -	- -
RT3112	Callionymus lyra	- -	- -	- -	- -	- -
RT3113	Agonus cataphractus	- -	- -	- -	- -	- -
RT3114	Trisopterus minutus	- luscus	- -	- sp.	- luscus	- -
RT3115	Merlangius merlangus	- -	- -	- [merlangius]	- -	- -
RT3116	Raja montagui	- -	- -	- clavata	- -	- -
RT3117	Aspitrigla cuculus	- -	Trigla lucerna	Triglidae -	- -	- -
RT3118	Eutrigla gurnardus	- -	- -	Triglidae -	- -	- -
RT3119	Syngnathus rostellatus	- -	[Synganthus] typhle	Signathodiae -	- -	- -
RT3120	Ammodytes marinus	- tobianus	- tobianus	Ammodytidae -	Hyperoplus ?	- tobianus
RT3121	Clupea harengus	- -	- -	- -	- -	- -
RT3122	Osmerus eperlanus	- -	- -	- [eperlamus?]	- -	Atherina presbyter
RT3123	Arnoglossus laterna	- -	- -	Lepidorhombus whiffiagonis	Lepidorhombus whiffiagonis	Solea solea
RT3124	Lophius piscatorius	- -	- -	- -	- -	- -
RT3125	Ammodytes tobianus	Hyperoplus lanceolatus	Hyperoplus lanceolatus	Ammodytidae -	- -	Hyperoplus lanceolatus

RT31	Taxon	LB1313b	LB1313c	LB1313d	LB1313e	LB1313f
RT3101	Echiichthys vipera	- -	- -	- -	- -	- -
RT3102	Dicentrarchus labrax	- -	[Dicentrachus] -	- -	- -	- -
RT3103	Platichthys flesus	Pleuronectes platessa	[Pleuonectes] -	Pleuronectes platessa	Plueronectes platessa	[Pleuronectes] -
RT3104	Sprattus sprattus	- -	- -	- -	- -	- -
RT3105	Gaidropsarus mediterraneus	Rhinonemus cimbrius	Enchelyopus cimbrus	Enchelyopus cimbrius	Enchelyopus cimbrius	Enchelyopus cimbrius
RT3106	Mullus surmuletus	- -	- -	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -	- -	- -
RT3108	Limanda limanda	- -	- -	- -	- -	- -
RT3109	Scyliorhinus canicula	- -	- -	- -	- -	- -
RT3110	Trachurus trachurus	- -	- -	- -	Trispterus luscus	Trisopterus luscus
RT3111	Scomber scombrus	- -	- -	- -	- -	- -
RT3112	Callionymus lyra	- -	- -	- -	- -	- -
RT3113	Agonus cataphractus	- -	- -	- -	- -	- -
RT3114	Trisopterus minutus	- luscus	- -	- luscus	- -	- -
RT3115	Merlangius merlangus	- -	- -	[Merlangus] -	- -	- -
RT3116	Raja montagui	- -	- -	- -	- -	- -
RT3117	Aspitrigla cuculus	- -	- -	Eutrigla gurnardus	- -	- -
RT3118	Eutrigla gurnardus	- -	- -	Aspitrigla cuculus	- -	- -
RT3119	Syngnathus rostellatus	- -	- -	- -	- -	- -
RT3120	Ammodytes marinus	- tobianus	- tobianus	Ammodytidae -	- tobianus	- tobianus
RT3121	Clupea harengus	- -	- -	- -	- -	- -
RT3122	Osmerus eperlanus	- -	Atherina presbyter	- -	Atherina presbyter	Atherina presbyter
RT3123	Arnoglossus laterna	Solea solea	Solea solea	Solea solea	Solea solea	Solea solea
RT3124	Lophius piscatorius	- -	- -	- -	- -	- -
RT3125	Ammodytes tobianus	Hyperoplus lanceolatus	Hyperoplus lanceolatus	Hyperoplus laceolatus	Hyperoplus lanceolatus	Hyperoplus lanceolatus

Table 14. The identifications of the fauna made by participating laboratories for RT31. Names are given only where different from the AQC identification.

RT31	Taxon	LB1313g	LB1313h	LB1314a	LB1314b
RT3101	Echiichthys vipera	- -	- -	- -	- -
RT3102	Dicentrarchus labrax	- -	- -	- -	- -
RT3103	Platichthys flesus	Pleuronectes platessa	[Pleuronectes] [lessus]	- -	- -
RT3104	Sprattus sprattus	- -	- -	- -	- -
RT3105	Gaidropsarus mediterraneus	Enchelyopus cimbrius	- sp.	Ciliata mustela	Phcis blennoides
RT3106	Mullus surmuletus	- -	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -	- -
RT3108	Limanda limanda	- -	- -	- -	- -
RT3109	Scyliorhinus canicula	[Scyliorbinus] -	- [caniculus]	[Syllorhinus] [canulus]	- -
RT3110	Trachurus trachurus	- -	- -	- -	- -
RT3111	Scomber scombrus	- -	- -	- -	- -
RT3112	Callionymus lyra	- -	- -	[Callionymas] -	- -
RT3113	Agonus cataphractus	- -	- -	- -	- -
RT3114	Trisopterus minutus	- luscus	- -	- -	- -
RT3115	Merlangius merlangus	- -	- -	- -	- -
RT3116	Raja montagui	- [montaguii]	- [montaguii]	- clavata	- -
RT3117	Aspitrigla cuculus	Trigla lucerna	- -	[Astrigla] -	- -
RT3118	Eutrigla gurnardus	Aspitrigla cuculus	- -	- -	- -
RT3119	Syngnathus rostellatus	- -	- -	- -	- -
RT3120	Ammodytes marinus	- tobianus	- tobianus	- -	Hyperoplus lanceolatus
RT3121	Clupea harengus	- -	- -	- -	- [herengus]
RT3122	Osmerus eperlanus	- -	Atherina presbyter	- -	- [eperlandus]
RT3123	Arnoglossus laterna	Solea solea	Solea solea	- -	Lepidorhombus whiffiagonis
RT3124	Lophius piscatorius	- -	- -	- -	- -
RT3125	Ammodytes tobianus	Hyperoplus lanceolatus	Hyperoplus lanceolatus	- marinus	- -

RT31	Taxon	LB1314c	LB1314d	LB1315a	LB1316a
RT3101	Echiichthys vipera	- -	- -	Trachinus draco	[Trachinus] -
RT3102	Dicentrarchus labrax	- -	Pollachius virens	- -	[Dicentrachus] -
RT3103	Platichthys flesus	- -	- -	- -	- -
RT3104	Sprattus sprattus	- -	- -	- -	- -
RT3105	Gaidropsarus mediterraneus	Ciliata mustela	Phycis blennoides	- vulgaris	- -
RT3106	Mullus surmuletus	- -	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -	- -
RT3108	Limanda limanda	- -	- -	- -	- -
RT3109	Scyliorhinus canicula	- -	- [caniculus]	- [caniculus]	[Scylorhinus] [caniculus]
RT3110	Trachurus trachurus	- -	- -	- -	- -
RT3111	Scomber scombrus	- -	- -	- -	- -
RT3112	Callionymus lyra	- -	- -	- -	- -
RT3113	Agonus cataphractus	- -	- -	- -	- -
RT3114	Trisopterus minutus	- -	- -	- -	- -
RT3115	Merlangius merlangus	- -	- -	- -	- -
RT3116	Raja montagui	- brachyura	- brachyura	- clauata	- -
RT3117	Aspitrigla cuculus	- -	- -	- -	- -
RT3118	Eutrigla gurnardus	[Eutriglia] -	- -	- -	- -
RT3119	Syngnathus rostellatus	- -	- acus	- -	- -
RT3120	Ammodytes marinus	Hyperoplus immaculatus	Hyperoplus immaculatus	- tobianus	- tobianus
RT3121	Clupea harengus	- -	- -	- -	- -
RT3122	Osmerus eperlanus	- -	Alosa fallax	- -	- -
RT3123	Arnoglossus laterna	Lepidorhombus whiffiagonis	Lepidorhombus whiffiagonis	Microstomus kitt	- [lanterna]
RT3124	Lophius piscatorius	- -	- -	- -	- -
RT3125	Ammodytes tobianus	- -	Hyperoplus lanceolatus	Hyperoplus lanceolatus	- -

Table 14. The identifications of the fauna made by participating laboratories for RT31. Names are given only where different from the AQC identification.

RT31	Taxon	LB1323a	LB1323b	LB1325a
RT3101	Echiichthys vipera	- -	- -	- -
RT3102	Dicentrarchus labrax	- -	- -	- -
RT3103	Platichthys flesus	[Pleuronectes] -	[Pleuronectes] -	Pleuronectes platessa
RT3104	Sprattus sprattus	- -	- -	Clupea herringus
RT3105	Gaidropsarus mediterraneus	- -	- -	Molva molva
RT3106	Mullus surmuletus	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -
RT3108	Limanda limanda	- -	- -	Solea solea
RT3109	Scyliorhinus canicula	- -	- -	- [canucula]
RT3110	Trachurus trachurus	- -	- -	- -
RT3111	Scomber scombrus	- -	- -	- -
RT3112	Callionymus lyra	- reticulatus	- -	- -
RT3113	Agonus cataphractus	- -	- -	- -
RT3114	Trisopterus minutus	- luscus	- luscus	- -
RT3115	Merlangius merlangus	- -	- -	- -
RT3116	Raja montagui	- -	- -	- -
RT3117	Aspitrigla cuculus	- -	- -	Trigla lucerna
RT3118	Eutrigla gurnardus	- -	- -	Aspitrigla cuculus
RT3119	Syngnathus rostellatus	- acus	- acus	Nerophis lumbriciformis
RT3120	Ammodytes marinus	- -	Hyperoplus lanceolatus	- tobianus
RT3121	Clupea harengus	- -	- -	- -
RT3122	Osmerus eperlanus	- -	- -	- -
RT3123	Arnoglossus laterna	[Arnglossus] -	- -	- -
RT3124	Lophius piscatorius	- -	- -	Squatina squatina
RT3125	Ammodytes tobianus	- -	- -	Gymanammodytes circerelus

RT31	Taxon	LB1325b	LB1325c	LB1326a
RT3101	Echiichthys vipera	[Trachinus] -	[Trachinus] -	[Trachinus] -
RT3102	Dicentrarchus labrax	- -	- -	- -
RT3103	Platichthys flesus	- -	- -	- -
RT3104	Sprattus sprattus	- -	- -	- -
RT3105	Gaidropsarus mediterraneus	Atherina presbyter	Atherina presbyter	[Gaidropsaurus] -
RT3106	Mullus surmuletus	- -	- -	- -
RT3107	Zeus faber	- -	- -	- -
RT3108	Limanda limanda	- -	- -	- -
RT3109	Scyliorhinus canicula	[Scyliorhynus] [caniculus]	[Scyliorhynus] [caniculus]	- [caniculus]
RT3110	Trachurus trachurus	- -	Alosa sp.	- -
RT3111	Scomber scombrus	- -	- -	- -
RT3112	Callionymus lyra	[Callionmus] -	Scorpaena sp.	- reticulatus
RT3113	Agonus cataphractus	- -	Scorpaena scofa	- -
RT3114	Trisopterus minutus	- -	- -	- luscus
RT3115	Merlangius merlangus	- -	- -	- -
RT3116	Raja montagui	- clavata	- brachyura	- clavata
RT3117	Aspitrigla cuculus	- -	- -	- -
RT3118	Eutrigla gurnardus	Trigla lucerna	- -	- -
RT3119	Syngnathus rostellatus	- -	Enterulus aequeorus	- acus
RT3120	Ammodytes marinus	Lumpenus lamlretaeformis	- tobianus	- -
RT3121	Clupea harengus	[Culpea] -	[Culpea] -	Sardina pilchardus
RT3122	Osmerus eperlanus	- -	- -	- -
RT3123	Arnoglossus laterna	Solea solea	Solea solea	- -
RT3124	Lophius piscatorius	- -	- -	- -
RT3125	Ammodytes tobianus	- -	Hyperoplus lanceolatus	- -

Table 15. Results from the Own Samples (OS32-34) with respect to the NMBAQC / UK NMMP standards.

1		2			3	4	5	6	7	8	9	10	11			12	13	14	15	16	17	18	19	20	21	22	23
		Estimation of Taxa								Taxonomic Errors			Estimation of Abundance								Estimation of Biomass			Similarity Index			NMBAQCS/NMMP
LabCode		Lab.	Min	Max	Target	Flag	Missed	% Missed	Remedial Action	Lab.	%	Remedial Action	Lab.	Min	Max	Target	Flag	Missed	% Missed	Remedial Action	Lab.	Target	Flag	Target	Lab.	Flag	Sample Flag
LB1301	OS32	66	61.2	74.8	61.2 - 74.8	PASS	2	2.9		0	0.0		151	148.5	181.5	148.5 - 181.5	PASS	11	6.7		1.0610	0.8197 - 1.2295	*PASS*	90.0	96.07	PASS	Pass-Good
LB1301	OS33	7	5.0	9.0	5.0 - 9.0	PASS	0	0.0		0	0.0		22	19.8	24.2	19.8 - 24.2	PASS	0	0.0		0.4497	0.3805 - 0.5707	*PASS*	90.0	100.00	PASS	Pass-Excellent
LB1301	OS34	2	0.0	4.0	0.0 - 4.0	PASS	0	0.0		0	0.0		1	-1.0	3.0	-1.0 - 3.0	PASS	0	0.0		0.7373	0.5510 - 0.8266	*PASS*	90.0	100.00	PASS	Pass-Excellent
LB1302	OS32	150	135.9	166.1	135.9 - 166.1	PASS	1	0.7		1	0.7		6605	5931.0	7249.0	5931.0 - 7249.0	PASS	21	0.3		67.1262	54.0684 - 81.1026	*PASS*	90.0	99.59	PASS	Pass-Good
LB1302	OS33	77	69.3	84.7	69.3 - 84.7	PASS	0	0.0		1	1.3		962	871.2	1064.8	871.2 - 1064.8	PASS	9	0.9		19.8220	15.9532 - 23.9298	*PASS*	90.0	99.28	PASS	Pass-Good
LB1302	OS34	41	36.9	45.1	36.9 - 45.1	PASS	0	0.0		0	0.0		121	108.9	133.1	108.9 - 133.1	PASS	0	0.0		0.8664	0.6488 - 0.9732	*PASS*	90.0	100.00	PASS	Pass-Excellent
LB1303	OS32	9	7.0	11.0	7.0 - 11.0	PASS	0	0.0		0	0.0		25	23.4	28.6	23.4 - 28.6	PASS	1	3.8		2.0121	1.6032 - 2.4048	*PASS*	90.0	98.04	PASS	Pass-Good
LB1303	OS33	19	18.0	22.0	18.0 - 22.0	PASS	1	5.0		0	0.0		144	133.2	162.8	133.2 - 162.8	PASS	4	2.7		6.6714	5.2816 - 7.9224	*PASS*	90.0	98.63	PASS	Pass-Good
LB1303	OS34	6	5.0	9.0	5.0 - 9.0	PASS	1	14.3	Review	0	0.0		12	13.0	17.0	13.0 - 17.0	Fail	3	20.0	Reprocess	66.3403	55.5712 - 83.3568	*PASS*	90.0	88.89	Fail	Fail-Poor
LB1304	OS32	54	47.7	58.3	47.7 - 58.3	PASS	0	0.0		1	1.9		138	121.5	148.5	121.5 - 148.5	PASS	0	0.0		1.4438	0.9314 - 1.3970	*Fail*	90.0	98.17	PASS	Pass-Good
LB1304	OS33	133	122.4	149.6	122.4 - 149.6	PASS	1	0.7		11	8.1		1732	1535.4	1876.6	1535.4 - 1876.6	PASS	8	0.5		173.2021	133.1139 - 199.6709	*PASS*	90.0	96.66	PASS	Pass-Good
LB1304	OS34	42	36.9	45.1	36.9 - 45.1	PASS	0	0.0		1	2.4		100	90.0	110.0	90.0 - 110.0	PASS	0	0.0		1.1783	0.8310 - 1.2466	*PASS*	90.0	99.01	PASS	Pass-Good
LB1305	OS32	36	33.3	40.7	33.3 - 40.7	PASS	0	0.0		8	21.6		115	106.2	129.8	106.2 - 129.8	PASS	1	0.8		1.6044	1.1618 - 1.7426	*PASS*	90.0	90.13	PASS	Pass-Acceptable
LB1305	OS33	40	35.1	42.9	35.1 - 42.9	PASS	0	0.0		2	5.1	Review	260	234.9	287.1	234.9 - 287.1	PASS	0	0.0		0.4708	0.3250 - 0.4876	*PASS*	90.0	85.99	Fail	Fail-Poor
LB1305	OS34	25	23.4	28.6	23.4 - 28.6	PASS	1	3.8		4	16.0		88	84.6	103.4	84.6 - 103.4	PASS	7	7.4		8.9230	6.3854 - 9.5780	*PASS*	90.0	90.11	PASS	Pass-Acceptable
LB1306	OS32	66	63.0	77.0	63.0 - 77.0	PASS	1	1.4		6	8.7		1142	1028.7	1257.3	1028.7 - 1257.3	PASS	13	1.1		3.7800	3.2603 - 4.8905	*PASS*	90.0	96.11	PASS	Pass-Good
LB1306	OS33	39	35.1	42.9	35.1 - 42.9	PASS	0	0.0		0	0.0		345	319.5	390.5	319.5 - 390.5	PASS	9	2.5		0.4894	0.4495 - 0.6743	*PASS*	90.0	98.59	PASS	Pass-Good
LB1306	OS34	68	62.1	75.9	62.1 - 75.9	PASS	1	1.4		4	5.9		308	277.2	338.8	277.2 - 338.8	PASS	3	1.0		10.9533	8.4317 - 12.6475	*PASS*	90.0	96.92	PASS	Pass-Good
LB1307	OS32	13	11.0	15.0	11.0 - 15.0	PASS	0	0.0		0	0.0		34	30.6	37.4	30.6 - 37.4	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1307	OS33	39	36.0	44.0	36.0 - 44.0	PASS	0	0.0		2	5.0		80	72.0	88.0	72.0 - 88.0	PASS	0	0.0		-	-	-	90.0	90.00	PASS	Pass-Acceptable
LB1307	OS34	5	3.0	7.0	3.0 - 7.0	PASS	0	0.0		1	20.0	Review	5	3.0	7.0	3.0 - 7.0	PASS	0	0.0		-	-	-	90.0	80.00	Fail	Fail-Bad
LB1308	OS32	90	76.5	93.5	76.5 - 93.5	PASS	0	0.0		5	5.9		510	450.9	551.1	450.9 - 551.1	PASS	0	0.0		-	-	-	90.0	96.34	PASS	Pass-Good
LB1308	OS33	55	49.5	60.5	49.5 - 60.5	PASS	0	0.0		2	3.6		114	100.8	123.2	100.8 - 123.2	PASS	1	0.9		-	-	-	90.0	94.69	PASS	Pass-Acceptable
LB1308	OS34	64	56.7	69.3	56.7 - 69.3	PASS	0	0.0		3	4.8		200	163.8	200.2	163.8 - 200.2	PASS	0	0.0		-	-	-	90.0	93.19	PASS	Pass-Acceptable
LB1309	OS32	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		1175	1071.0	1309.0	1071.0 - 1309.0	PASS	0	0.0		-	-	-	90.0	99.37	PASS	Pass-Good
LB1309	OS33	82	78.3	95.7	78.3 - 95.7	PASS	3	3.4		15	17.9	Reprocess	165	158.4	193.6	158.4 - 193.6	PASS	10	5.7	Review	-	-	-	90.0	84.04	Fail	Fail-Bad
LB1309	OS34	37	33.3	40.7	33.3 - 40.7	PASS	0	0.0		3	8.1		61	55.8	68.2	55.8 - 68.2	PASS	1	1.6		-	-	-	90.0	94.66	PASS	Pass-Acceptable
LB1310	OS32	62	55.8	68.2	55.8 - 68.2	PASS	0	0.0		1	1.6		2233	2014.2	2461.8	2014.2 - 2461.8	PASS	8	0.4		-	-	-	90.0	99.49	PASS	Pass-Good
LB1310	OS33	19	17.0	21.0	17.0 - 21.0	PASS	0	0.0		0	0.0		1246	1118.7	1367.3	1118.7 - 1367.3	PASS	3	0.2		-	-	-	90.0	99.88	PASS	Pass-Good
LB1310	OS34	52	46.8	57.2	46.8 - 57.2	PASS	0	0.0		0	0.0		726	644.4	787.6	644.4 - 787.6	PASS	0	0.0		-	-	-	90.0	98.91	PASS	Pass-Good
LB1311	OS32	9	7.0	11.0	7.0 - 11.0	PASS	0	0.0		1	11.1		14	12.0	16.0	12.0 - 16.0	PASS	0	0.0		0.2083	0.1682 - 0.2524	*PASS*	90.0	92.86	PASS	Pass-Acceptable
LB1311	OS33	28	25.2	30.8	25.2 - 30.8	PASS	0	0.0		0	0.0		141	126.9	155.1	126.9 - 155.1	PASS	0	0.0		0.4875	0.4258 - 0.6388	*PASS*	90.0	100.00	PASS	Pass-Excellent
LB1311	OS34	19	17.0	21.0	17.0 - 21.0	PASS	0	0.0		1	5.3		99	89.1	108.9	89.1 - 108.9	PASS	0	0.0		0.8099	0.6338 - 0.9508	*PASS*	90.0	97.98	PASS	Pass-Good
LB1312	OS32	-	-	-	-	-	-	-		-	-		-	-	-	-	-	-	-		-	-	-	90.0	-	-	
LB1312	OS33	-	-	-	-	-	-	-		-	-		-	-	-	-	-	-	-		-	-	-	90.0	-	-	
LB1312	OS34	-	-	-	-	-	-	-		-	-		-	-	-	-	-	-	-		-	-	-	90.0	-	-	
LB1313	OS32	4	2.0	6.0	2.0 - 6.0	PASS	0	0.0		1	25.0		69	61.2	74.8	61.2 - 74.8	PASS	0	0.0		0.0500	0.0265 - 0.0397	*Fail*	90.0	97.81	PASS	Pass-Good
LB1313	OS33	9	7.0	11.0	7.0 - 11.0	PASS	0	0.0		0	0.0		468	402.3	491.7	402.3 - 491.7	PASS	0	0.0		2.2340	1.7706 - 2.6560	*PASS*	90.0	97.27	PASS	Pass-Good
LB1313	OS34	8	6.0	10.0	6.0 - 10.0	PASS	0	0.0		1	12.5		142	128.7	157.3	128.7 - 157.3	PASS	0	0.0		0.0980	0.0621 - 0.0931	*Fail*	90.0	98.25	PASS	Pass-Good
LB1314	OS32	23	20.7	25.3	20.7 - 25.3	PASS	0	0.0		0	0.0		747	672.3	821.7	672.3 - 821.7	PASS	0	0.0		-	-	-	90.0	99.73	PASS	Pass-Good
LB1314	OS33	13	11.0	15.0	11.0 - 15.0	PASS	0	0.0		0	0.0		117	106.2	129.8	106.2 - 129.8	PASS	1	0.8		-	-	-	90.0	99.59	PASS	Pass-Good
LB1314	OS34	92	82.8	101.2	82.8 - 101.2	PASS	0	0.0		0	0.0		206	185.4	226.6	185.4 - 226.6	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1315	OS32	32	28.8	35.2	28.8 - 35.2	PASS	0	0.0		2	6.3		464	412.2	503.8	412.2 - 503.8	PASS	2	0.4		43.0276	31.1014 - 46.6520	*PASS*	90.0	97.18	PASS	Pass-Good
LB1315	OS33	65	58.5	71.5	58.5 - 71.5	PASS	0	0.0		5	7.7		816	735.3	898.7	735.3 - 898.7	PASS	3	0.4		14.5392	11.1690 - 16.7536	*PASS*	90.0	96.88	PASS	Pass-Good
LB1315	OS34	15	13.0	17.0	13.0 - 17.0	PASS	0	0.0		2	13.3		424	372.6	455.4	372.6 - 455.4	PASS	2	0.5		0.4670	0.3525 - 0.5287	*PASS*	90.0	98.57	PASS	Pass-Good
LB1316	OS32	19	17.0	21.0	17.0 - 21.0	PASS	0	0.0		3	15.8		1574	1422.9	1739.1	1422.9 - 1739.1	PASS	21	1.3		2.3319	1.4250 - 2.1376	*Fail*	90.0	99.37	PASS	Pass-Good
LB1316	OS33	20	18.0	22.0	18.0 - 22.0	PASS	0	0.0		2	10.0		653	586.8	717.2	586.8 - 717.2	PASS	2	0.3		0.5399	0.7457 - 1.1185	*Fail*	90.0	98.70	PASS	Pass-Good
LB1316	OS34	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		371	339.3	414.7	339.3 - 414.7	PASS	15	4.0		3.7693	2.8783 - 4.3175	*PASS*	90.0	98.40	PASS	Pass-Good
LB1317	OS32	54	47.7	58.3	47.7 - 58.3	PASS	0	0.0		2	3.8		141	126.0	154.0	126.0 - 154.0	PASS	1	0.7		1.1831	0.7756 - 1.1634	*Fail*	90.0	97.51	PASS	Pass-Good
LB1317	OS33	20	18.0	22.0	18.0 - 22.0	PASS	0	0.0		0	0.0		42	37.8	46.2	37.8 - 46.2	PASS	0	0.0		3.6673	2.8032 - 4.2048	*PASS*	90.0	100.00	PASS	Pass-Excellent
LB1317	OS34	25	23.4	28.6	23.4 - 28.6	PASS	1	3.8		0	0.0		60	54.0	66.0	54.0 - 66.0	PASS	1	1.7		0.2989	0.2166 - 0.3248	*PASS*	90.0	96.67	PASS	Pass-Good
LB1318	OS32	3	3.0	7.0	3.0 - 7.0	PASS	2	40.0		0	0.0		507	475.2	580.8	475.2 - 580.8	PASS	22	4.2		-	-	-	90.0	97.88	PASS	Pass-Good
LB1318	OS33	31	29.7	36.3	29.7 - 36.3	PASS	2	6.1		0	0.0		114	117.0	143.0	117.0 - 143.0	Fail	16	12.3		-	-	-	90.0	93.44	PASS	Pass-Acceptable
LB1318	OS34	23	26.1	31.9	26.1 - 31.9	Fail	5	17.2		1	4.2		1043	1047.6	1280.4	1047.6 - 1280.4	Fail	129	11.1		-	-	-	90.0	93.84	PASS	Pass-Acceptable
LB1320	OS32	52	46.8	57.2	46.8 - 57.2	PASS	0	0.0		1	1.9		166	155.7	190.3	155.7 - 190.3	PASS	7	4.0		-	-	-	90.0	97.49	PASS	Pass-Good
LB1320	OS33	3	1.0	5.0	1.0 - 5.0	PASS	0	0.0		0	0.0		10	8.0	12.0	8.0 - 12.0	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1320	OS34	18	16.0	20.0	16.0 - 20.0	PASS	0	0.0		0	0.0		74	66.6	81.4	66.6 - 81.4	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1321	OS32	73	65.7	80.3	65.7 - 80.3	PASS	1	1.4		4	5.6		425	384.3	469.7	384.3 - 469.7	PASS	4	0.9		-	-	-	90.0	98.12	PASS	Pass-Good
LB1321	OS33	52	49.5	60.5	49.5 - 60.5	PASS	1	1.8		2	3.7		167	153.0	187.0	153.0 - 187.0	PASS	2	1.2		-	-	-	90.0	97.92	PASS	Pass-Good
LB1321	OS34	64	60.3	73.7	60.3 - 73.7	PASS	3	4.5		7	10.9	Reprocess	327	347.4	424.6	347.4 - 424.6	Fail	60	15.5	Reprocess	-	-	-	90.0	87.52	Fail	Fail-Poor
LB1322	OS32	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		31	29.7	36.3	29.7 - 36.3	PASS	2	6.1		0.3121	0.2036 - 0.3054	*Fail*	90.0	96.97	PASS	Pass-Good
LB1322	OS33	47	44.1	53.9	44.1 - 53.9	PASS	2	4.1		1	2.1		341	306.0	374.0	306.0 - 374.0	PASS	3	0.9		9.9358	8.4691 - 12.7037	*PASS*	90.0	98.68	PASS	Pass-Good
LB1322	OS34	22	22.5	27.5	22.5 - 27.5	Fail	1	4.0		0	0.0		97	90.0	110.0	90.0 - 110.0	PASS	2	2.0		17.5625	13.3716 - 20.0574	*PASS*	90.0	97.46	PASS	Pass-Good
LB1323	OS32	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		215	205.2	250.8	205.2 - 250.8	PASS	0	0.0		-	-	-	90.0	97.07	PASS	Pass-Good
LB1323	OS33	20	18.0	22.0	18.0 - 22.0	PASS	0	0.0		0	0.0		2549	2282.4	2789.6	2282.4 - 2789.6	PASS	0	0.0		-	-	-	90.0	99.55	PASS	Pass-Good
LB1323	OS34	6	4.0	8.0	4.0 - 8.0	PASS	0	0.0		0	0.0		9	7.0	11.0	7.0 - 11.0	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1324	OS32	18	15.0	19.0	15.0 - 19.0	PASS	0	0.0		0	0.0		189	174.6	213.4	174.6 - 213.4	PASS	1	0.5		1.1110	0.6987 - 1.0481	*Fail*	90.0	96.61	PASS	Pass-Good
LB1324	OS33	9	8.0	12.0	8.0 - 12.0	PASS	0	0.0		2	20.0		102	91.8	112.2	91.8 - 112.2	PASS	0	0.0		16.2570	11.3117 - 16.9675	*PASS*	90.0	90.20	PASS	Pass-Acceptable
LB1324	OS34	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		135	175.5	214.5	175.5 - 214.5	Fail	0	0.0		3.0140	1.5801 - 2.3701	*Fail*	90.0	80.00	Fail	Fail-Bad
LB1325	OS32	21	19.8	24.2	19.8 - 24.2	PASS	1	4.5		0	0.0		1403	1260.0	1540.0	1260.0 - 1540.0	PASS	7	0.5		89.6909	39.9038 - 59.8558	*Fail*	90.0	99.47	PASS	Pass-Good
LB1325	OS33	5	3.0	7.0	3.0 - 7.0	PASS	0	0.0		0	0.0		15	13.0	17.0	13.0 - 17.0	PASS	0	0.0		0.0120	0.0084 - 0.0126	*PASS*	90.0	100.00	PASS	Pass-Excellent
LB1325	OS34	34	31.5	38.5	31.5 - 38.5	PASS	1	2.9		1	2.9		564	517.5	632.5	517.5 - 632.5	PASS	11	1.9		16.8696	10.5976 - 15.8964	*Fail*	90.0	98.51	PASS	Pass-Good

Table 16. Z-score results for the derived statistics supplied by participating laboratories for the particle size (PS) exercises - PS28 and PS29 - NMBAQC / UK NMMP standards applied.

PS28

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description: pre/post analysis
Laser1RepAv	94.83	0.89	PASS	6.90	0.87	PASS	6.96	1.06	PASS	1.96	0.55	PASS	0.049	0.36	PASS	-
Laser2RepAv	100	2.09	Fail	7.094	1.28	PASS	7.28	1.49	PASS	1.44	-1.60	PASS	-0.572	-2.02	Fail	-
LB1301	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-/-
LB1302	90.89	-0.03	PASS	6.74	0.52	PASS	6.65	0.63	PASS	1.96	0.53	Fail	0.050	0.37	PASS	M/M
LB1303	89.6	-0.33	PASS	6.44	-0.14	PASS	6.11	-0.11	PASS	1.70	-0.53	PASS	-0.260	-0.82	PASS	Mud/Mud
LB1304	95.2	0.96	PASS	7.02	1.12	PASS	6.91	0.98	PASS	1.73	-0.41	PASS	0.070	0.44	PASS	Mud(anoxic)/Mud
LB1305	90.0	-0.24	PASS	5.81	-1.50	PASS	5.95	-0.33	PASS	1.74	-0.37	PASS	0.220	1.02	PASS	Thick dk brown mud + occ. shell fragments/(g)M
LB1306*	89.58	-0.33	PASS	6.44	-0.14	PASS	6.11	-0.11	PASS	1.70	-0.53	PASS	-0.260	-0.82	PASS	Mud/Mud
LB1307	82.0	-2.08	Fail	6.07	-0.94	PASS	6.16	-0.04	PASS	3.13	5.32	Fail	-0.62	-2.20	Fail	mud/mud
LB1308	96.12	1.19	PASS	7.00	1.08	PASS	6.82	0.86	PASS	1.4	-1.76	PASS	-0.260	-0.82	PASS	mud/mud
LB1314	88.57	-0.57	PASS	6.58	0.17	PASS	5.20	-1.36	PASS	1.91	0.33	PASS	0.120	0.64	PASS	mud/-
LB1317	91.94	0.22	PASS	5.96	-1.18	PASS	4.97	-1.68	PASS	1.71	-0.49	PASS	0.170	0.83	PASS	muddy silt/medium silt
LB1320	38.61	-12.16	Fail	3.624	-6.24	Fail	4.54	-2.26	Fail	2.31	1.98	PASS	0.565	2.34	Fail	Mud/Muddy sand

"-" no return and/or data from laboratory. See Section 6 for details.
"*" = centralised analysis

PS29

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description
Laser1RepAv	1.14	0.65	PASS	1.76	-0.20	PASS	1.74	0.20	PASS	0.62	-0.91	PASS	-0.047	-0.08	PASS	Unspecified
Laser2RepAv	0.77	-0.04	PASS	1.65	-0.76	PASS	1.64	-0.28	PASS	0.712857	0.59	PASS	-0.42	-4.90	Fail	Sand/Sand
LB1301	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-/-
LB1302	0	-1.45	PASS	2.05	1.22	PASS	2.00	1.36	PASS	0.54	-2.34	Fail	-0.180	-1.80	PASS	Medium sand/Sand
LB1303	0.69	-0.18	PASS	1.4	-1.98	PASS	1.42	-1.26	PASS	0.71	0.54	PASS	0.030	0.92	PASS	Coarse sand/Sand
LB1305	0.87	0.15	PASS	1.65	-0.75	PASS	1.67	-0.13	PASS	0.74	1.05	PASS	0.020	0.79	PASS	Very sl. gravelly (shelly) sand/ Sand
LB1306*	0.69	-0.18	PASS	1.4	-1.98	PASS	1.42	-1.26	PASS	0.71	0.54	PASS	0.030	0.92	PASS	Coarse sand/Sand
LB1307	4.72	7.24	Fail	1.99	0.93	PASS	1.26	-1.98	PASS	0.81	2.23	Fail	0.16	2.60	Fail	Sand/Sand
LB1308	0.89	0.19	PASS	2.13	1.62	PASS	2.11	1.86	PASS	0.57	-1.83	PASS	-0.090	-0.63	PASS	Sand/Sand
LB1314	0.00	-1.45	PASS	1.63	-0.85	PASS	1.47	-1.03	PASS	0.69	0.20	PASS	0.010	0.66	PASS	Sandy/-
LB1317	1.76	1.79	PASS	1.61	-0.95	PASS	1.62	-0.36	PASS	0.73	0.88	PASS	0.030	0.92	PASS	Muddy sand/Medium sand
LB1320	0.20	-1.09	PASS	2.08	1.36	PASS	2.03	1.49	PASS	0.65	-0.51	PASS	-0.102	-0.79	PASS	Sand/Sand

"-" no return and/or data from laboratory. See Section 6 for details.
"*" = centralised analysis

Table 17. Comparison of the overall performance of laboratories in the Own Sample exercises from 1995/96 to 2006/07 with respect to the NMBAQC / UK NMMP standards. Initial OS results excluding remedial action.

Scheme Year	Exercise	Pass (>90% BCSI)	Fail (<90% BCSI)	% Pass
02 (1995/96)	01	14	0	100
03 (1996/97)	02, 03, 04	27	11	71
04 (1997/98)	05, 06, 07	33	7	83
05 (1998/99)	08, 09, 10	30	12	71
06 (1999/00)	11, 12, 13	37	14	73
07 (2000/01)	14, 15, 16	30	15	67
08 (2001/02)*	17, 18, 19	35	10	78
09 (2002/03)*	20, 21, 22	33	11	75
10 (2003/04)*	23, 24, 25	43	8	84
11 (2004/05)*	26, 27, 28	51	3	94
12 (2005/06)*	29, 30, 31	49	4	92
13 (2006/07)*	32, 33, 34	63	6	91
	In Total	445	101	82

Key: * - Own Samples selected from completed data matrices, *i.e.* 'blind audits'
BCSI - Bray Curtis similarity index (untransformed)

Table 18. Comparison of each laboratory's performance in the Own Sample exercises from Scheme year 02 (1995/96) to Scheme year 13 (2006/07).

	Scheme Year 2	Scheme Year 3			Scheme Year 4			Scheme Year 5			Scheme Year 6			Scheme Year 7			Scheme Year 8			Scheme Year 9			Scheme Year 10			Scheme Year 11			Scheme Year 12			Scheme Year 13		
LabCode	**OS01**	**OS02**	**OS03**	**OS04**	**OS05**	**OS06**	**OS07**	**OS08**	**OS09**	**OS10**	**OS11**	**OS12**	**OS13**	**OS14**	**OS15**	**OS16**	**OS17**	**OS18**	**OS19**	**OS20**	**OS21**	**OS22**	**OS23**	**OS24**	**OS25**	**OS26**	**OS27**	**OS28**	**OS29**	**OS30**	**OS31**	**OS32**	**OS33**	**OS34**
LB1301	-	-	-	-	60	62.5	83.82	87.5	93.5	94.12	74.21	76.6	70.98	74.02	81.74	78.47	78.95	90.36	100	70.25	94.68	78.57	98.11	100	100	100	100	96.3	100	80.00	100	96.07	100	100
LB1302	97.94	-	92.08	-	74.34	94.64	96.43	71.03	96.48	99.17	98.32	97.65	96.3	96.67	98.21	96.96	92.41	96.74	89.86	98.54	98.2	99.54	99.6	97.85	98.86	99.46	100	97.33	99.26	99.65	99.91	99.59	99.28	100
LB1303	97.91	96.3	85.8	89.82	75.29	95.44	74.89	73.3	97.33	93.01	73.02	99.5	90.5	93.13	94.57	90.32	96.67	94.12	90.39	94.27	96.43	96.77	83.74	90.72	96.77	100	96.42	94.55	96.97	85.11	90.72	98	98.6	88.9
LB1304	-	-	-	-	-	-	-	95.08	53.66	60.42	-	-	-	-	-	-	84.32	100	80.31	-	-	-	93.7	83.94	91.23	-	-	-	99.35	95.65	97.87	98.2	96.7	99
LB1305	-	-	-	-	89.9	-	-	-	-	-	95.8	49.56	67.28	72.73	89.52	70.87	55.86	71.28	90.77	72.58	98.56	99.61	95.89	95.82	97.62	100	98.9	98.52	100	95.86	98.85	90.1	86	90.1
LB1306	100	100	100	100	98.88	100	100	97.46	100	83.33	89.29	95.65	94.48	76.92	92.82	95.43	92.68	96.68	97.43	96.91	93.74	91.23	93.29	97.35	94.12	98.82	91.48	90.48	97.55	91.97	97.97	96.1	98.6	96.9
LB1307	-	-	-	-	95.75	92.56	96.37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	98.21	96.45	90.77	49.37	96.54	96.32	100	90	80
LB1308	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.68	91.36	93.63	98.66	96.44	92.46	100	98.46	98	99.45	95.08	100	99.25	98.63	100	96.3	94.7	93.2
LB1309	-	-	-	-	-	-	-	-	-	-	-	-	-	92.09	96.52	82.22	91.5	99.34	97.22	84.94	76.92	80.46	89.16	99.83	96.18	98.04	100	100	100	91.8	99.24	99.4	84	94.7
LB1310	97.17	98.93	96.58	98.4	100	98.8	98.04	91.32	98.8	98.35	99.23	90.38	98.13	99.21	91.1	96.22	99.55	93.98	95.24	99.07	96.69	98.14	96.68	92.27	77.38	82.37	98.44	71.38	92.08	93.94	86.17	99.49	99.88	98.91
LB1311	92.83	94.19	99.04	97.96	99.45	99.03	95.72	100	99.66	99.79	100	70	75.56	83.58	77.62	99.71	98.39	95.87	100	100	100	95.24	96.85	90.26	96.55	98.49	97.73	99.44	98.84	100	100	92.9	100	98
LB1312		73.15	68.7	96.12	-	-	-	93.33	90.46	93.1	87.15	98.56	98.24	95.9	92.57	91.22	-	-	-	86.15	98.43	96.78	95.23	96.92	95.97	98.48	96.15	98.62	93.61	96.23	99.68	81.8	98.8	98.8
LB1313	98.1	98.48	100	88.89	100	100	98.67	96.39	89.13	100	99.16	97.92	95.87	98.98	85.19	72.15	95.65	57.98	91.2	98.06	94.44	-	89.55	83.33	73.75	92.75	100	91.96	-	-	-	97.8	97.3	98.2
LB1314	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	99.73	99.59	100
LB1315	99.44	98.39	100	100	100	99.31	99.75	98.59	98.59	100	98.14	66.26	88.78	96.95	99.09	98.95	98.99	84.62	91.09	99.37	99.24	98.67	96.48	97.92	99.37	99.7	100	98.92	99.69	99.77	99.04	97.2	96.9	98.6
LB1316	98.54	-	-	-	99.68	99.87	90.2	91.73	43.85	35.71	97.27	98.7	97.56	94.12	97.4	98.08	96.94	95.4	98.84	-	-	-	98.26	96.21	98.72	98.62	98.78	98.00	99.12	98	99.14	99.4	98.7	98.40
LB1317	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(99.2)	(98.7)	(98.7)	97.5	100	96.7
LB1318	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	96.89	72.07	56.22	-	-	-	-	-	-	-	-	-	-	-	-	97.9	93.4	93.8
LB1319	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1320	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	97.97	100	97.5	100	100
LB1321	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	88.89	43.32	83.72	99	94.6	85.11	94.74	95.89	96.43	99.19	95.89	96.3	98.1	97.9	87.5
LB1322	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.22	90.00	93.85	98.59	97.93	98.94	97	98.7	97.5
LB1323	98.18	100	83.33	95.77	100	100	94.74	-	-	-	98.21	97.79	100	-	-	-	-	-	-	97.52	99.43	92.86	98.76	92.31	99.5	99.02	100	99.40	99.73	99.77	98.52	97.1	99.5	100
LB1324	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.5	92.07	100	95.58	91.49	70.95	-	-	-	96.6	90.2	80.0
LB1325	-	-	-	-	-	-	-	-	-	-	100	98.96	85.71	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	93.64	100	87.5	99.5	100	98.5
LB1326	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Key: Yellow shaded cells = 'Fail' flag; no record of subsequent remedial action.
Green shaded cells = Remedial action sucessfully completed.
Pink shaded cells = Data changed following external review.
Red text = no sample residue supplied (excluded from statistics).
"(data)"= Remedial action Extra Own Sample data due to initial non-submission (excluded from statistics).

Figures

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS28. Seven samples analysed by Malvern Laser and seven samples analysed by Coulter Laser.

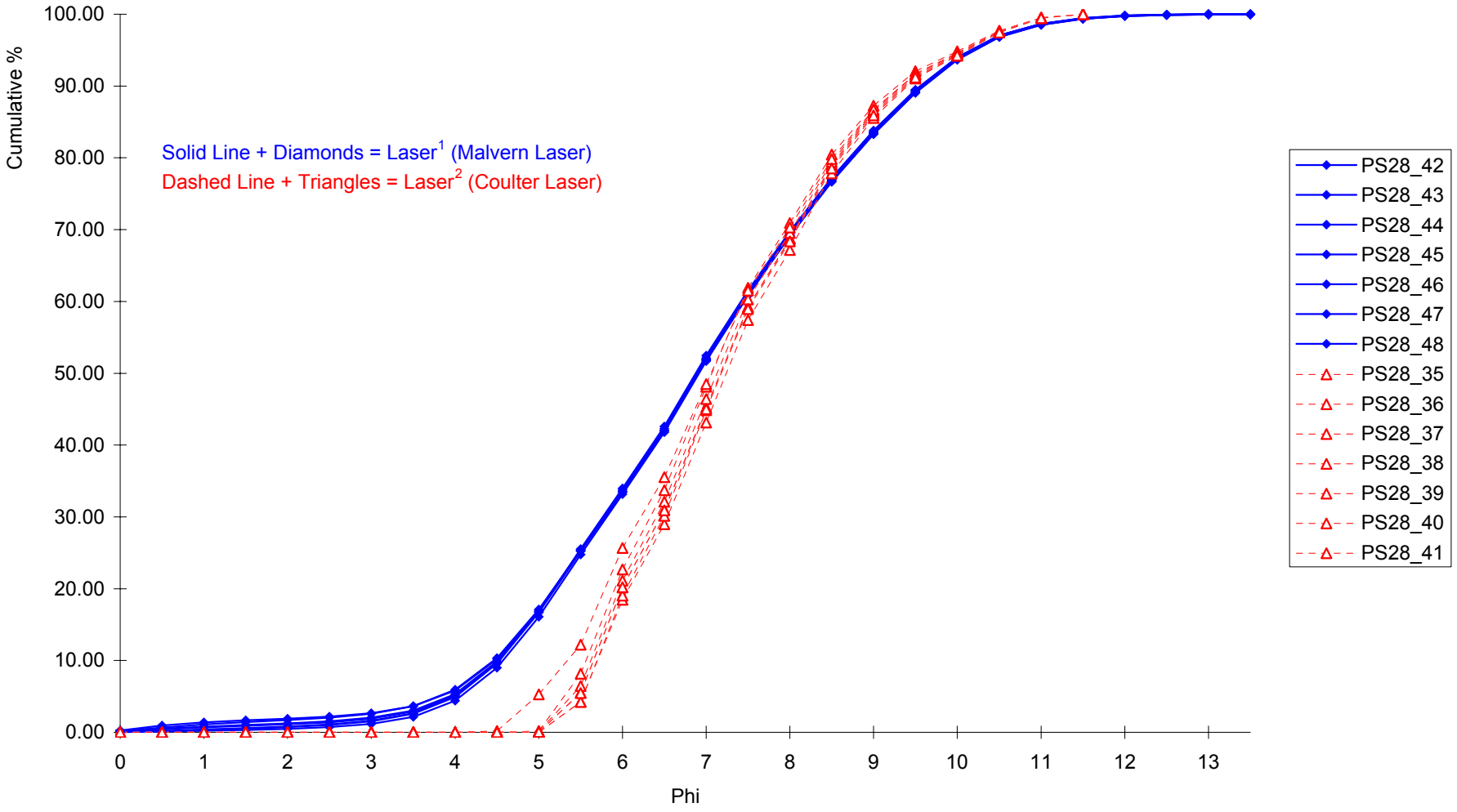


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS29. Seven samples analysed by Malvern Laser and seven samples analysed by Coulter Laser.

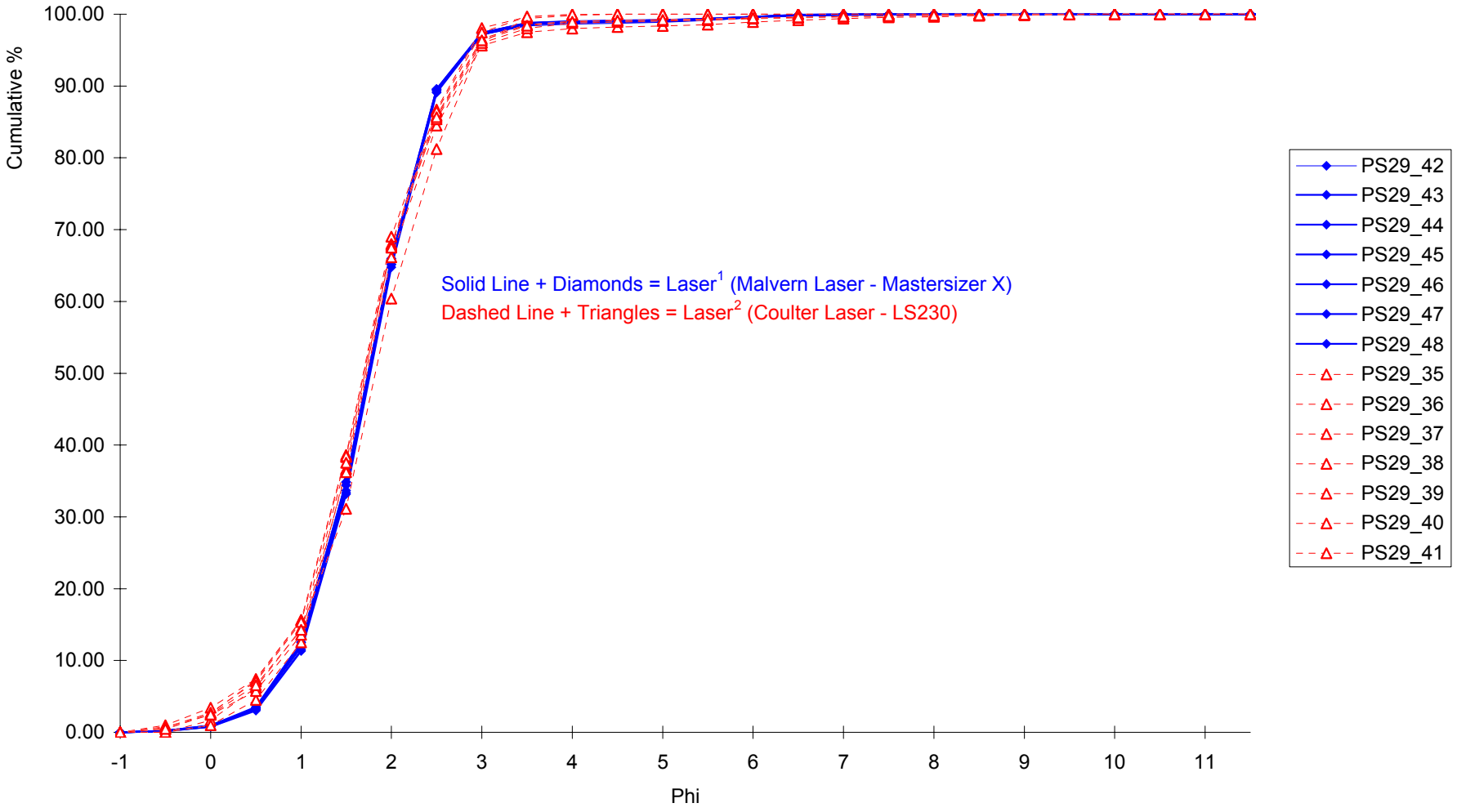


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS28.

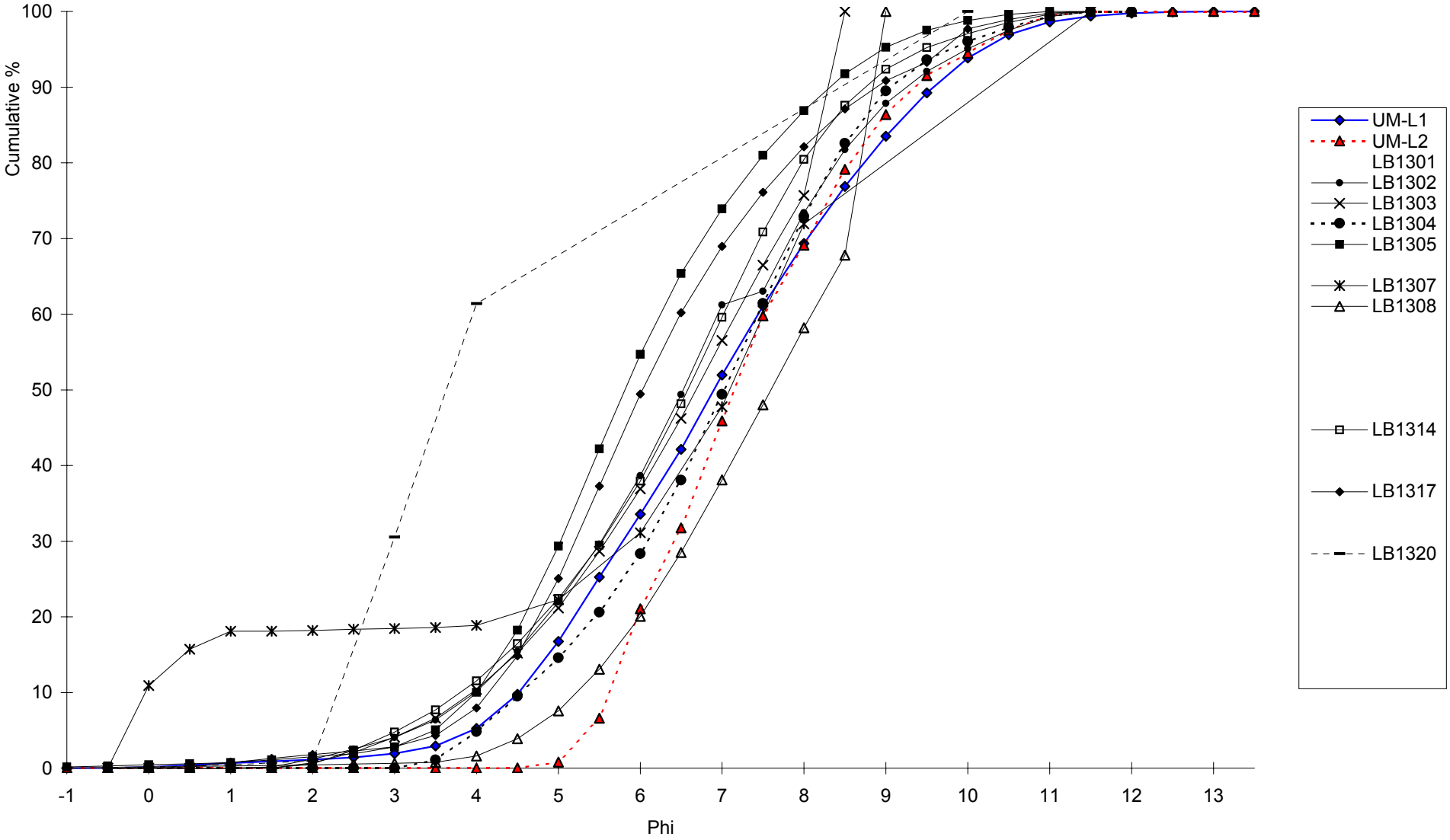


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS29.

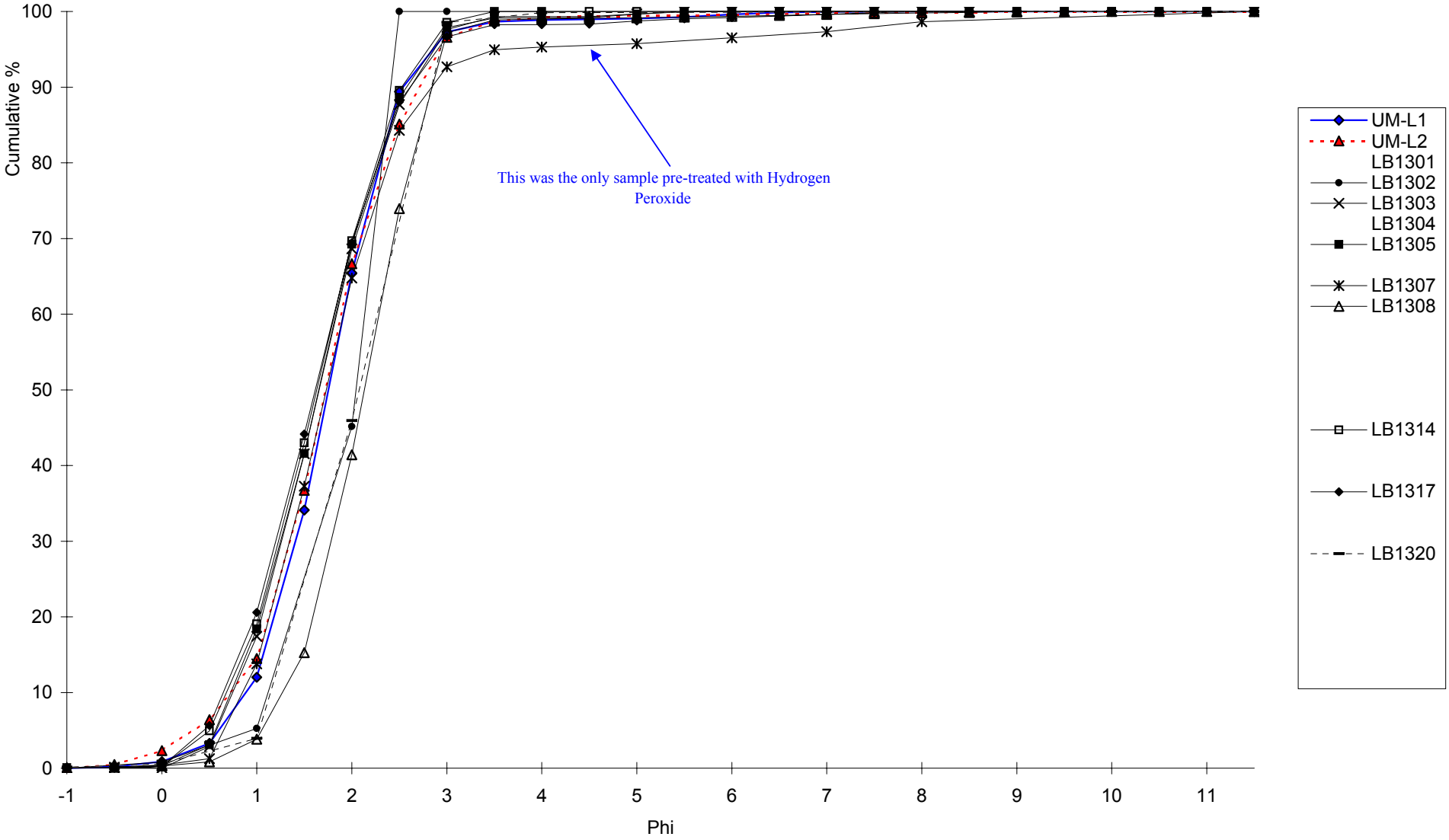


Figure 5. Z-scores for PS28 derived statistics (replicated data not displayed).

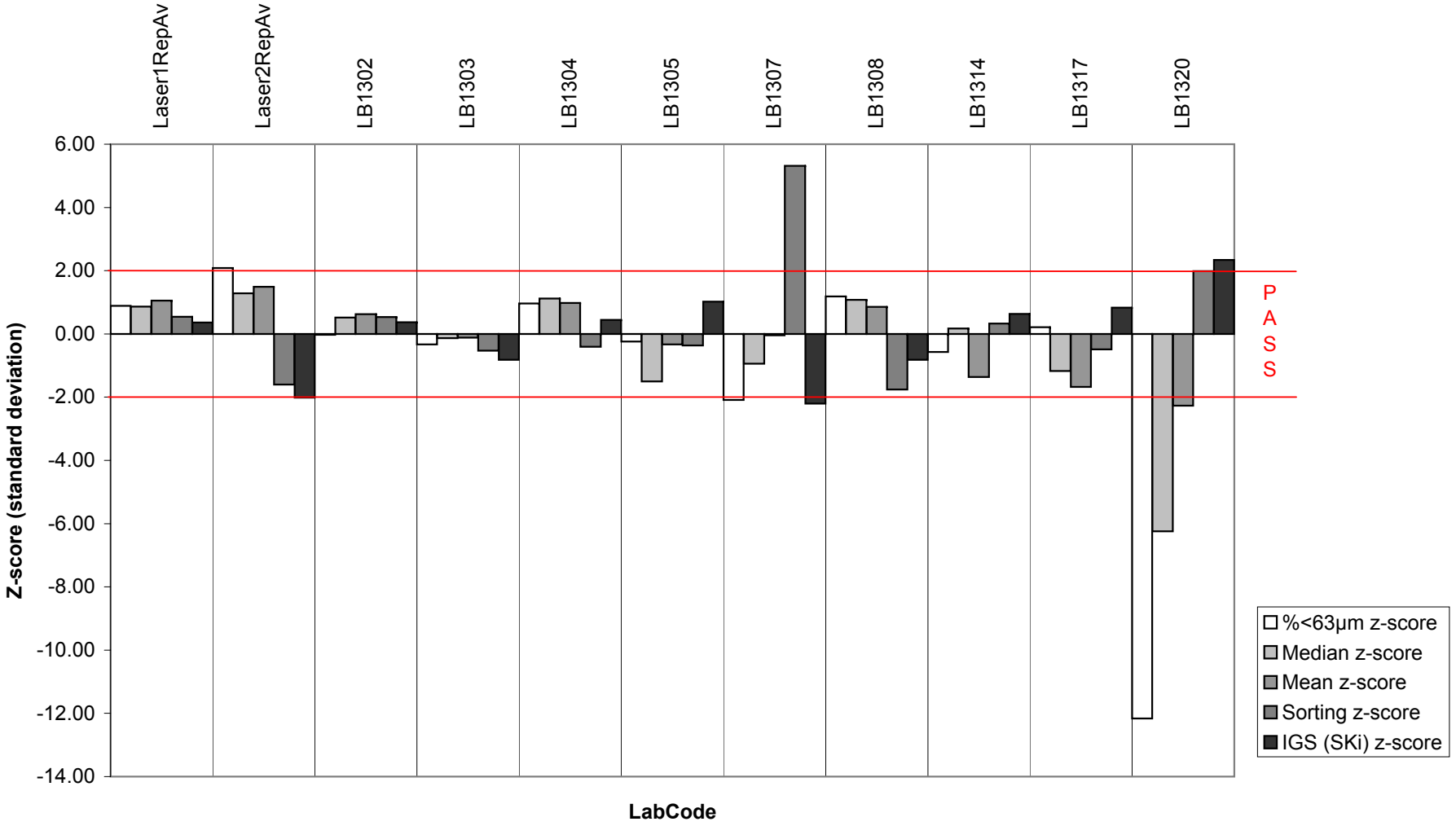


Figure 6. Z-scores for PS29 derived statistics (replicated data not displayed).

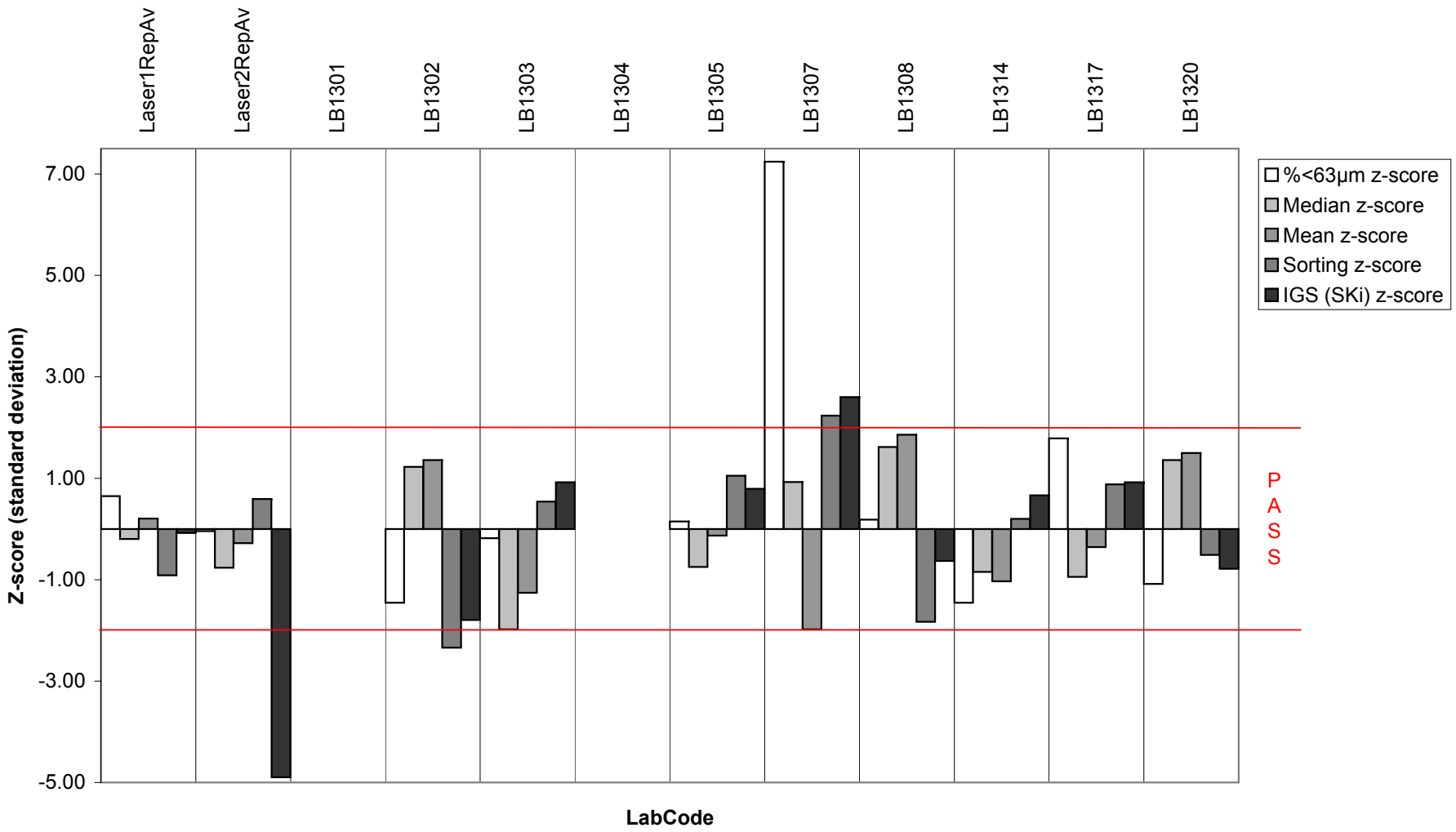


Figure 7. The number of differences from the AQC identification of specimens distributed in RT29 for each of the participating laboratories. Arranged in order of increasing number of differences.

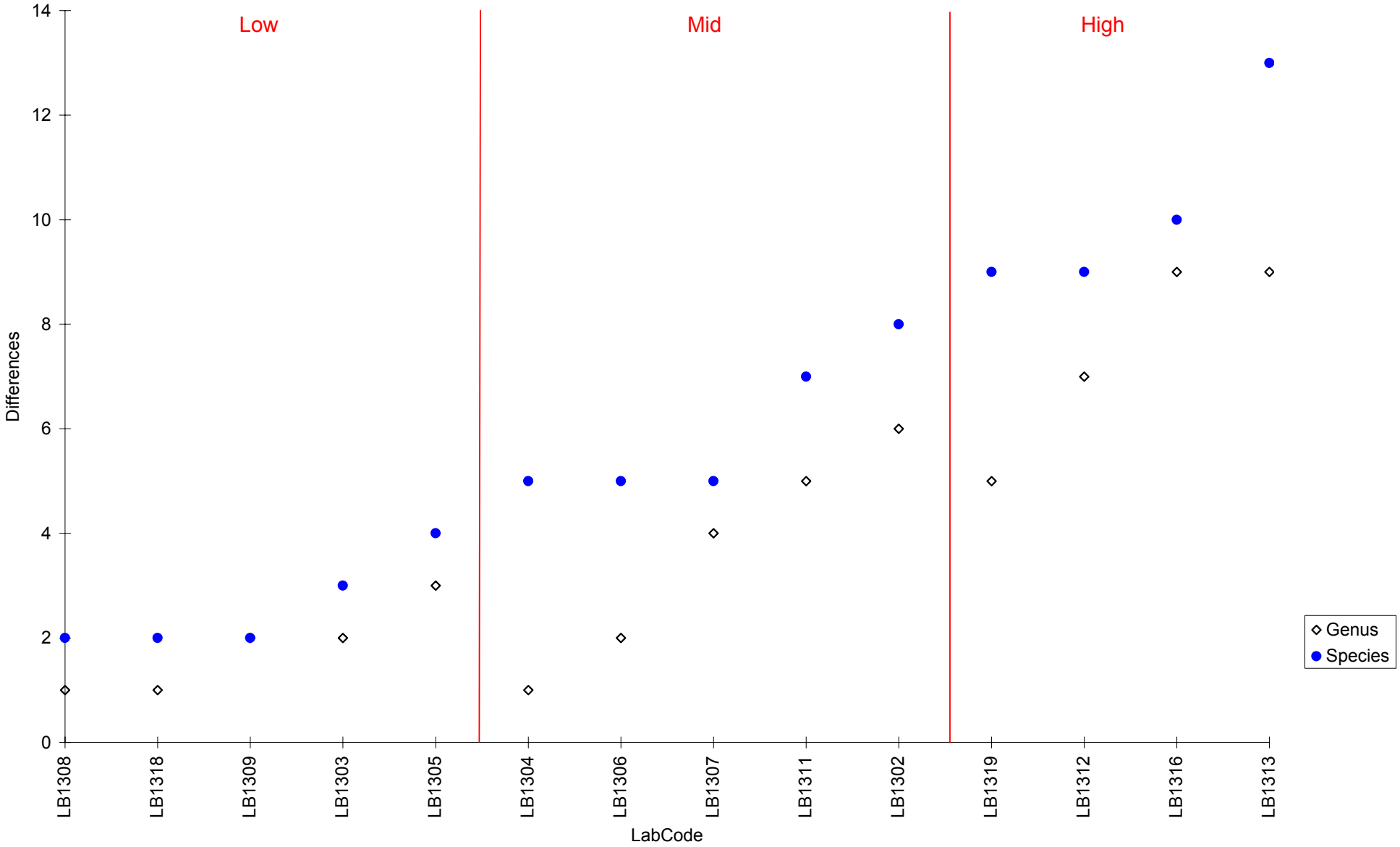


Figure 8. The number of differences from the AQC identification of specimens distributed in RT30 for each of the participating laboratories. Arranged in order of increasing number of differences.

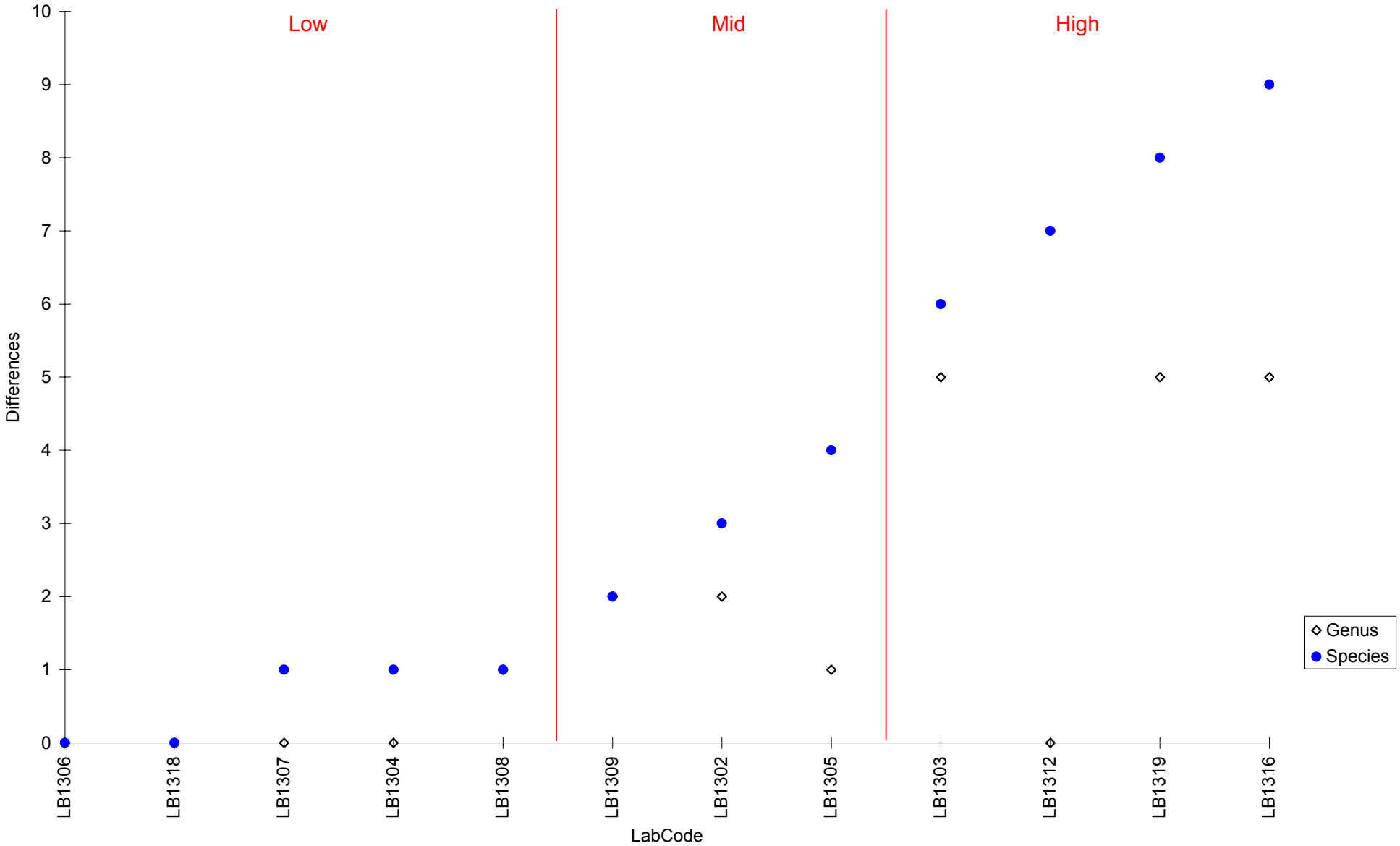
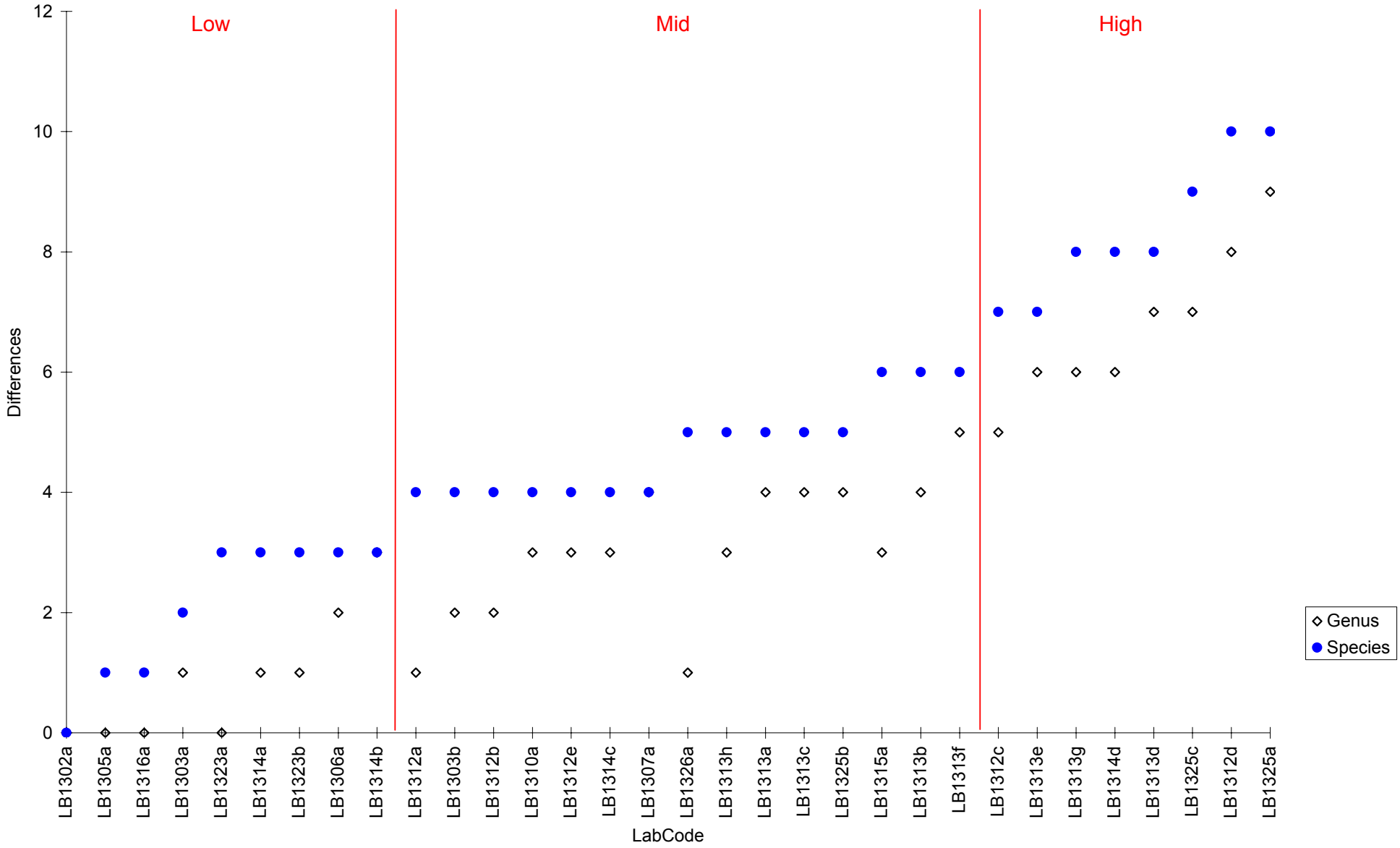


Figure 9. The number of differences from the AQC identification of specimens distributed in RT31 for each of the participating laboratories. Arranged in order of increasing number of differences.



Appendices

Appendix 1.

National Marine Biological Analytical Quality Control Scheme

Participant Laboratory Reference Collection exercise (LR)

Objective:

- To examine the accuracy of identification of fauna recorded in the 'home' area of each participating laboratory
- To encourage the assemblage and use of collections of reference specimens

LR11 is an **'identification amnesty'** exercise – all of the submitted specimens can be deemed unidentifiable or of uncertain identity by the participant laboratory (*i.e.* problem taxa). Submission of problem taxa is optional and laboratories can use this exercise for the verification of normal reference specimens as in previous LR exercises. If unidentified specimens are provided please give as much habitat data as possible to assist identification.

Protocol:

Twenty-five specimens from your laboratory reference material are to be submitted. Free choice is given for specimen selection. All fauna selected should be from waters around the British Isles. If possible, the species selected should differ from those submitted as part of a previous circulation. Duplicate examples of species can be submitted for the purpose of establishing growth series. **Some or all of the twenty-five specimens supplied can be unidentified problem taxa** (these specimens should be indicated as such on the data sheet). The specimens received will be identified according to Unicomarine Ltd. standard practice. If there are any disagreements, upon return of the specimens, we will provide full explanations of our identifications using reference material and images, where necessary. Unicomarine reserve the right to return specimens 'unidentified' if unacceptable mixtures of species are contained within a single taxon vial.

Preparation:

All specimens should be supplied in 70% IMS in individually labelled vials. A LR data sheet is provided for entering details of the specimen name, origin, key used and other details. This sheet has labels attached that should be placed in each of the reference vials. All material will be returned when analysis is complete unless it has been indicated that we may keep material for reference purposes or inclusion in a future NMBAQCS Ring Test.

Timescale:

Please send specimens to Unicomarine Ltd. by 10th November 2006. Results and specimens will be returned as soon after receipt as practicable.

Appendix 2.

1. Description of Scheme Standards

In the third year of the NMBAQC Scheme (1996/97) required levels of performance were set by the NMBAQC steering committee for the Own Sample (OS) and Particle Size analysis (PS) exercises and flags were placed upon the results. The flags applied are based on a comparison of the results from sample analysis by Unicomarine Ltd. with those from the participating laboratories. The Own Sample flagging criteria were reviewed during the seventh Scheme year (2000/01). A new set of NMBAQC standards and exercise protocols was devised (Unicomarine, 2001) and introduced in Scheme year eight (2001/02).

The OS exercise has several aspects, each with a separate standard. Each of the standards has been calculated independently for the three Own Samples received from each laboratory. The PS standard was also altered in Scheme year eight and is no longer based solely upon the determination of the Silt-Clay fraction in the samples. Each particle size sample is now given z-scores for each of the major derived statistics.

The process of assigning the flags for each component is described below. The target standards and recommended protocols may be modified in the future. A single standard 'averaged' value calculated across several components was found to be impracticable.

1.1 Own Sample Standards

Protocol changes introduced in Scheme year eight (2001/02):

- NMMP data to be audited one year in arrears.
- Own Samples to be selected from completed data matrices.
- Remedial Action to be encouraged to improve upon 'fail' flags.

1.1.1 Primary Performance Targets

These targets are stated for all Own Samples and give a clear indication of the samples performance.

1.1.1.1 Extraction/Sorting efficiency - Total taxa target

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted and sorted from the OS samples. The 'correct' total number of taxa is assumed to be that resulting from re-analysis of the samples by Unicomarine Ltd. To achieve a pass the total number of taxa recorded should be within ±10% or ±2 taxa (whichever is greater) of this total.

1.1.1.2 Extraction/Sorting/Enumeration efficiency - Total individuals target

This flag reflects the efficiency with which the laboratory estimated the total number of individuals in the sample. The total should be within ±10% or ±2 individuals (whichever is greater) of the total resulting from re-analysis of the samples by Unicomarine Ltd.

1.1.1.3 Biomass estimation accuracy - Total biomass target

The total value should be within ±20% of the value obtained from re-analysis of the sample.

1.1.1.4 Bray-Curtis comparison target

Comparison of the two data sets, from re-analysis by Unicomarine Ltd. and by the participating laboratory, should result in a Bray-Curtis similarity index of ≥ 90%.

1.1.2 Secondary Performance Targets

These targets are analysed to determine specific areas of processing for remedial action.

1.1.2.1 Extraction efficiency - Taxa in residue target

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted from the sample residue. The total number of taxa is assumed to be that resulting from re-analysis of the fauna and residue by Unicomarine Ltd. To achieve a 'pass' the number of taxa not extracted should be <10% or <2 taxa (whichever is greater) of this total.

1.1.2.2 Identification accuracy – Taxonomic errors target

This flag relates to the performance of the laboratory with respect to the identification of the animals extracted from the sample residue by the participating laboratory. The 'correct' identification is assumed to be that resulting from re-analysis of the sample by Unicomarine Ltd. (following any appeals). To achieve a 'pass' the number of taxa incorrectly identified should be <10% or <2 taxa (whichever is greater) of the number of taxa extracted by the participating laboratory.

1.1.2.3 Extraction efficiency - Individuals in residue target

This flag reflects the efficiency with which the laboratory extracted the individuals from the sample residue. The number of individuals not extracted from the residue should be <10% or <2 individuals (whichever is greater) of the total resulting from re-analysis of the fauna and residue by Unicomarine Ltd.

1.1.2.4 Enumeration efficiency – Enumeration of extracted individuals target

This flag reflects the efficiency with which the laboratory has enumerated the individuals extracted by the participating laboratory. The count variance should be ±10% or 2 individuals (whichever is greater) of the total resulting from re-enumeration of the fauna by Unicomarine Ltd.

1.1.3 Overall Sample Flag

Each Own Sample is assigned an individual flag based upon their Bray-Curtis similarity indices. A five tier system of classifying individual Own Samples is used:

100% BCSI	**Excellent**
95 - <100	**Good**
90 - <95	**Acceptable**
85 - <90	**Fail - Poor – Remedial Action Suggested**
<85	**Fail – Bad - Remedial Action Required**

If an Own Sample achieves a BCSI of less than 90% remedial action is required. The nature of this remedial action can be ascertained by examining the secondary performance targets (See 1.1.2). A remedial action guidance table is utilised to structure any resultant action:

	<5%	**5 – 10%**	**>10% & < or = 2 units**	**>10% & > 2 units**
Individuals missed in residue	-	Review Extraction	Review Extraction	Reprocess – Resort Residues
Taxa missed in residue	-	Review Extraction	Review Extraction	Reprocess – Resort Residues
Taxonomic errors in extracted fauna	-	Review Identification	Review Identification	Reprocess – Reanalyse Fauna
Count variance	-	Review Enumeration	Review Enumeration	Reprocess – Recount Fauna

Version 1.1 Remedial Action Protocol August 2002

Considerable variation in the estimation of biomass (as discussed in earlier reports; NMBAQC Scheme Annual report, 1996/97, Section 3.2.5) has led to the flag for this component being excluded from the determination of the overall sample flag for the OS exercises. Laboratories failing to supply OS data have automatically been assigned a fail flag by default.

1.2 Particle Size Standards

1.2.1 Derived Statistics targets

The derived statistics of %silt-clay, mean particle size, median particle size, sorting and IGS(Ski) are expressed as z-scores based upon all data returned from participating laboratories and the average results obtained from the laser and sieve replicates (analysed by Unicomarine Ltd. to examine sample conformity). The z-scores must fall within ±2SD of the mean for each statistic to achieve a pass:

% silt-clay	**±2SD of all data**
Mean particle size	**±2SD of all data**
Median particle size	**±2SD of all data**
Sorting	**±2SD of all data**
IGS(Ski)	**±2SD of all data**

A “Deemed fail” flag is to be assigned when the required summary statistics are not provided by the laboratory.