BEQUALM - NMBAQC

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report

Year 10

2003/2004

National Marine Biological AQC Coordinating Committee – July 2005

BEQUALM

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Section A – Report from the NMBAQC Co-ordinating Committee

Section B – Report from the Contractor

1. OVERALL SUMMARY

- The NMBAQC Scheme completed its Year 10 in 2003/2004.

- From Year 10 the Scheme has operated under the European BEQUALM (Benthic Effects Quality Assurance in Monitoring) programme and now aims to include participants from other European countries.

- Management of the scheme finances has transferred from the Scottish Environment Protection Agency to the Environmental Agency to facilitate fund flow flexibility, and to save VAT costs.

- Components of the scheme continue to be based on: a whole MacroBenthic sample (MB), Own Samples (OS), Ring Tests (RT), and a Laboratory Reference (LR) for biological determinands, plus Particle Size (PS) tests.

- Participation in the scheme remained high with a total of twenty-four laboratories participating. Thirteen of these laboratories submitted data for NMMP. However only one continental European lab joined the scheme. Participation in scheme components remains variable and several of the **NMMP labs are not fulfilling their requirement to undertake all biological components**.

- Detailed results of the circulations are presented in the contractors report (Section B) where individual laboratory performance is described and standards of achievement against the targets tabulated.

- **Sorting accuracy remains a significant problem**. Laboratories should assess their own procedures with reference to the recommendations now provided by the NMBAQC Review of Standard Operating Procedures (Cooper & Rees, 2002*).

- **The proposed protocol to standardise the faunal groups to be extracted from NMMP samples remains to be completed**.

- **Biomass analysis discrepancies were again evident**, with a great deal of variation amongst labs. The scheme still requires to investigate this issue and to revise the "blotted wet weight technique" for biomass determination.

- In Year 10, seventeen labs submitted 51 Own Samples. **Overall performance was very improved on Years 8 or 9** with over 80% of samples achieving pass levels.

- Five NMMP samples were initially graded unacceptable (*i.e.* Poor or Fail) but remedial action on the relevant replicate batches has been completed on only one sample site to date. **Some NMMP labs are not undertaking mandatory remedial action**.

- The remedial action and flagging procedure for NMMP sites may require modification to ensure non-audited sites are of acceptable quality.

- Guidance notes are required for post audit data amendments.

- The proportion of samples audited per lab may need to be standardised. The current status of NMMP benthic sites needs clarification to ensure that all required data sets are being collected and presented for audit.

- Further procedural guidance on presentation and interpretation of PS data is required. A protocol for applying an overall 'Pass/Fail' flag on the Particle Size (PS) exercise remains to be devised.

- The provision of a standard database of taxonomic literature used for invertebrate identification would be beneficial.

- The identification status of specimens submitted for the Laboratory Reference (LR) exercise requires clarification by individual laboratories.

- A second epibiota ring test is now available on the NMBAQC website. The format is interactive with sets of images of different biota groups. Other pages of the website now require updating and re-vamping.

- The scheme contributed to a workshop on Seabed Mapping at the Dunstaffnage Marine Lab and organised an identification workshop on benthic invertebrate groups at the Dove Marine Lab.

* Ref:. Cooper K.M. & Rees, H.L. (2002). National Marine Biological Control Scheme (NMBAQC): Review of Standard Operating Procedures. NMBAQC/CEFAS Science Series, Aquatic Environment Protection: Analytical Methods No.13. 57pp.

2. SCOPE OF THE SCHEME

The Biological Effects Quality Assurance in Monitoring Programmes (BEQUALM) scheme has adopted the UK Marine Biological AQC (NMBAQC) Scheme as a model to progress its community structure analysis component. This involved offering the services of the present UK NMBAQC scheme's contractor to other European laboratories who participate in international or national monitoring programmes, since April 2003.

The tenth year of the NMBAQC Scheme followed previous years with the emphasis on assessment of participant analytical performance on "own samples" of macrobenthos, along with contractor supplied ring test sets of faunal specimens and sediments. In total seventeen participants supplied macrobenthic own samples and have now been judged against the NMBAQC standards (derived in 1996/97) as modified in 2001/02.

Scheduled circulations:

a) 1 contractor supplied MacroBenthic sample (MB).

b) 3 participant supplied macrobenthic Own Samples (OS) to be (re)analysed by Unicomarine.

c) 2 contractor supplied Particle Size (PS) sediment samples.

d) Ring Tests (RT) as follows:

1 contractor supplied ring test of 25 diverse species.
1 contractor supplied ring test targeted 25 taxa from a marine gravel habitat.

e) 1 participant supplied Lab Reference (LR) set of 25 different reference specimens.

The samples were sent out to participants at staggered intervals during the year with set time scales for sample or data returns to Unicomarine Ltd.

A detailed breakdown of the results for Year 10, are contained in the contractors report in Section B.

3. ISSUES ARISING

3.1 The aims and composition of the scheme.

The scheme is now encompassed within BEQUALM which aims to develop appropriate quality standards for biological techniques and operate a quality assurance system for labs submitting data for national and international monitoring programmes (see Appendix 5.1). In practice this means improving laboratory skills, improving the consistency and quality of marine biological benthic data, and screening data for the UK NMMP programme.

MacroBenthic Sample: This exercise is designed to examine sample processing skills, in addition to taxonomic skills, based on a sample from a geographical location unfamiliar to participants. In contrast to previous years the MB11 sample was artificially created using pre-sorted muddy sand and adding known species and numbers of taxa along with a set number of pebbles and faunal fragments. Although most of the labs achieved >90% BC similarity, the sorting efficiency of these samples is of concern. None of the participants extracted all the individuals planted in the sample and up to 5 taxa were "lost". In some cases the planted pebbles and fragments of worms and colonial bryozoans were not returned with the residue or faunal fragments vials. The allocation of indeterminate or juvenile specimens to different nominal "taxa" also created additional discrepancies.

Similarly difficulties also persist with determining biomass. Although labs should be following the same protocol, as detailed in the Green Book, the results ranged from 26% below to 11% above the nominal biomass.

Own Samples: The OS exercise is a core element of the scheme and aims to assess laboratory performance on their own samples with the focus on samples collected for the NMMP programme. From Year 8 pre-submission of sample data sets was required to allow a randomised "blind" sample selection. The scoring of the Own Sample exercise also changed in Year 8 to a graded system related to the untransformed Bray-Curtis scores. Data flags are now applied on a sample-by-sample basis. Remedial action was also introduced in Year 8 to improve the quality of data held in the NMMP database. **Completion of remedial action is now mandatory for labs submitting data to the NMMP database and is strongly encouraged for non-NMMP labs.**

Although the performance on the Own Samples shows an improvement from Year 9, there are still a variety of surprising anomalies. One lab apparently carried out an in-situ count and left 600 specimens within the sorted residue. Some labs had failed to supply accompanying

biomass data or supplied data in the wrong format, while others failed to supply split taxa to allow abiomass audit or supplied damaged or dried material.

The Committee are developing a **protocol to standardise the faunal groups to be extracted from NMMP samples**, and to determine what is a reasonable level of identification for all taxa likely to be encountered. This follows on from the NMBAQC Review of Standard Operating Procedures (Cooper & Rees, 2002) and when completed should be included in the Green Book.

Particle Size: The particle size determinands are accepted as a routine biological descriptor and can be carried out by a variety of techniques each of which appears to be fairly consistent in its reproducibility. Most laboratories in this scheme carried out the analysis by either laser granulometry or dry sieving.

This analysis is assigned a pass / fail standard and must be completed by NMMP labs. In Year 9 a new set of pass/fail criteria was introduced, along with an attempt to standardise sediment descriptions using the Folk triangle. The pass/fail criteria are based on z-scores of five determinands. Some labs did not return data for some of these determinands and were deemed fail. Almost all labs provided a pre and post analysis description based on the Folk triangle, although some of the latter were clearly inconsistent with the supplied sample. For the PS23 sample the participants analyses were significantly lower from the Unicomarine Ltd. replicate results for the % silt & clay determinand. An investigation carried out by Unicomarine on the possible impact of sample storage procedures showed that peroxide treatment shifted the cumulative curve about half a phi to the right (*ie* finer sediment) and hence did not explain the silt & clay underestimate. It has been suggested that poor disaggregation of samples after drying may contribute to the anomaly and that this may be compounded by use of lasers with limited ranges. Anomalous results of one lab were traced to errors in a customised spreadsheet used to calculate PSA determinands.

It appears that some procedural inconsistencies which may affect analytical results are not being detailed by labs. It may be worthwhile for labs to check or validate spreadsheets or programmes used to calculate PSA determinands and to protect these from unauthorised customisation. **It is clear that further guidance on procedural documentation as well as presentation and interpretation of particle size data would be beneficial**. Utilisation of soil charts such as the Munsell Soil Color Chart or the Archaeological Soil Recording Chart may be worth investigation.

Ring Tests: The standard ring tests form part of the core programme. The tests provide an excellent training opportunity for analysts allowing them to broaden their taxonomic expertise. Problematical faunal groups may be tackled using targeted ring tests enabling analysts to hone their identification skills on difficult taxa. Analysts receive bulletins updating them on how the various labs have performed and, if discrepancies persist, individual feedback with the contractor is encouraged. As the ring tests are intended for training purposes only, they have not been used to set a pass / fail standard.

Laboratories generally achieved good results on the ring test. Both ring tests comprised a mixture of various taxa but the second test focused on fauna from marine gravel habitats. Minor issues were once again raised in relation to literature used for identification by some labs for scaleworms, amphipods, tanaids, and bivalves. **The provision of a standard literature database could help avoid such problems.**

Laboratory Reference: The initial aim of this component was to encourage labs to establish marine voucher collections from NMMP sites and apply quality control to these 'own specimens'. Assessment of performance in this exercise is difficult as there is currently no clear distinction between specimens, with confident identifications, derived from a reference collection, and difficult specimens, provisionally put forward, pending a second opinion from an external consultant. Participants have been permitted to include up to 2 uncertain taxa within their submission.

The average number of specific differences has changed little from last year, at 3.3 (= 13.2%) from 25 taxa. If it is assumed that each participant includes 2 uncertain taxa, then the results suggest that on average these 2 taxa, along with 1.3 of the remaining 23 "certain taxa" are usually misidentified. Although the LR exercise is not assigned a pass / fail standard, **it would be beneficial if participants clarified the status of their submitted specimens. This would help distinguish mis-identification of assigned reference specimens from that of recognised problematical material.**

3.2 Participation

The number of participating labs has marginally increased in year 10, from 22 to 24, although the level of participation is quite variable (See Appendix 5.2). The participants in 2003/2004 comprised private contractors, university labs and Government labs in Scotland, Northern Ireland, England and Wales. Only one European lab, from Germany, has taken up the services of the scheme via BEQUALM. It seems that the imperative driving participation in AQC schemes is not yet as strong in continental Europe. Thirteen laboratories provide data or analytical services for NMMP components and submit data to the NMMP database. A number of the participants subcontract to a second or third party. While it is in the interest of all laboratories to participate in all components of the scheme, in order to gauge their performance, some laboratories opt to undertake only those components that they regard as compatible with their commercial interests, budgets or time constraints. **However, all laboratories submitting data to the NMMP database must complete all components and are required to carry out remedial actions if needed to achieve a "pass" standard.**

All primary correspondence for the scheme is now via e-mail. Hard copies of data sheets will only be provided where appropriate.

3.3 Submission of data

Participating laboratories are responsible for informing Unicomarine Ltd. of their level of participation in the Scheme. Laboratories must give adequate priority to the NMBAQC Scheme components and endeavour to report within the requested time limits. Laboratories which subcontract work to a second or third party should make the contractor fully aware of the Scheme deadlines.

It remains of concern that some "NMMP labs" which ought to be undertaking all components are not participating in, or not completing, some components. 'Fail flags' which are applied when no data is submitted are perceived as far worse than a participatory 'fail flag'.

3.4 Data feedback

As in previous years some problems were encountered feeding back data due to late or non returns. **Laboratories that miss data or sample return deadlines will be deemed to have failed.**

Participating laboratories are informed of the timetable of circulations and data deadlines at the beginning of each scheme year. They must give adequate priority to the NMBAQC Scheme components.

Laboratories have been issued with their individual results for circulations to allow review of their own performance. The introduction of ring test bulletins (RTB) has improved feedback and emphasised the learning aspect of this component.

3.5 Targets and Standards

The Co-ordinating Committee decided to alter the application of the pass/fail criteria for the Own Sample exercise in scheme Year 8. Data flags are now applied on a sample-by-sample basis using a graded system related to the untransformed Bray-Curtis scores. The five tier system is as follows:

100% BCSI	Excellent
95-<100% BCSI	Good
90-95% BCSI	Acceptable
85-90% BCSI	Poor – Remedial action suggested
<85% BCSI	Fail – Remedial action required

Samples not achieving the required standards (*i.e.* Acceptable or above) are flagged, along with the remaining replicates from the same NMMP site.

The NMBAQC Committee has produced guidelines for remedial action (see Appendix 5.3). Specific details of appropriate remedial action for individual laboratories will be approved by the Committee. Those labs submitting data to the NMMP data set MUST complete the remedial action and re-submit samples for audit. **Data flags will only be removed from all the site replicates once a PASS has been achieved.** Non-NMMP laboratories will have remedial action recommended, although completion of such is optional. There is some confusion among NMMP labs about procedural details of amending data of audited samples prior to re-submission. This should apply both to initial Pass samples and remedial Pass samples. **Further guidance notes on this process are required.**

Seventeen labs participated in the OS exercise, submitting fifty-one samples for audit. The grading of the samples in Year 10 was improved on Years 8 and 9 with only eight samples being graded as less than Acceptable. The percentage of samples achieving Pass level in Year 10 is 84%, the highest pass rate since Year 02 (see Section B, Table 17).

Status	Year .8	Year .9	Year .10
Excellent	3	2	4
Good	17	23	28
Acceptable	15	8	11
Poor	1	2	3
Fail	9	9	5
Total	**45**	**44**	**51**

3.6 Flagging of NMMP data.

Selection of samples for the OS exercise has been randomised from Scheme Year 9. All participating laboratories must submit their previous years completed NMMP data set prior to sample selection. Data submitted to the NMMP database is assumed to be flagged until the NMBAQC auditing process and reporting is completed. Sample sites are then validated if the relevant Own Sample achieves acceptable quality.

The NMMP data matrices submitted for Own Sample audits are shown in Appendix 5.4. Most of the data is derived from the year 2002 except one lab which submitted 2003 data. Although the NMMP Green Book (v.8, Nov.2003 – see www.sep.org.uk) cites 73 sites for benthos analysis, data for only 56 sites has been presented. Moreover 7 of the sites presented (275, 305, 315, 325, 565, and 820) do not match sites in the Green Book. It is evident that for some sites data has either not been generated and/or has not been made available for audit. It is probable that some sites for benthos analysis may have been dropped, and some new sites created in the interim. **Clarification of the current site status should be provided by the monitoring authorities to facilitate the audit process and allow the Green Book to be updated.**

Of the Year 10 samples, five NMMP were originally graded as less then acceptable. To date remedial action has only been carried out on only one of the relevant NMMP sample site batches. Four audited sample sites and their associated replicate samples remain flagged until required remedial action is completed. **It is imperative that all labs submitting data to the NMMP database complete the required remedial actions in order to validate their samples.**

At present the data flagging and remedial action is applied on a sample/site basis and non-audited samples are deemed valid by default. Moreover only 3 samples are selected for auditing per lab irrespective of how many sites the lab monitors. **This procedure appears to raise anomalies with potential quality impacts**. For example one of the labs shown has failed to achieve acceptable grades on all 3 audited samples and has not yet carried out any remedial action. However only the audited sample sites remain flagged and the other non-audited sites are deemed valid by default. Other labs may have quite serious failures on a single sample yet are only currently requested to carry out remedial action on the remaining replicates of that site. **It is apparent that to ensure consistent quality then the proportion of samples audited needs to be standardised. In addition where serious or multiple failures are attributed to a lab then the need to apply remedial action across all the relevant samples from the labs should be investigated and where this is the case then it may be appropriate to flag all these samples until the remedial action is completed.**

Two PS exercises (PS22 & PS23) were distributed in Year 10. Ten laboratories participated but some failed to return completed data. A new pass/fail criteria scheme was introduced in scheme year 8 with assessment using z-scores applied to five parameters; percentage silt and clay, median particle size, mean particle size, sorting coefficient and inclusive graphic skewness. The z-score represents the deviation of a result from the mean population of data in units of standard deviation.

The equation for calculating the z-score is as follows:

$$z = \left| \frac{(x_i - A)}{s} \right|$$

Xi = value obtained by the lab
A = true or assigned value from all the samples (mean with outliers removed)
s = population standard deviation (calculated from results excluding outliers)

As the required confidence limits of the data are **95%** then the limits of acceptable values of z are +2 or –2.

The Z-score Pass/Fail results for the five parameters now appear on the Statement of Performance. **However, a protocol for applying an overall 'Pass/Fail' flag on the PS exercise still remains to be devised. The production of standardised written sediment descriptions based on the summary statistics and/or the Folk Triangle (British Geological Society) is also needed.**

There appears to be some disparity between the sediment parameters requested in the NMMP Green Book, those requested on the NMMP benthos submission spreadsheets, and those requested as supporting parameters on the NMMP database front end. Moreover there appears to be no flagging mechanism operating at present for sediment data or cross-referencing of sediment data held on separate parts of the NMMP database system. **This area requires some clarification to ensure all the relevant data is submitted and that the quality control system is working effectively.**

4. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

The membership of the committee, its role, and that of the contract manager, are outlined in Appendices 5.5, 5.6, and 5.7.

The full report on the NMBAQC Humber Field Methods Workshop held at the University of Hull in 1997 has finally been published (Proudfoot *et al.*2003)[1] by the Environment Agency bringing the wealth of information generated in this exercise into the public domain.

A second epibiota ring test has been constructed by the Joint Nature Conservation Committee and placed on the NMBAQC website (www.nmbaqcs.org). This interactive Epibiota Photographic Identification Test is a compilation of a wide range of images of epifauna (and flora) from UK waters and includes both common and rare species. It provides an opportunity to test identification skills from photos and aims to assist with identification of difficult taxonomic groups with the long term objective of improving the quality of epifaunal survey data. On completion of the test the recorded distribution and conservation status of each species are presented. Scores from previous tests are also available so the site forms a reference source over time. While the addition of the ring test facility has augmented the NMBAQC website, it is now apparent the other information on the website about the scheme is somewhat out of date. A revision of the site structure is clearly needed.

The NMBAQC scheme contributed to a joint workshop on Acoustic Ground Discrimination methods for Monitoring Seabed habitats in UK waters, held at the Dunstaffnage Marine Laboratory, Oban in September 2003. Other sponsors of this workshop included JNCC, SNH, and Argyll & Isles Enterprise. The workshop was hosted by SAMS (Scottish Association of Marine Science) and a full report has since been produced (Brown *et al.*, 2003)[2]. A summary is provided in Appendix 5.8.

The committee's delayed plan for a training workshop on "difficult taxa" was eventually realised with a benthic invertebrate taxonomic workshop held at the Dove Marine Laboratory, Newcastle in November 2003 (see Appendix 5.9 for programme). Participants provided positive feedback on this workshop via a questionnaire. Bernard Picton's revised version of

Southern's Echinoderm Key (yet to be finished) along with Tim Worsfold's draft Oligochaete Key and Eivind Oug's Lumbrinerid Key were all well received.

As in previous years committee members have been involved in the development of benthic biology as a monitoring tool by the statutory agencies for the forthcoming Water Framework Directive (WFD). Committee Members have formed part of the Marine Benthic Invertebrate Task Team (MBITT) - a sub-group of the Marine Task Team for the Water Framework Directive. This group oversees a project being undertaken by the Environment Agency which involves testing classification tools appropriate for the ecological status assessment of benthic invertebrate communities for the purposes of the Water Framework Directive. The report on Phases I & II of this study was published in May 2004 (Prior *et al.*2004)[3] and a summary is provided in Appendix 5.10.

The core role of the NMBAQC Scheme is to provide the quality data on benthic fauna for the UK NMMP. Committee members have been actively involved in analysis and interpretation of benthic data for Phase 2 (99-2001) of the UK NMMP and the results of this analysis of the benthic community structure are summarised in the UK National Marine Monitoring Programme – Second Report (1999-2001)[4], published by the Marine Environment Monitoring Group in August 2004 .

References:

[1] Proudfoot, R.K., Elliott, M., Dyer, M.F., Barnett, B.E., Allen, J.H., Proctor, N.L., Cutts, N., Nikitik, C., Turner, G., Breen, J., Hemmingway, K.L.,and Mackie, T. (2003). Proceedings of the Humber Benthic Field Methods Workshop, Hull University 1997. Collection and Processing of macrobenthic samples from soft sediments; a best practice review. Environment Agency. R & D Technical Report E1 – 13/TR, 128pp.

[2] Brown, C., Golding, N., Mitchell, A., Limpenny, D., Robertson, M., and Service, M., (2003). Mapping seabed habitats in UK waters. Practical Acoustic Ground Discrimination Workshop, September 2003. Workshop Report, Scottish Association of Marine Science Dunstaffnage Marine Laboratory, 47 pp.

[3] Prior, A., Miles, A.C., Sparrow, A. J. & Price, N. ,(2004) Development of a Classification Scheme for the Marine Benthic Invertebrate Component, Water Framework Directive. Phase I & II - Transitional and Coastal Waters. Environment Agency R & D Technical Report E1-116, E1-132, pp.1-83, App. I-VII.

[4] Marine Environment Monitoring Group (2004). UK National Marine Monitoring Programme – Second Report (1999-2001), published by CEFAS, 136pp.

NMBAQC – Section A: Report from the Committee - Appendices

5. APPENDICES

Appendix 5.1 - Role of BEQUALM

The Biological Effects Quality Assurance in Monitoring Programmes (BEQUALM) project was initiated through members of the ICES Working Group on the Biological Effects of Contaminants (ICES WGBEC) and commenced in 1998 as an EU funded research programme, through the Standards, Measurements and Testing Programme of the European Commission. Its aim was to develop quality standards for a range of biological effects techniques and devise a method for monitoring compliance of laboratories generating data from these techniques for national and international monitoring programmes (primarily the OSPAR JAMP CEMP) and also for regulatory purposes. The ultimate goal was to develop a Quality Assurance (QA) system that would be self-financing. All OSPAR JAMP CEMP biological effects data submitted to the ICES database should have accompanying QA provided by BEQUALM.

The BEQUALM self-funded comprises three components –

i) Whole Organism (bioassays and fish disease), led by the Centre for Environment, Fisheries and Aquaculture Science (CEFAS),

ii) Biomarkers, led by the Norwegian Institute for Water Research (NIVA)

iii) Community Analysis, led by the UK National Marine Biological Analytical Quality Control Scheme (NMBAQC).

The BEQUALM Project Office (CEFAS) acts as the overall administrative and co-ordinating centre for the whole scheme.

Each lead laboratory will be organising and conducting a yearly programme of AQC activities, including training workshops and intercalibration exercises, for a range of biological effects techniques. The focus will initially be on establishing QA for techniques that are an integral part of the OSPAR JAMP and CEMP, but it is anticipated that the range of techniques will be extended year on year to include, for example, those standard bioassays that are used for regulatory purposes. Organisations participating in the BEQUALM scheme will be able to demonstrate that they are producing data that is compliant with appropriate, defined quality standards and is Quality Controlled.

Details of the scheme, the programme of events for each component, registration fees and contacts are available on the website www.bequalm.org.

Appendix 5.2 - NMBAQC Participants - Scheme Year 10 - 2003/2004

a) Laboratories

AstraZeneca Ltd., (Brixham Environmental Laboratory)

CEFAS (Centre for Environment, Fisheries and Aquaculture Science, Burnham Lab.)

DARDNI (Department of Agriculture and Rural Development for Northern Ireland)

Ecomaris Ltd. (Huntingdon, Cambridgeshire)

Environment Agency (North East, Newcastle)

Environment Agency (Anglian, Lincoln)

Environment Agency (Thames, Camberley)

Environment Agency (Southern, West Malling)

Environment Agency (South West, Blandford Forum)

Environment Agency (Wales – Cardiff)

Environment Agency (Wales – Llanelli)

EHS (Water Management Unit, Environment & Heritage Service, Lisburn, Northern Ireland. Formerly Industrial Research & Technology Unit, IRTU)

Emu Ltd. (Hayling Island Marine Lab., Hampshire)

ERT (Scotland) Ltd. (Environment & Resource Technology, Edinburgh)

Environmental Services (Institute of Aquaculture, University of Stirling, Scotland)

Federal Environmental Agency (UBA), Berlin, Germany

Fugro Survey Ltd. (Environmental Division, Great Yarmouth)
(formerly Svitzer Ltd.)

Hebog Environmental (Gwynedd, Wales)

IECS (Institute of Estuarine and Coastal Sciences, University of Hull)

MES Ltd. (Marine Ecological Surveys Ltd., St.Ives, Cornwall)
(now moved to Bath)

SAMS Research Services Ltd. (Dunstaffnage Marine Laboratory, Oban, Scotland)
(formerly SEAS Ltd.)

Scottish Environment Protection Agency (Highlands, Islands & Grampian Area, Dingwall)

Scottish Environment Protection Agency (South East Area, Edinburgh)

Scottish Environment Protection Agency (South West Area, Glasgow)

Appendix 5.2 Contd. - NMBAQC Participants - Scheme Year 10 -

b) Laboratory Participation Levels

Year 10 (2003/04) Labs.	MB	OS	PS	RT	LR
AstraZeneca, Brixham Environmental Lab	0	1	1	1	1
CEFAS - Burnham	1	1	1	1	1
DARDNI - Belfast	1	1	1	1	1
Ecomaris Ltd.	0	1	0	0	0
EA NE - Newcastle	0	1	0	0	0
EA Anglian - Lincoln	0	1	0	0	0
EA Thames - Camberley	0	1	0	1	0
EA Southern - West Malling	0	1	0	1	1
EA SW - Blandford	0	1	0	1	1
EA Wales - Cardiff	0	1	0	1	0
EA Wales - Llanelli	0	0	1	0	0
EHS (formerly IRTU)	1	1	1	1	1
Emu Ltd.	1	1	1	1	1
ERT (Scotland) Ltd.	1	0	1	1	1
Environmental Services (Inst. of Aquaculture)	0	0	0	1	1
Federal Environmental Agency (UBA)	1	0	0	1	0
Fugro Survey Ltd. (formerly Svitzer)	0	1	0	0	0
Hebog Environmental	0	0	0	1	1
IECS - University of Hull	0	1	1	1	1
Marine Ecological Surveys Ltd.	1	0	0	0	0
SAMS Research Services Ltd. (formerly SEAS Ltd.)	1	0	0	1	1
SEPA Highlands Islands and Grampian - Dingwall	1	1	0	1	1
SEPA Southeast Area - Edinburgh	1	1	1	1	1
SEPA Southwest Area - Glasgow	1	1	1	1	1
Tots.	11	17	10	18	15

MB – Macrobenthos exercise
OS – Own Sample exercise.
PS – Particle Size exercise.
RT – Ring Test exercise
LR – Laboratory Reference exercise.

c) Other Participating Organisations

Other organisations contribute to the scheme but only participate at an information exchange level. These include:

English Nature (EN)
Scottish Natural Heritage (SNH)
Countryside Commission for Wales (CCW)
Environment & Heritage Service, Dept.of Environment, Northern Ireland (EHSNI)
FRS / SEERAD (Fisheries Research Services, Scottish Executive Environment & Rural Affairs Department)

Appendix 5.3 Remedial Action Guidelines

If an Own Sample achieves either a 'Poor' or a 'Fail' NMBAQCS flag (i.e. <90% BCSI) then the sample is reviewed by the NMBAQC Committee to ascertain whether any remedial action needs to be applied to the remaining NMMP replicates. The remedial action required is then based upon the samples performance in following criteria:

	<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**

*Note that allowances are made for small samples in which single errors can represent significant percentage errors. If the % error is greater than 10% but the number of error units (i.e. missed individuals, missed taxa or taxonomic errors) is less than or equal to 2, a review of the failing category is suggested rather than reprocessing.

NMBAQC Year 8 examples:

Shaded cells with bold type represent a failing category in need of reprocessing (i.e. data and/or residue to be reaudited following remedial action). Bold type represent a category in need of review by participant (i.e data to be altered in-house prior to submission to the client).

	% - Units shown in brackets				
LabCode; OS Code (%BCSI)	**Individuals missed in residue**	**Taxa missed in residue**	**Taxonomic errors in extracted fauna**	**Count Variance**	**Remedial Action**
LB08XX; OSXX (55.86%)	**32.3% (21)**	**23.1% (6)**	**30% (6)**	3.1% (2)	**Reanalyse remaining replicates**
LB08XX; OSXX (89.86%)	0% (0)	0% (0)	**8.1% (3)**	0.6% (1)	**Review identification**
LB08XX; OSXX (72.07%)	**44.4% (157)**	**25% (1)**	0% (0)	0.8% (3)	**Resort remaining residues**
LB08XX; OSXX (84.62%)	**14.3% (2)**	0% (0)	**16.7% (1)**	0% (0)	**Review extraction; Review identification**
LB08XX; OSXX (84.32%)	0% (0)	0% (0)	**19.4% (6)**	1.1% (1)	**Reanalyse remaining fauna**
LB08XX; OSXX (80.31%)	**9.9% (20)**	**23.4% (11)**	**19.4% (7)**	0.5% (1)	**Reanalyse remaining replicates**
LB08XX; OSXX (78.95%)	**27.3% (6)**	**15.4% (2)**	**9.1% (1)**	0% (0)	**Resort remaining residues; Review identification**

Appendix 5.3 (Cont.)

NMBAQC Scheme Action Protocol for NMMP Own Samples

	Criteria	Category	Remedial Action	
			Review SOP	Reprocess (remaining replicates)
Individuals	Count Variance	Enumeration	Counter malfunction	Recount - submit for audit (excl. residue)
			Biomass loss/damage	-
			Handling care	-
			'Countable' recording policy	Recount - submit for audit (excl. residue)
			In situ approximation	Recount - submit for audit (excl. residue)
	Missed Individuals In Residue	Extraction	Floating & blasting methods	Resort residue - submit residue for audit
			Petri dish searching methods	Resort residue - submit residue for audit
			Tray extraction procedures	Resort residue - submit residue for audit
			Quality Assurance mechanisms	Resort residue - submit residue for audit
Taxa	Missed Taxa In Residue	Extraction	Floating & blasting methods	Resort residue - submit residue for audit
			Petri dish searching methods	Resort residue - submit residue for audit
			Tray extraction procedures	Resort residue - submit residue for audit
			Quality Assurance mechanisms	Resort residue - submit residue for audit
	Taxonomic Errors	Identification	Literature	Rework fauna (In part or complete)
			Reference collection	Rework fauna (In part or complete)
			Staff training/contractor	Rework fauna (In part or complete)
			Quality Assurance mechanisms	Rework fauna (In part or complete)

Appendix 5.4
NMMP Sample Flagging - Year 10

Lab	Data Matrices Submitted	Own Samples	Grade	Flag Status
	Year Site - Location			
A	2002_45 CMT5	-		Deemed validated
	2002_55 CMT7	Rep3 (OS23)	Acceptable	Validated
	2002_70 STN H	Rep1 (OS24)	Acceptable	Validated
	2002_76 L.Linnhe	Rep5 (OS25)	Good	Validated
B	2002_175 Kingston Hudds	Rep1 (OS23)	Acceptable	Validated
	2002_175 Kingston Hudds	Rep 5 (OS24)	Good	Validated
	2002_208 Kincardine	Rep 4 (OS25)	Acceptable	Validated
C	2002_210 Yarrow Slake	RepB (OS23)	Good	Validated
	2002_220 Budle Bay	-		Deemed validated
	2002_225 Hebburn	-		Deemed validated
	2002_235 Ferry Crossing	-		Deemed validated
	2002_265 Alex. Bridge	RepB (OS24)	Acceptable	Validated
	2002_270 Off Seaham	-		Deemed validated
	2002_275 Sandy Point	-		Deemed validated
	2002_305 Bamlett's Bight	-		Deemed validated
	2002_315 No23 Buoy	RepA (OS25)	Fail	Flagged
	2002_325 Phillips Buoy	-		Deemed validated
	2002_755 Seacombe Ferry	-		Deemed validated
	2002_765 Ch. C1 Buoy	-		Deemed validated
	2002_766 u/s 11 mile post	-		Deemed validated
	2002_767 North Bay	-		Deemed validated
	2002_768 St. Bees	-		Deemed validated
D	2002_357 Grimsby Roads	RepC (OS23)	Good	Validated
	2002_358 Sunk Island	RepC (OS24)	Acceptable	Validated
	2002_388 WW19 off Boston	RepC (OS25)	Good	Validated
E	2002_389 W45 (Reps.B,C)	(OS23,OS24)	Acceptable	Validated
	2002_389 W45	RepD (OS25)	Excellent	Validated
F	2002_435 Woolwich (Reps.2,5)	(OS23/OS24)	Good	Validated
	2002_455 Mucking	Rep4 (OS25)	Good	Validated
G	2002_505 Dock Head	RepA (OS23)	Good	Validated
	2002_526 Burham	RepA (OS24)	Good	Validated
	2002_527 Sun Pier	RepA (OS25)	Good	Validated
H	2002_245 NSTF14	RepC (OS23)	Good	Validated
	2002_345 NSTF53	RepC (OS24)	Good	Validated
	2002_536 Lyme Bay	-		Deemed validated
	2002_605 Celtic Deep	RepC (OS25)	Good	Validated
I	2002_555 Warren Point	-		Validated
	2002_565 Hamoaze	RepB (OS24)	Good	Validated
	2002_566 Upper South Deep	RepD (OS25)	Good	Validated
	2002_567 Wytch	-		Validated
	2002_576 Jennycliffe	RepC (OS23)	Good	Validated

Appendix 5.4 Contd. –

NMMP Sample Flagging Year 10

Lab	Data Matrices Submitted	Own Samples	Grade	Flag Status
	Year Site - Location			
J	2002_625 Purton	RepD (OS23)	Poor	Flagged
	2002_635 Bedwin	-		Deemed validated
	2002_645 Peterstone	-		Deemed validated
	2002_646 Cosheston Point	-		Deemed validated
	2002_647 Ynys-hir	RepB (OS24)	Fail	Flagged
	2002_648 Bontddu	RepE (OS25)	Fail	Flagged
	2002_690 Mostyn Bank	-		Deemed validated
K	2003_845 BL5	RepD (OS23)	Good	Validated
	2003_820 BR3	-		Deemed validated
	2003_880 Kilderry	RepC (OS24)	Good	Validated
	2003_825 IS1	RepD (OS25)	Good	Validated
L	2002_806 NMP4	-		Deemed validated
	2002_807 NMP5	RepA (OS23)	Good	Validated
	2002_808 Buoy(NMP6)	RepA (OS24)	Excellent	Validated
	2002_865 NC2(NMP2)	-		Deemed validated
	2002_875 NC1(NMP1)	-		Deemed validated
	(2002_NMMPtrialsite grab)	Rep1 (OS25)	Excellent	Validated

Appendix 5.5

NATIONAL MARINE BIOLOGICAL AOC COORDINATING COMMITTEE
Membership - Scheme Year 10 (2003/04)

Dr. M. Service (Chair)	DARD(NI) - (Department of Agriculture & Rural Development (Northern Ireland), Agriculture, Food and Environmental Science Division.
Mrs. E . Hamilton (Contract Manager)	SEPA South East (Scottish Environment Protection Agency)
Mr. T. Mackie (Secretary)	EHS, DOENI (Environment & Heritage Service, Department of Environment, Northern Ireland)
Mr. N. Proctor*	IECS (Institute of Estuarine & Coastal Studies. University of Hull)
Mr. M. Robertson	FRS / SEERAD (Fisheries Research Services, Scottish Executive Environment & Rural Affairs Department)
Dr. H. Rees	CEFAS (Centre for Environment, Fisheries and Aquaculture Science)
Mr. K. Cooper	CEFAS
Ms. S. Peaty**	Environment Agency, North-east
Ms. L. Richardson	Environment Agency, Wales
Mr C. Ashcroft	Environment Agency
Dr. J. Davies***	JNCC (Joint Nature Conservation Committee, Peterborough)
Mr. M. O'Reilly	SEPA South West (Temporary Contract Manager – April-Dec.2003)

* Nominated representative for non-agency labs/independent consultancies.
** Replaced by C. Ashcroft as EA/finance manager in Dec. 2003.
***Represents the nature conservation agencies (JNCC, EN, SNH, CCW, EHSNI)

Appendix 5.6 - ROLE OF THE NATIONAL MARINE BIOLOGICAL AQC COMMITTEE

The functions and role of the committee for the scheme are as follows:

1. Define what services are required with particular reference to the UK NMP.

2. Interact with Environmental Agency (EA) as managers of the contract.

3. Review other organisations/laboratories that should be approached to join the scheme.

4. Agree and set an annual budget and itemise contributions from individual participants.

5. Agree the funding requirements of EA to service the scheme and the committee.

6. Develop all necessary definitions.

7. Develop and document an overall plan for the scheme.

8. Receive and review reports from participating laboratories on any problems arising from internal and external AQC exercises.

9. Receive and review reports from EA on the management of the scheme.

10. Establish the frequency and location of committee meetings.

11. Receive and review reports from the tendering organisation on AQC exercises.

12. As necessary, establish ad-hoc groups to address problems as they arise and provide members to chair each sub-group.

13. Produce an annual report which will be presented to MPMMG for information.

14. Establish links and stimulate collaboration with international intercomparison exercises.

15. Encourage accreditation and co-ordinate in-house AQC policy.

16. Make recommendations and receive reports from participating laboratories on in-house AQC.

17. Establish a timetable and dates for reports.

Appendix 5.7 - NATIONAL MARINE BIOLOGICAL AQC SCHEME

ROLE OF THE CONTRACT MANAGER

Objectives

1. To establish a managed national marine biological quality control scheme.

2. To recommend quality materials where appropriate.

3. To manage the scheme's finances

Schedule of Work

1. Provide operational support for the National Co-ordinating Committee.

2. Implement the plan of the national AQC scheme.

3. Receive and manage funds donated by participating members of the AQC consortium.

4. Co-ordinate with the Committee the contents of the tender document, issue to relevant laboratories, evaluate tenders, provide a report with recommendations to the Committee and agree the contract.

Appendix 5.8 Mapping Seabed Habitats in the UK. Practical Acoustic Ground Discrimination Workshop, Dunstaffnage Marine Laboratory, September 2003.

Workshop Report –Executive Summary

In recent years the application of acoustic mapping methodologies, in particular the use of acoustic ground discrimination systems (AGDS) used in conjunction with ground-truth sampling, has become common practice in monitoring and mapping seabed habitats at a number of Special Areas of Conservation (SACs) around the UK coastline. Whilst this approach offers advantages over more traditional style benthic grab surveys, the accuracy of the spatial distribution maps produced from such surveys has on occasions been questionable.

Previous investigations into the application of AGDS have gone some way to assess the benefits and limitations of such systems for continuous coverage seabed mapping. The findings from many of these previous studies were used to develop procedural guidelines for conducting AGDS surveys which are presented as part of the Joint Nature Conservation Committee (JNCC) Marine Monitoring Handbook. However, as the number of research/contract groups undertaking broad-scale seabed mapping activities at various sites around the UK coastline increases it is essential to improve communication between these groups and to further refine guidelines and recommendations on best practice for the production of full-coverage seabed biotope maps using AGDS. To address these issues a UK National Acoustic Ground Discrimination Workshop was hosted by the Scottish Association for Marine Science at Dunstaffnage Marine Laboratory from 6-11th September 2003.

The workshop brought together a number of UK research/contract groups who use the AGDS, RoxAnn, for the production of biotope maps. The main aim was to critically evaluate this acoustic system for use in mapping seabed biotopes. A small test site on the west coast of Scotland, within the Firth of Lorn candidate SAC, encompassing a wide range of benthic habitats was chosen as the study site. Prior to the workshop, the area was surveyed using sidescan sonar to accurately map seabed features and two contingency RoxAnn data sets were collected. Ground-truthing using a drop-down video system was also carried out at various sites across the area for the purposes of external validation of the final habitat maps. The first two days of the workshop were held at sea and participants were invited to apply their own mapping methodology over this study area using at least 2 separate RoxAnn systems. Issues such as survey design, system set up and data quality assessment were addressed. A common ground-truthing data set (underwater video data) was also collected from within the test site during this time, and issues relating to the selection of ground-truthing stations were discussed.

The common ground-truthing data set was then used during the processing of the RoxAnn data sets back at the laboratory during a 2-day data-processing workshop.

Appendix 5.8 Contd. Mapping Seabed Habitats in the UK.

Workshop sessions were run covering various aspects of data handling, quality assessment and data processing to review methods of best practice. Spatial coverage maps were produced from each of the RoxAnn data sets and the accuracy and predictive capability of each map was then tested against the external ground-truthing data set collected prior to the workshop. A total of four different RoxAnn data sets were collected and processed during the workshop to assess aspects such as between-system variability, survey design and data quality.

The final session of the workshop was open to all interested parties within the UK; the primary focus of this session was to present the findings of the workshop to non-specialist environmental managers/advisors involved in the implementation and end use of biotope maps. Issues relating to accuracy, predictive capability and system limitations were discussed to provide a better understanding of this type of mapping approach to non-specialists who regularly use the out-puts from such surveys.

Comparisons between the four maximum likelihood classification maps produced from the four RoxAnn datasets collected was done using internal and external accuracy assessment techniques based on the video ground-truth data sets. These results revealed a moderate level of agreement in terms of the spatial distribution of the six habitat classes (life-forms) identified within the study area between the four data sets. The ability of the RoxAnn system to identify discrete seabed features mapped using sidescan sonar was also tested. RoxAnn consistently overestimated the percentage of rocky reef habitat and underestimated the percentage of mud habitat within the area compared to that measured by sidescan sonar. A number of recommendations relating to the use of AGDS for the production of continuous coverage maps and relating to the JNCC Marine Monitoring Handbook guidelines are proposed.

Appendix 5.9 - BENTHIC INVERTEBRATE TAXONOMIC WORKSHOP PROGRAMME

NMBAQC Scheme Taxonomic Workshop 24th-28th November 2003 (Dove Marine Laboratory, Cullercoats, Tynemouth)

Day	Session	Programme	Aims	Leader
24th Nov 2003	am	Arrival. Registration. Laboratory set-up.	Register participants. To prepare laboratory equipment for practical sessions the following day.	-
	2:00pm	Introduction. General information.	Welcome participants. Q&A session regarding workshop. Outline timetable.	Tim Mackie (NMBAQCC) David Hall (Unicomarine Ltd.)
	2:30pm	Talk – The Dove Marine Laboratory. History. Research. Local attractions. Lab. rules (H&S issues).	To give history of Dove Marine Lab. and facilities. Tour/Maps – areas of local interest (biological and otherwise). Pub & food guide.	Jane Delany (Dove Mar. Lab.)
	3:45pm	Talk – Impacts of trawling on benthic biogeochemistry – PhD thesis.	Outline one of the research projects at the Dove.	Phil Percival (Dove Mar. Lab.)
	4:30pm	Talk – Ecological functioning of the marine benthos and the impacts of human activities – PhD thesis.	Outline one of the research projects at the Dove.	Julie Bremner (Dove Mar. Lab.)
25th Nov 2003	9:00am	Discussion / Demonstration – Oligochaeta. Literature. Problem areas. Identification techniques.	To introduce literature containing details of gross morphological features for species identification.	Tim Worsfold (Unicomarine Ltd.)
		Practical - Examination & identification of range of Oligochaeta taxa from reference material.	To use new literature to view own and supplied specimens. View / verify reference material.	Tim Worsfold (Unicomarine Ltd.)
	4:30pm	Talk – European Fisheries Ecosystem Plan – EU funded project (www.efep.org).	Outline one of the research projects at the Dove.	Odette Paramor (Dove Mar. Lab.)

26th Nov 2003	9:00am	Discussion / Demonstration - Introduction to Echinodermata. The five classes. Literature. Problem areas. Demonstration of the classes. Important morphological features of Echinoidea, Holothurioidea, Ophiuroidea. Identification techniques.	To introduce the major features / terminology used for echinoderm identification.	Bernard Picton (Ulster Museum)
		Practical - Examination & identification of range of Echinoderm taxa from reference material.	To obtain identification experience. View / verify reference material.	Bernard Picton (Ulster Museum)
	4:30pm	Sea Life Aquarium group trip.	Visit local aquarium and view live examples of local fauna.	-
27th Nov 2003	9:00am	Discussion / Demonstration - Introduction to Lumbrineridae / Dorvilleidae. Literature. Problem areas. Identification techniques.	To obtain familiarity with the major features of lumbrinerids and dorvilleids.	Eivind Oug (NIVA)
		Practical - Examination & identification of range of Lumbrineridae and Dorvilleidae taxa from reference material.	To obtain familiarity with the major identification features. Gain greater experience of identifying lumbrinerids and dorvilleids. View / verify reference material.	Eivind Oug (NIVA)
	7:30pm	Workshop Dinner – Newcastle City Centre, Spanish restaurant, menu and prices TBA	-	-
28th Nov 2003	9:00am	Discussion - Summary of week. Q&A session.	Distribute/collect workshop feedback forms.	Tim Mackie (NMBAQCC) David Hall (Unicomarine Ltd.)
	am	Departure.	-	-

Appendix 5.10

Summary of Development of a Classification Scheme for the Marine Benthic Invertebrate Component, Water Framework Directive. Phases I & II.

CLASSIFICATION TOOLS: ASSESSING BENTHIC INVERTEBRATE COMMUNITIES

The Marine Benthic Invertebrate Task Team (MBITT) is currently testing benthic macroinvertebrate classification tools, in order to identify those suitable for assessing the ecological status of transitional and coastal waters for the Water Framework Directive (WFD). The project aims to identify WFD compliant classification tools for the marine invertebrate component by November 2004 (Phase III). Currently, MBITT is only considering soft sediment benthic invertebrate communities.

The first two phases of the Project have focused on sourcing and collating historic macrobenthic faunal abundance data into a biological database, UNICORN© (copyright© 1995-2004 Unicomarine Ltd). Without extensive, quality assured data, in an easily accessible format, adequate testing of the classification tools cannot be achieved. Modifications to the UNICORN© database have been developed to assist with testing of the WFD classification tools. Quality assurance (QA) of the electronic data and confirmation of those samples having undergone laboratory analysis has been carried out. The project database now holds over 400 benthic invertebrate surveys (13,000 samples) from UK coastal and transitional waters. The database therefore provides the resource for the project to help (i) establish reference conditions, (ii) set ecological class boundary criteria and (iii) test the suitability of proposed classification indices. Data truncation rules have been established to standardise datasets prior to statistical analysis (required due to discrepancies in the level of taxonomic identification in national datasets).

For benthic invertebrate assessment, 'habitat-specific' reference conditions will be required in order to establish the 'type-specific' reference conditions. Habitats will be defined by the European Nature Identification System (EUNIS) system and assessments carried out at EUNIS level 4. Suggested qualitative reference conditions relate to the EUNIS description for the dominant habitat/s in the water body type. Quantitative reference conditions will be set using expert opinion and existing spatial and temporal datasets to create 'virtual' reference conditions.

Classification tools relating to the benthic invertebrate community were reviewed in Phase I. The project does not aim to create new biological indices, rather it is assessing existing indices with respect to their use in WFD assessment. A 'multimetric' approach to ecological status classification will be adopted, as no single index is able to define the 'health' of the benthic community. The selection of metrics to be included in the multimetric will be established on a habitat basis through Principal Components Analysis (PCA) of the calculated metrics.

Many of the existing biological indices have previously been reviewed and as such the project is only evaluating their performance as part of the multimetric assessment.

Appendix 5.10 –Contd.

However, the individual performance of the two novel indices, Average Taxonomic Distinctness (AvTD) and AZTI Marine Biotic Index (AMBI), have been evaluated prior to considering their inclusion in the multimetric. Testing of these indices has been carried out on national datasets in order to assess their behaviour in the range of UK water body types. AMBI is being considered as a WFD compliant classification tool for UK coastal and transitional waters. Five hundred previously unassigned UK taxa have been identified and sent to the developers of the AMBI index, Borja *et al.*, for inclusion in the index taxon list (ensuring a 'master' European taxon list). The methods used by Borja *et al.*, for establishing boundary criteria are also being followed by the project. Testing of AvTD identified the need for inclusion of a frequency distribution in the index before its potential for WFD assessment can be established. Phase III will continue to address this index when the modification has been completed.

A more rapid approach to the assessment of marine benthic invertebrate communities was considered (both field and laboratory assessment). Ecological assessment of the benthic community in the field could be of potential use for WFD surveillance monitoring. However, the assessment would be reliant on the inclusion of highly trained benthic invertebrate identifiers in the field teams. The cost-benefit of training taxonomic staff for field assessment relative to sending traditional samples to the laboratory is not known and will be further evaluated in Phase III.

A scheme for testing the classification tools has been established (habitat-specific, truncated data, comparative to normative definitions) and this will be followed in Phase III. The variability of the benthic invertebrate community and the risk of misclassification will be evaluated using macrofaunal samples collected specifically for WFD classification tool testing.

NMBAQC – Section B: Report from the Contractor

SECTION B. - REPORT FROM THE CONTRACTOR

SCHEME OPERATION

Lists of Tables, Figures and Appendices

Tables

Lists of Tables, Figures and Appendices (contd.)

Figures

Appendices

Summary of Performance

This report presents the findings of the tenth year of operation of the National Marine Biological Analytical Quality Control Scheme.

The Scheme consisted of five components:

- Analysis of a single marine macrobenthic sample.
- Analysis of two sediment samples for physical description.
- Identification of two sets of twenty-five animal specimens.
- Re-analysis by Unicomarine Ltd. of three own samples supplied by each of the participating laboratories.
- Re-identification of a set of twenty-five specimens supplied by each of the participating laboratories.

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

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. This year, for the first time, the MB samples were artificially created by Unicomarine Ltd. to include set volumes of residue and known quantities of pre-identified fauna. Overall agreement between the laboratories and Unicomarine Ltd. was good and the results were generally higher than those achieved in this exercise for the previous Scheme year. The samples did pose some problems associated with faunal extraction and the degree of sieving effort verses faunal retention. Extraction efficiency, irrespective of sorting, was on average 92%, however three laboratories failed to extract 90% of the individuals 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 81.8% and 99.1% and was better than 90% in 80% of comparisons and better than 95% in 40% of comparisons.

The Scheme year nine protocol for 'blind' **Own Sample (OS)** audits was continued in this Scheme year. Laboratories were to submit full completed data matrices from their previous year's UK NMMP sampling programme (or alternative sampling programmes if not responsible for UK NMMP samples). The new OS flagging system, introduced in Scheme year eight, was continued (See Appendix 2: Description of the Scheme standards for each component). The results for the Own Samples were slightly improved compared to 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 88% of comparisons and better than 95% in 75% of all comparisons. The Bray-Curtis similarity index ranged from 74% to 100% with an average figure of 94%. The Bray-Curtis similarity index was greater than 95% in 63% of comparisons and in most cases (84%) the value of the index was greater than 90%, these samples all achieved 'pass' flags.

The **Particle Size exercises (PS)** were conducted as in the previous Scheme year. The original 'pass/fail' criteria, based upon the average percentage silt/clay figure recorded by all participating laboratories, was deemed unreliable. This was replaced, in Scheme year eight, with the statement of z-scores for the major derived statistics with an acceptable range of ±2 standard deviations (See Appendix 2: Description of the Scheme standards for each component). The influence of analytical technique on the results returned for the PS exercises was evident, especially for the muddy sediment circulated as PS23. As has been previously reported, in most cases there was good agreement between laboratories. The first particle size exercise of the Scheme year (PS22) resulted in five 'fail' flags and eight 'deemed fail' flags (no statistic/data supplied). One of the five 'fail' flags was the result of errors within the calculation for the IGS (Ski) figure. The second particle size exercise of the Scheme year (PS23) resulted in eight 'fail flags' and seven 'deemed fail' flags

(including replicated data). Two of the six 'fail' flags were due to an error in the calculation of IGS (SKi). The amount of silt/clay reported by participating laboratories was extremely variable. Additional preparation and processing information was requested from each participating laboratory to ascertain the cause of this variation. A series of experiments was conducted to assess potential causes of differing results. The experiments concentrated upon the potential impact of pre-analysis storage methods (frozen / unfrozen; refrigerated / room temperature; duration of storage) and sample preparation (peroxide treatment). The experiments concluded that, for PS23, the method of sample storage did not alter the particle size analysis results, however the use of peroxide resulted in a half phi shift in the cumulative curve (*i.e.* slightly finer results). The variation in reported silt/clay can be attributed to sub-sample preparation and laser procedural differences, predominantly the process of disaggregation of silt/clay material after drying.

Two **Ring Tests (RT)** of twenty-five animal specimens were distributed. One set contained general fauna and the other set consisted of twenty-five 'targeted' specimens belonging to offshore gravel habitats. For the general set of fauna (RT22) 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 2.0 generic errors and 6.3 specific errors, this generic error figure is much lower than that of the general ring test from the previous Scheme year. The majority of errors can be attributed to one polychaete and two crustacean taxa. The 'targeted' ring test (RT23 – offshore gravel habitats) posed far fewer problems for species identification. On average each participating laboratory recorded 2.3 generic errors and 3.8 specific errors. Mollusc specimens were responsible for the bulk of these errors (60% of all generic and specific errors recorded).

The identification of a set of twenty-five species selected and supplied by the participating laboratories, from a list distributed by Unicomarine Ltd., were generally accurate. No clear problem areas were identified. However there were differences in the approach to this **Laboratory Reference (LR)** 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 National Marine Monitoring Programme (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 tenth year of the Scheme (2003/04) followed the format of the ninth year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. Twenty-four laboratories participated in the Scheme. Fourteen laboratories were government laboratories (including one German laboratory); ten were private consultancies. Half of the participants (12) were responsible for 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 and standards were applied to agreed components.

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 Components

There are five components; Macrobenthic sample analysis (MB), Ring Test identification (RT), Particle Size analysis (PS), Laboratory Reference (LR) and Own Sample (OS) reanalysis.

Each of the Scheme components is described in more detail below. A brief outline of the information to be obtained from each component 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 details may be found in the 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 97 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 ten participant was given a confidential LabCode in April 2003, 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 4 in Scheme year ten will be recorded as LB1004.

In the present report all references to Laboratory Codes are the post-April 2003 codes (Scheme year ten).

2.2 Macrobenthic Samples (MB)

Artificial, uniformed grab samples containing 'known' marine fauna were created and distributed to each participating laboratory. This exercise has, in all previous years, comprised natural grab samples collected at anchor. The use of an artificial 'known' sample was agreed with the Scheme Contract Manager. Participating laboratories were not aware of this alteration. 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

The bulk of the fauna used for creating MB11 samples were obtained from MB01 samples, which were collected from the Wash using a 0.1m² Day Grab, or from previous ring tests. Each sample contained pre-counted and identified fauna of equal size and quality. In total two hundred and thirteen individuals comprising twenty-two taxa were distributed in each sample. Several faunal fragments and tubes were included to observe potential variances in their treatment. The residues were accurately measured from several components to reproduced a realistic sediment. For further details of the samples components refer to the MB11 Report (Hall, 2004a).

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 1 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, nematodes and copepods not 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 component; measurements were to be blotted wet weights to 0.0001g and to be made for each of the taxa recorded during the enumeration.

Twenty-two 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.* 2002 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 as long as a minimum of twelve samples were included in the data matrix.

2.3.1 *Analysis required*

Participating laboratories were instructed to carry out 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.

Five weeks were allowed for 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 was intended to provide information on the degree of variation between participating laboratories in the production of basic statistics on the sediment characteristics. Two samples of sediment, one coarse the other much finer, were distributed in 2003/04. Both samples were derived from natural sediments and prepared as described below. In each case replicates of the distributed samples were analysed using both laser diffraction and sieve analysis techniques to ensure sample consistency and illustrate variations in techniques.

2.4.1 *Preparation of the Samples – Natural Samples*

Sediment for each of the two circulations was collected from two different locations covering a range of sediment types. A minimum of 30 litres of sediment was removed from a small, visually uniformed, area for each circulation. This material was returned to the laboratory and coarse sieved (2 mm) to remove gravel. 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 laser and half by sieve and pipette. 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 carry out particle size analysis on the samples using their normal technique or sub-contractor 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. Approximately **nine weeks** were allowed for the analysis of each PS sample.

2.5 Ring Test Specimens (RT)

This component 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.

Two sets of twenty-five specimens were distributed in 2003/04. The first of the year's RT circulations (RT22) was of the same form as for the earlier years - the specimens included representatives of the major phyla and approximately 36% of the taxa were crustaceans, 32% were polychaete worms, 28% were molluscs and 4% were anthozoans. The second circulation (RT 23) 'targeted' specimens from marine gravel habitats. Details of substratum, salinity, depth and geographical location were provided for all ring test specimens to assist identifiaction.

2.5.1 Preparation of the Samples

The specimens distributed were obtained from a range of surveys from around the UK. 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 (RT22) and the 'targeted' RT (RT23), all specimens were taken from replicate 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. All specimens were to be returned to Unicomarine Ltd. for verification and resolution of any disputed identifications. This was the same procedure as for earlier circulations. Approximately **nine weeks** were allowed for the analysis of each RT exercise by the participating laboratories.

2.6 Laboratory Reference (LR)

This component aims to address the criticism that some of the taxa circulated in the Ring Tests were unlikely to be encountered by some of the laboratories, and thus were not a valid test of laboratory skills. The participants were required to submit a reference collection of twenty-five specimens for re-examination by Unicomarine Ltd. This exercise encourages laboratories to build extensive, verified reference collections to improve identification consistency. The creation and use of reference collections are viewed as best practice.

2.6.1 Selection of fauna

The different geographical distributions of species meant that a contractor 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. Each laboratory was invited to include, if they wished, two problematic specimens, these were to be excluded from the summary statistics. Specimens wherever possible were to be representatives from UK NMMP reference collections.

2.6.2 Analysis

A prepared results sheet was distributed with the list with attached labels for the laboratories to identify each of the specimens. Participating laboratories were permitted **fifteen 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 2003/04 were undertaken, in varying numbers, by twenty-four 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 component of the Scheme despite originally subscribing to the component.

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 artificial marine macrobenthic sample (MB11) was created from MB01 samples originally collected from the Wash with additional fauna from previous ring test material. The samples comprised approximately half a litre of slightly muddy sand with five pebbles. The samples contained twenty-two species and two hundred and thirteen individuals, covering a variety of phyla. Three out of the ten samples returned had been stained with Rose Bengal during sample processing. One laboratory (LB1018) processed the macrobenthic sample using the wrong sieve mesh (0.5 mm instead of 1 mm) due to the unavailability of the specified sieve. Ten of the eleven laboratories participating in this exercise returned samples and data. Detailed results have been reported to the participating laboratories (Hall, 2004a), additional comments are added below.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB11, a summary of the estimate of numbers of taxa and individuals made by each of the participating laboratories together with the corresponding count made by Unicomarine Ltd prior to sample dispatch. 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 were made to allow direct comparisons to be made, *e.g.* separating / combining adults and juveniles to reflect a common identification policy 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 that there was little variation between laboratories for the percentage of taxa identified in the samples. Up to three taxa (and 14% of the total taxa in the sample) were either not extracted, lost during sieving or not recognised within the picked material. Two laboratories recorded the same number of taxa as Unicomarine prepared within the artificial samples (LB1011 and LB1016). The simple comparison of numbers of taxa can be misleading as taxa counts are affected by inaccuracies in identification, *e.g.* 'oversplitting' (separating a single taxon incorrectly into multiple taxa). For example, one laboratory (LB1016) produced the correct summary number of taxa for the sample but missed five taxa in the residue.

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 or sieved from the artificial sample by the laboratory. Only one laboratory extracted representatives of all the species present in their sample (LB1011). The average number of missed taxa was over two, and in the worst instance five new taxa were missed during the picking or sieving stage of this exercise.

3.1.2.2 *Number of Individuals*

Re-sorting of the sample residue, following analysis by the participating laboratories, retrieved varied numbers of individuals for all ten samples. These data are presented in columns 11 and 12 of Table 1. It must be noted that several specimens not extracted by the participating laboratories were also not found during the residue resorting, these specimens have be attributed to processing loss, *e.g.* passing through or over the 1 mm sieve. The number of individuals not recorded (extracted) from the sample (column 11) is given as a percentage of the total number in the sample (including those missed / lost during processing) in column 12 (*i.e.* column 12 = column 11 / column 7 %). The proportion of missed individuals in 70% of the samples was less than 10% of the true total number in the sample. In the worst instance 14% of the total number of individuals were not extracted during the initial sample processing. The average number of missed / lost individuals was seventeen. A breakdown of the missed individuals by taxonomic group is presented in Table 2. All participating laboratories missed / lost polychaete and mollusc individuals during processing. Echinoderms were the best 'picked' faunal group with just two of the ten participating laboratories not extracting all the specimens.

3.1.2.3 *Uniformity of identification*

Most of the species in the distributed sample were identified correctly by the participating laboratories. Four of the participating laboratories had no taxonomic differences (Table 1, column 15). In the worst instances five taxonomic differences were recorded. On average over one and a half taxonomic differences were encountered per sample.

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 of fauna artificially created by Unicomarine Ltd. The comparison was made by calculating the Bray-Curtis similarity index for the pair of samples using non-transformed data. Prior to analyses of these data some minor adjustments were made to allow direct comparisons to be made, *e.g.* separating / combining adults and juveniles to reflect a common identification policy and remove artificial differences in these data. The results of the calculations are presented in Table 1 (column 13). There was variation among laboratories in the values calculated for the index, from 81.8% to 99.1%, with an average value of 93.5%. The index for the majority of laboratories (8 of 10) was in excess of 90%. Four of the participating laboratories achieved greater than 95% similarity. Two laboratories scored a Bray-Curtis similarity index below 90%; these were 81.8% and 87.6%. It must be noted that although the sample processing details (*i.e.* stated details of faunal groups extracted / not extracted as laboratory standard policy) varied greatly between participants, no countable examples of these variably recorded faunal groups were included in the artificial sample. 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 MB11 circulation is presented in Table 3. Four laboratories did not supply biomass data. The average difference between the two weight values was –3.1%, with the measurement made by Unicomarine Ltd. typically being greater (*i.e.* heavier) 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 –26.4% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +11.4% (measurements by laboratory were greater than those made by Unicomarine Ltd.). The average difference between estimations varied greatly between faunal groups, ranging from –7.6% to +14.1% (from echinoderms to crustaceans, respectively)

3.1.5 *Uniformity of sample sorting / degree of sieving effort*

MB11 was an artificial sample created by Unicomarine, the faunal content of the samples distributed is shown in Table 4. All fauna included in MB11 were obtained from samples previously analysed with a 1 mm sieve mesh. However, it was noted during MB11 preparation that a number of the specimens added to the residue could be lost according to the degree of sieving employed by the participating laboratories. One laboratory, LB1002, retained the residue that passed through the 1 mm sieve mesh. This material was subsequently analysed by Unicomarine to assess the efficiency of sieving by

analysing fauna passing through the 1 mm sieve mesh. Eight specimens from six different taxa were found in the <1 mm residue material, one of these specimens was an otherwise 'unpicked' taxon (*Protodorvillea kefersteini*).

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, fifty-one selected samples were received from seventeen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS23, OS24 and OS25 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 50 ml to 8 L of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 2 to 96, and the number of individuals from 7 to 4313. All seventeen laboratories participating in this exercise returned all three Own Samples, nine of these Own Samples were audited externally by Aquatic Environments due to Unicomarine Ltd. being responsible for the initial sample processing.

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 twenty-six samples (51% 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-five exceptions, the difference was at most eleven taxa and the average difference was one taxon.

The data for the numbers of individuals recorded (columns 6 and 7) shows a range of differences from re-analysis of between 0% and 29%. The average difference was 5.2% (sixteen samples exceeded this average). Seventeen of the samples received, one third of all samples, showed 100% extraction of fauna from the residue (column 12), and in fourteen 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 eleven new taxa found in the residue (column 10). In the worst instance residue was found to contain six hundred individuals, however this is likely to be the result of unspecified *in-situ* recording. 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 twenty-six, and the average number of missed taxa was less than one.

3.2.3 Uniformity of identification

Taxonomic differences between Unicomarine Ltd. and participating laboratorys' results were found in twenty-two (43%) of the fifty-one samples received. An average of just under two and a quarter taxonomic differences per laboratory were recorded; in the worst instance ten 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 74% to 100%, with an average figure of 94%. Five samples from four different laboratories achieved a similarity figure of less than 85%. Four samples gave a similarity figure of 100%, these were submitted by three different laboratories (LB1002, LB1004 and LB1006). The best overall results were achieved by laboratory LB1004, whose results comprised 98.11%, 100% and 100%. The worst overall results were achieved by laboratory LB1020, whose results comprised 89.55%, 83.33% and 73.75%. It is worth noting 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; three laboratories did not supply biomass data; five samples were reported to five decimal places; two laboratories provided biomass data to species but combined all fauna in one vial; one sample contained dried fauna due to storage difficulties. Table 7 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. Thirty-five of the fifty-one samples received have been used for comparative analysis. The total biomass values obtained by the participating laboratories varied greatly with those obtained by Unicomarine Ltd. The average was a +6.2% difference between the two sets of results (*i.e.* heavier than Unicomarine Ltd.), the range was from –56.2% to +45.5%. 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 +1.8% for polychaetes, +3.2% for oligochaetes, +11.4% for nemerteans, +5.4% for crustaceans, +40.3% for Chelicerata, -42.9% for echinoderms, +2.8% for molluscs and –23.5% for all remaining faunal groups. These figures are different to those produced by this same exercise in each of the previous six 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 PS22, nine out of ten participating laboratories returned data (including laboratories with grouped results); one laboratory did not provide data. For PS23, nine out of the ten participating laboratories returned data; one laboratory did not provide data.

3.3.2 *Analysis of sample replicates*

Replicate samples of the sediment used for the two PS distributions were analysed using both sieve and laser techniques. This was adopted after initial exercise results indicated a clear difference according to the analytical technique used to obtain them. Half of the *replicates* were analysed using the Malvern laser and half by the sieve and pipette technique. *Replicate* analyses were performed by Sediment Analysis Services (sieve and pipette technique) and Plymouth University, Geography Department (laser technique).

There was very good agreement between the *replicate* samples from the sandy sediment circulated as PS22; the shape of the distribution curves was similar for the two analytical techniques and they were closely grouped with the sieve curves displaced to the right of the laser curves. This sample had a very low percentage of sediment in the fine fraction (average of 0.48% <63μm). The derived statistic for median particle size (ϕ) were markedly different between the two techniques. The average median particle size from laser analyses was 1.39ϕ, compared with 1.53ϕ from sieve and pipette analyses. Results for the individual *replicates* are provided in Table 8 and are displayed in Figure 1.

Sample PS23 was of a muddy sediment (average of 95.76% <63μm) and the cumulative distribution curves differed between the two techniques. The derived statistic for median particle size (ϕ) were markedly different between the two techniques. The average median particle size from laser analyses was 6.90ϕ, compared with 8.47ϕ from sieve and pipette analyses. The sieve technique showed a larger component of clay and smaller components of coarse and medium silt compared to the laser technique. 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. Figures 5 and 6 show the z-scores for each of the derived statistics. The z-scores were calculated with outliers and replicated data removed from the mean estimations of each of the major derived statistics.

It should be noted that this year one laboratory which normally sub-contract their particle size analysis to another laboratory (also participating), elected to utilise the results from this laboratories for PS22 and PS23. 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 PS22 and PS23 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-second distribution – PS22

There was generally good agreement for PS22 between the results from the analysis of *replicates* and those from the majority of participating laboratories. The results for a single laboratory (LB1013) were adrift due to a higher estimation of the coarse sand fraction. The difference between the analytical techniques was less marked than has been seen for other PS circulations (see Figures 1 and 3).

3.3.3.2 Twenty-third distribution – PS23

There was significantly more spread in the results for this sample (which had a much higher proportion of sediment in the silt-clay fraction) and the difference between the techniques was again evident in the *replicate* samples analysed by Unicomarine Ltd. (see Figures 2 and 4). Table 11 shows the marked variation in data received from the participating laboratories. The derived statistic for %silt/clay ranged from 75.5% to 96.3%, with the majority of laboratories producing figures significantly lower than the *replicate* analyses produced by Unicomarine Ltd. These low values for %silt/clay were clearly anomalous and such variety in results should not be produced by laboratories all using the same technique (laser). Additional processing and preparation information was sought and a series of experiments was conducted to evaluate the potential impacts of storage (freezing, refrigeration, light/dark storage conditions and duration prior to analysis) and preparation (use of peroxide). These experiments have been reported to the NMBAQC Committee (Hall, 2004b). In summary, all experiments showed that storage methods had no obvious effect upon the resultant particle size data for PS23, however peroxide treatment was found to produce a cumulative curve shifted half phi to the right, *i.e.* half phi finer data. Hence, the use of peroxide could not be responsible for such high underestimation of the silt / clay fraction.

The sample responsible for the lowest %silt/clay data (initially analysed by laboratory LB1002) was retrieved and reanalysed by the laser *replicate* analyst to examine possible reasons for the anomalous data. As the laboratory had not indicated the use of peroxide, six subsamples were analysed half of these were treated with peroxide. The reanalyses resulted in cumulative curves that were very similar to those produced by the other *replicates,* therefore no natural differences in the replicate were observed to account for the differing results produced by LB1002. Following discussion with sedimentologists the variance in results, notably the underestimation of the silt/clay proportion, can probably be attributed to poor disaggregation of particles after drying. This has been further exaggerated in sample LB1002 data by the use of laser equipment with a limited range, *i.e.* data range ends at 8ϕ.

3.4 Ring Test Circulations (RT)

3.4.1 General comments

The implementation of this part of the Scheme was the same as previous years. Both RT circulations were accompanied by details of each specimen's habitat details (depth, salinity, substratum, and geographical location). A number of laboratories use this component of the Scheme for training purposes and have selected it preferentially over other components. UK NMMP labs are required to

participate in this component though it is not used when assigning 'pass' or 'fail' flags. Two circulations of twenty-five specimens were made. For RT22 the species were from a variety of Phyla while for RT23 twenty-five specimens from subtidal gravel habitats were 'targeted' for circulation. Other aspects of the two circulations, in particular the method of scoring results, were the same as for previous circulations. In total eighteen laboratories were distributed with RT22 specimens and eighteen laboratories received RT23 specimens. For RT22, thirteen laboratories returned data; three laboratories specified non-participation for this exercise; two did not supply data or indicate non-participation. For RT23, fifteen laboratories returned data; one laboratory specified non-participation for this exercise; two did not supply data or indicate non-participation.

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 species, *e.g. Cirrophorus lyra* for *Paradoneis lyra.*
- Simple mis-spelling of a name, *e.g. Pomatoceros lamarckii* for *Pomatoceros lamarcki.*

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 and 13, respectively, present the identifications made by each of the participating laboratories for each of the twenty-five specimens in RT circulations RT22 and RT23. 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 and 13. 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 2002/03 as there was only a single 'standard' exercise (RT22). RT23 was targeted on fauna from subtidal gravel habitats. 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 (RTB22 and RTB23), outlining the reasons for each individual identification discrepancy. Participating laboratories were instructed to retain their ring test specimens, for approximately two week after the arrival of their results, to facilitate an improved learning dimension via the essential 'second look'.

3.4.3.1 *Twenty-second distribution – RT22*

Table 12 presents the results for the RT22. The agreement at the generic level was relatively good, twenty-six errors were recorded from the thirteen participating laboratories. Agreement at the specific level was also relatively poor, eighty-two errors were recorded. For over half of the distributed taxa there was good agreement between participating laboratories and the identification made by Unicomarine Ltd. The remaining taxa were responsible for the majority of differences, some are described briefly below.

Over one third of the ring test comprised crustacean taxa and these caused problems for several laboratories; specifically *Pseudarachna hirsuta* (adult specimens), *Aora gracilis* (medium sized male specimens), *Tanaopsis graciloides* (medium sized specimens), *Corophium lacustre* (large male specimens), *Sphaeroma hookeri* (juvenile specimen revised as *Lekanesphera hookeri*) and *Orchomene nanus* (large specimens). These accounted for 58% of the generic and 41% of the specific differences recorded. Five of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Potamopyrgus antipodarum, Anaitides mucosa, Pseudoprotella phasma, Levinsenia gracilis* and *Protodorvillea kefersteini*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB22 - Hall & Worsfold, 2003) which was circulated to each laboratory that supplied results for this exercise.

Two of the taxa circulated in RT22 (*Nephtys kersivalensis* and *Sphaeroma hookeri*) were sent for external verification due to significant numbers of participating laboratories agreeing upon alternative identifications. The *Nephtys kersivalensis* were sent to Dr. Peter Garwood of Identichaet (UK). Dr. Sebastien Rainer of CSIRO (Australia) has also offered to review these specimens at a later date. The *Sphaeroma hookeri* were sent to Dr. Niel Bruce of NIWAR (New Zealand).

Dr. Peter Garwood identified the *Nephtys* specimens as *Nephtys hombergii.* He stated that *N. kersivalensis* would have a stout bodyform and would not have branchiae commencing from chaeiger five. He also stated that specimens of such size (<3 cm) are often identified as *Nephtys* sp. juvenile due to uncertainty. His identification concurs with the majority of laboratories for this exercise. Eight laboratories identified this taxon as *N. hombergii*; two as *N. kersivalensis*; one as *N. caeca*; one as *N. cirrosa*; and one as *Nephtys* sp. juvenile. Participating laboratories will be informed of Dr. Sebastian Rainer's external review in due course.

Dr. Niel Bruce identified the *Sphaeroma* specimens as *Lekanesphaera hookeri.* He added that several of the UK species have changed genus. *Sphaeroma serratum* (Fabricius, 1787) remain unchanged; the others are *Lekanesphaera* (*hookeri, monodi* and *rugicauda*). This identification agrees with that of Unicomarine, but disagrees with all except one of the participating laboratories. Ten laboratories identified this taxon as *Sphaeroma rugicauda*; one as *S. monodi*; one as *Cirolana cranchii*; and one as *S. hookeri.*

3.4.3.2 *Twenty-third distribution – RT23*

RT23 contained twenty-five specimens from to marine gravel habitats. The results from the circulation are presented in Table 13 in the same manner as for the other circulations. Only a few of the taxa were responsible for the majority of differences and these are described briefly below.

The agreement at the generic level was relatively good, thirty-five errors were recorded from the fifteen participating laboratories. Agreement at the specific level was also relatively good, fifty-seven errors were recorded. Nine of the twenty-five specimens circulated were polychaetes; seven were molluscs; six were crustaceans; two were echinoderms; and one was a Chelicerata specimen. The bulk of the errors recorded could be attributed to the molluscs. The molluscs accounted for a total of 60% of all generic and 60% of all the specific differences recorded. Seven of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Lepidonotus squamatus, Crangon allmanni, Echinocyamus pusillus, Mysella bidentata, Atylus falcatus, Lumbrineris gracilis* and *Asterias rubens*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB23 – Hall & Worsfold, 2004) which was circulated to each laboratory that supplied results for this exercise.

3.4.4 *Differences between participating laboratories*

Figures 7 and 8 present the number of differences recorded at the level of genus and species for each of the participating laboratories, for RT circulations RT22 and RT23 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 RT22 were of crustaceans. Crustacean specimens (nine specimens in total) were responsible for 62% of generic differences and 45% of the total number of specific differences. Eight of the twenty-five specimens circulated were polychaetes and these produced 20% of the generic and 24% of the specific differences recorded. Molluscs, despite only seven specimens being circulated, accounted for 12% of the total number of generic differences and 28% of specific differences. The single anthozoan specimen circulated produced 8% of the generic and 2% of the specific differences recorded.

Most of the differences of identification in RT23 were of molluscs. Seven mollusc specimens accounted for approximately 60% of the total number of generic differences and 60% of specific differences. Crustacean specimens (six specimens in total) were responsible for 20% of generic differences and 19% of the total number of specific differences. Nine of the twenty-five specimens circulated were polychaetes and these produced 14% of the generic and 18% of the specific differences recorded. Echinoderm specimens (two specimens) were correctly identified by all participants. The single Chelicerata specimen circulated produced 6% of the generic and 4% of the specific differences recorded.

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 to assess the ability of participating laboratories to identify material from their own area, or with which they were familiar. Of the fifteen laboratories participating in this exercise, eleven laboratories supplied specimens for verification; four laboratories decided not to participate.

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. The results for this component are presented in Table 14. There was generally good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd.

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 MB11 comprised an artificial, but typical, coastal marine muddy sand sample. The relatively high numbers of *Mysella bidentata* and the difficulty of separating these from the coarse residue fraction complicated the full extraction of fauna from the sediment. None of the participating laboratories extracted all the countable material from the residue. The overall efficiency of faunal individual extraction was very similar compared to the previous year's exercise (MB10), on average approximately 8% of the individuals were not extracted from the residue. Identification caused various problems for a minority of laboratories; four of the ten participating laboratories correctly identified their entire extracted fauna. Some taxonomic mistakes were noted including *Fabulina fabula, Abra alba, Nephtys hombergii, Ampelisca tenuicornis/Ampelisca brevicornis* and *Nucula nitidosa* misidentifications. Only two of the ten returning laboratories attained a Bray-Curtis similarity index

lower than 90%. The highest Bray-Curtis similarity index achieved was a very high value, 99.05% (LB1011). The average Bray-Curtis figure of 93% is similar to those recorded for MB10 (88%), MB09 (93%), MB08 (95%), MB07 (88%), MB06 (91%), MB05 (85%) and MB04 (82%).

Table 4 shows the variation, by major Phyla, between reported data from the participating laboratories for those artificial samples circulated for the macrobenthic exercise (MB11). All differences can be attributed to sample processing (sieving / extracting / identification) procedures. All samples were provided with exact components of residue and fauna, including faunal fragments. Some laboratories failed to return all of the residue material and faunal fragments, *e.g.* LB1008 did not return the five pebbles, unattached *Flustra foliacea* and *Nereis longissima* fragments. It is assumed that in such instances these components have been disposed during processing.

The need for a standard macrobenthic sample processing policy was clearly emphasised by this exercise. Ten exact replicate samples produced some relatively poor similarity figures from the participant laboratories prior to data adjustments to improve recording differences. The adjustments included several faunal groups; *Urothoe* cf. *elegans* combined with *U. elegans*; *Pholoe synophthalmica* combined with *P. inornata*; Ophiuridae juveniles and *Ophiura* sp. juveniles combined with *O. albida*; *Nephtys kersivalensis* juveniles and *N. caeca* juveniles combined with *Nephtys* spp. juveniles; *Notomastus latericeus* combined with *Notomastus* sp.; *Fabulina fabula* juveniles combined with *F. fabula* adults. Such adjustments could not be possible in 'normal' samples with data processed by 'remote' database managers and consequently, in the absence of a standard policy, these processing differences are etched into each individual laboratory's data.

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. Six laboratories provided biomass data, one laboratory (LB1017) supplied data to five decimal places; two provided a total biomass figure that was lighter than Unicomarine Ltd.; four supplied data that was heavier than Unicomarine Ltd. estimations, one of which was only 1% heavier (LB1008). The extremes recorded were 26% lighter (LB1002) and 11% heavier (LB1016) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories and Unicomarine Ltd. was –3.1% (*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. Last year's average biomass difference figure was –13.3% (MB10).

It seems likely that the main reasons for the observed differences between the biomass 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 MB09 was –14.6%, while for 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 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 techniques specified are derived from the conversion factors used, *i.e.* which technique best reflects the methods specified by the conversion factors to be subsequently used. 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 similarly in the OS exercises and the MB11 exercise. The average value of the index was 94% for the OS, compared with 93% for MB11. The most apparent difference between these exercises was the far better extraction of individuals and taxa from the residue in the Own Samples, the average %

individuals and number of taxa not extracted from the residue for the MB11 samples were approximately double that of the OS returns. This was also true of last year's Own Samples (OS20-22) compared to MB10, but is the complete opposite to these exercises in Scheme year eight, where the MB09 samples showed far better extraction efficiency figures than the Own Samples (OS17-19).

There were fifty-one samples submitted for this component. This was facilitated by the distribution of timely reminders. Approximately 80% of fifty-one samples received exceeded the 90% Bray-Curtis pass mark and approximately 75% of the samples exceeded 95% Bray-Curtis similarity. The average Bray-Curtis similarity index achieved was 94%. These figures show an improvement upon the good results from previous OS exercises. 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 three hundred and sixty-nine samples have been received (OS01-25). The average Bray-Curtis similarity figure is 91.94%. Eighty-eight samples have fallen below the 90% pass mark (24%). Thirty-six samples have achieved a similarity figure of 100% (10% 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 high possibility of being unrepresentative regardless of the quality of subsequent faunal identifications, and should the sorted residue be disposed of 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.

4.3 Particle Size Analyses

The difference between the two main techniques employed for analysis of the samples (laser and sieve) was again evident in the results from the analysis of the replicates samples. The sample distributed as PS22 appeared from an analysis of replicates (Figure 1) to be very uniform and the results from participating laboratories (Figure 3) were closely grouped. Figure 5 shows the z-scores for each of the major statistics supplied by the participating laboratories. Data received from LB1009 and LB1013 indicated much higher proportions of silt/clay than the other data returns for PS22 and hence these results are displaced in the cumulative curve figure (Figure 3).

There was a significant amount of scatter in the results for PS23 from participating laboratories (Figure 4), this was not expected based upon the replicate analysis results (Figure 2) produced prior to the sample dispatch. Figure 6 shows the z-scores for each of the major statistics supplied by the participating laboratories. The data received from several laboratories indicated a much lower silt-clay fraction compared to the *replicate* sample data produced prior to the exercise. A series of experiments deduced that the replicates distributed showed very little natural variation and observed differences were the result of a processing methods within the laser technique, especially affected by differing equipment and particle disaggregation methods after drying.

Participating laboratories were asked to provide a visual description of the PS22 and PS23 samples prior to analysis. The results varied greatly (Table 16, final column). Participating laboratories were also instructed to describe the sediment using the Folk triangle after analysis. Data were provided by eight laboratories for PS22 and seven laboratories for PS23. The majority of laboratories (6) described PS22, using the Folk triangle, as 'sand'; one recorded 'fine sand'; all remaining laboratories did not supply descriptions. The majority of laboratories (4) providing sediment descriptions described PS23, using the

Folk triangle, as 'sandy mud'; one recorded 'silt'; one laboratory recorded 'gravely sandy mud'; all remaining laboratories did not supply descriptions. All PS samples are pre-sieved at 2 mm prior to circulation therefore the description of gravel particles (>2 mm) is extremely unlikely.

It is essential that the analytical methods be stated when reporting or attempting to compare results. The situation is complicated further by the fact that the difference between the techniques also varies with the nature of the sediment sample. In the majority of cases laser analysis was used, however, as demonstrated in PS23 the possible variations in equipment and methods within this technique 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 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. RT22 identified discrepancies with literature used by some participating laboratories for their identification of the *Aora gracilis, Tanaopsis graciloides,* and *Pholoe baltica* specimens. RT23 identified discrepancies with literature used by some participating laboratories for their identification of the *Chamelea striatula* and *Iphimedia minuta* specimens. All participating laboratories have been made aware of this via the ring test bulletins (RTB22 & RTB23).

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. For the laboratories returning a collection, the average number of differences at the level of genus was 1.5, and in many cases (7 of 11) laboratories had no differences or only a single difference at the generic level. The situation was similar for identification at the level of species where the majority of laboratories achieved at most three differences in identification (8 of 11 laboratories). The average number of specific differences was 3.3. In the majority of instances identifications made by the participating laboratories were in agreement with those made by Unicomarine Ltd. In view of 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. The results presented in Table 14 are arranged by LabCode; 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

The primary purpose 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 components 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 for each component. Laboratories meeting or exceeding the required standard for a given component would be considered to have performed satisfactorily for that particular component. A flag indicating a 'Pass' or 'Fail' would be assigned to each laboratory for each of the components 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 components may be included. In the meantime, the other components 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 components 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 had elected not to participate in a particular component of the Scheme.

5.1 Laboratory Performance

The target values for each component 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 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 the 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 92% of the comparisons were considered to have passed the enumeration of taxa standard; 86% exceeded the enumeration of individuals standard and 84% passed the Bray-Curtis comparison standard. UK NMMP sample flags have been applied to each of the Own Sample in accordance with the performance flagging criteria introduced in Scheme year eight (Table 15, column 23); five of the fifty-one samples are flagged as 'Fail'; three are flagged as 'Poor'; eleven are flagged as 'Acceptable'; twenty-eight are flagged as 'Good'; and four are flagged as 'Excellent' for achieving 100% Bray-Curtis similarity indices.

Performance with respect to the biomass standard was slightly poorer (Table 15, column 19) with only 63% 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 component standards, introduced in the last Scheme year, (See Appendix 2: Description of the Scheme standards for each component) is shown in Table 16. The upper section of Table 16 shows the results for the PS22 exercise. Three participating laboratories did not submit all five requested statistics, these statistics have been flagged as 'Deemed Fail'. One laboratory (LB1009), which submitted data for %<63μm, failed to meet the standard for this statistic; one laboratory (LB1013) failed to meet the standard for median (ϕ); one laboratory (LB1013) failed to meet the standard for mean (ϕ); one laboratory (LB1016) failed to meet the standard for sorting; one laboratory (LB1009) failed to meet the standard for IGS(Ski). Half of the participating laboratories submitted data for all statistics and passed all standards, although one of these laboratories was utilising data from a centralised source. The lower section of Table 16 shows the results for the PS23 exercise. Two participating laboratories did not submit all five requested statistics, these statistics have been flagged as 'Deemed Fail'. One laboratory (LB1002), which submitted data for %<63μm, failed to meet the standard for this statistic; one laboratory (LB1011) failed to meet the standard for median (ϕ); one laboratory (LB1013) failed to meet the standard for mean (ϕ); two laboratories (LB1001 and LB1017) failed to meet the standard for sorting; three laboratories (LB1001, LB1013 and LB1017) failed to meet the standard for IGS(Ski). Four out of ten laboratories submitted data for all statistics and passed all standards.

5.2 Statement of Performance

Each participating laboratory have received a 'Statement of Performance', which includes a summary of results for each of the Schemes components and details the resulting flags where appropriate. These statements were first circulated in 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 last nine years based upon the current NMBAQC Scheme standards (See Appendix 2: Description of the Scheme standards for each component). This year's fifty-one Own Samples resulted in the second highest percentage pass rate, 84% (the highest being 100% achieved in exercise 01 that involved just ten samples) since the beginning of the Own Sample component. 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 flags for each participating laboratories over the past nine years (the 'pass / fail' flags shown do not reflect any subsequent remedial action that has been undertaken). There appears to be a fairly high level of consistency within each laboratory. 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 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 for each component). A failing Own Sample is categorised by the achievement of a Bray-Curtis similarity indices of <90%; eight samples 'failed' in this Scheme year (including five UK NMMP samples). 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 reviewed by the NMBAQC Committee and appropriate remedial action is decided. The participating laboratories are notified, of such decisions, in writing by the NMBAQC Scheme Contract Manager. Any remedial action performed should be examined externally for effectiveness before UK NMMP data flags are altered. The following remedial action has been proposed by the NMBAQC Committee for the remaining NMMP replicates, where relevant:

LB1001 OS23 - Check *Abra* spp. identification.
LB1005 OS23 - Check *Abra* spp. and *Tharyx killariensis* identification.
LB1007 OS25 - Resort and re-audit.
LB1019 OS25 - Check *Diastylis* spp. identification and make taxonomic corrections.
LB1020 OS23 - Make corrections.
LB1020 OS24 - Resort and re-audit.
LB1020 OS25 - Resort and re-audit.
LB1023 OS24 - Make taxonomic corrections and check enumeration.

The recommended remedial action for 'failing' Own Samples from two laboratories (LB1001 and LB1023) has been successfully conducted following a review of identification throughout all their replicate samples. These samples has now been awarded a 'pass' flag. One of these samples was from a UK NMMP sampling station and therefore the station data flag can now be amended and the 'fail' flag removed.

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 RT's 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 RT22 and RT23 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 component' then the laboratory has not subscribed to the component. If an exercise contains the comment 'not participating in this exercise' then the laboratory, despite subscribing to this component, has decided not to submit data for the exercise.

Laboratory – LB1001

Macrobenthos (Training Component)

MB11 – Artificial sample. Four taxonomic differences. Three taxa not recorded/extracted (*Urothoe elegans*, *Pholoe inornata* and *Protodorvillea kefersteini*). Nineteen individuals not picked/lost from the residue. Bray-Curtis similarity index of 93.86%. Biomass on average 4.9% heavier than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT22 – Five specific differences. Number of AQC identifications in Mid group.
RT23 – Three generic and three specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR08 – Three specific differences.

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

OS23 – NMBAQCS sample flag – 'Fail'. Remedial action has subsequently been successfully performed upon the remaining replicates from this station (*i.e. Abra* spp. review).
Five taxonomic differences. Count variance of two individuals. Two individuals not picked from the residue, including one previously unpicked taxon. Bray-Curtis similarity index of 83.74%. Biomass on average 20.97% heavier than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Acceptable'.
Five taxonomic differences. Count variance of sixteen individuals. One individual not picked from the residue. Bray-Curtis similarity index of 90.72%. Biomass on average 8.43% lighter than Unicomarine Ltd.
OS25 – NMBAQCS sample flag – 'Good'.
One individual not picked from the residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 96.77%. Biomass on average 1.73% heavier than Unicomarine Ltd.

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

PS22 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'sand with shell fragments' prior to analysis; described as sand using the Folk triangle.
PS23 – NMBAQCS standards for sorting and IGS(SKi) failed. All remaining NMBAQCS standards passed.

No major differences in size distribution curve. Incorrect IGS (Ski) figure submitted due to spreadsheet errors. Sediment described as 'black mud' prior to analysis; described as sandy mud using the Folk triangle.

Laboratory – LB1002

Macrobenthos (Training Component)

MB11 – Artificial sample. No taxonomic differences. Two taxa not recorded/extracted (*Nephtys* sp. juv. and *Protodorvillea kefersteini*). Twenty-two individuals not picked/lost from the residue. Bray-Curtis similarity index of 94.55%. Biomass on average 26.4% lighter than Unicomarine Ltd. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT22 – One generic and four specific differences. Number of AQC identifications in Low group.
RT23 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR08 – One specific difference.

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

OS23 – NMBAQCS sample flag – 'Excellent'.
All individuals picked from the residue. Bray-Curtis similarity index of 100%. Biomass on average 6.05% lighter than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Good'.
One individual not picked from the residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 98.46%. Biomass on average 42.9% heavier than Unicomarine Ltd. (major variance due to *Echinocardium cordatum* specimen - broken in transport).
OS25 – NMBAQCS sample flag – 'Good'.
One taxonomic difference. All individuals picked from residue. Bray-Curtis similarity index of 98%. Biomass on average 3.34% lighter than Unicomarine Ltd.

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

PS22 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'sand' prior to analysis; described as sand using the Folk triangle.
PS23 – NMBAQCS standard for %silt/clay failed. All remaining NMBAQCS standards passed.
Size distribution curve to the left of the majority of curves. Sediment described as 'mud' prior to analysis; described as sandy mud using the Folk triangle.

Laboratory – LB1003

Macrobenthos (Training Component)

MB11 - Artificial sample. No taxonomic differences. One taxon not recorded/extracted (*Mediomastus fragilis*). Nine individuals not picked/lost from the residue. Bray-Curtis similarity index of 97.61%. Biomass on average 3.7% heavier than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT22 – Not participating in this exercise.
RT23 – Five generic and seven specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR08 – All specimens correctly identified.

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

OS23 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
Count variance of fourteen individuals. Six individuals not picked from the residue. Bray-Curtis similarity index of 99.6%. Biomass on average 0.7% heavier than Aquatic Environments.
OS24 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
Count variance of fourteen individuals. All individuals extracted from the residue. Bray-Curtis similarity index of 97.8%. Biomass on average 0.6% lighter than Aquatic Environments.
OS25 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
Count variance of fifteen individuals. All individuals extracted from the residue. Bray-Curtis similarity index of 98.9%. Biomass on average 1.9% heavier than Aquatic Environments.

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

PS22 - All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'medium-coarse sand' prior to analysis; described as sand using the Folk triangle.
PS23 – All NMBAQCS standards passed.
Size distribution curve to the left of the majority of curves. Sediment described as 'muddy sand' prior to analysis; described as sandy mud using the Folk triangle.

Laboratory – LB1004

Macrobenthos (Training Component)

MB11 – Not participating in this exercise.

Ring Test (Training Component)

RT22 – Not participating in this exercise.
RT23 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR08 – Not participating in this exercise.

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

OS23 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
One individual not picked from the residue. Bray-Curtis similarity index of 98.1%. Biomass on average 0.9% heavier than Aquatic Environments.
OS24 – NMBAQCS sample flag – 'Excellent'. External audit conducted by Aquatic Environments.
All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 6.2% heavier than Aquatic Environments.
OS25 – NMBAQCS sample flag – 'Excellent'. External audit conducted by Aquatic Environments.
All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 0.8% lighter than Aquatic Environments.

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

PS22 – No data received.
PS23 – No data received.

Laboratory – LB1005

Macrobenthos (Training Component)

MB11 - Artificial sample. Two taxonomic differences. Three taxa not recorded/extracted (*Mediomastus fragilis, Pholoe inornata* and *Protodorvillea kefersteini*). Fifteen individuals not picked/lost from the residue. Bray-Curtis similarity index of 95.38%. No biomass data supplied. Laboratory policy stated that copepods are were not extracted.

Ring Test (Training Component)

RT22 – Three generic and seven specific differences. Number of AQC identifications in Mid group.
RT23 – Two specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR08 - Eight generic and eleven specific differences.

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

OS23 – NMBAQCS sample flag – 'Poor'.
Three taxonomic differences. One individual not picked from the residue. Bray-Curtis similarity index of 89.16%. No biomass data supplied.
OS24 – NMBAQCS sample flag – 'Good'.
Four individuals not picked from the residue, including one previously unpicked taxon. Count variance of two individuals. Bray-Curtis similarity index of 99.83%. No biomass data supplied.
OS25 – NMBAQCS sample flag – 'Good'.
Four taxonomic differences. Eleven individuals not picked from the residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 96.18%. No biomass data supplied.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1006

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this component.
RT23 – Not participating in this component.

Laboratory Reference (Training Component)

LR08 – Not participating in this component.

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

OS23 – NMBAQCS sample flag – 'Acceptable'.
One taxonomic difference. Fifty-nine individuals not picked from residue, including five previously unpicked taxa. Count variance of twenty-two individuals. Bray-Curtis similarity index of 92.5%. Biomass audit not conducted (taxa received in single fauna vial).
OS24 – NMBAQCS sample flag – 'Acceptable'.
Six hundred individuals not picked from residue (mostly unspecified *in situ* recording), including one previously unpicked taxon. Count variance of five hundred and seven individuals (predominantly *in situ* enumeration related). Bray-Curtis similarity index of 92.07%. Biomass audit not conducted (taxa received in single fauna vial).
OS25 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass audit not conducted (taxa received in single fauna vial).

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1007

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this component.
RT23 – Not participating in this component.

Laboratory Reference (Training Component)

LR08 – Not participating in this component.

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

OS23 – NMBAQCS sample flag – 'Good'.
Twenty-six individuals not picked from residue. Count variance of ten individuals. Bray-Curtis similarity index of 96.68%. Biomass audit not conducted (taxa received in single fauna vial).
OS24 – NMBAQCS sample flag – 'Acceptable'.
Six individuals not picked from residue, including one previously unpicked taxon. Count variance of five individuals. Bray-Curtis similarity index of 92.27%. Biomass audit not conducted (taxa received in single fauna vial).
OS25 – NMBAQCS sample flag – 'Fail'.
Eleven individuals not picked from residue, including three previously unpicked taxa. Count variance of ninety-eight individuals (mostly the result of transcription errors). Bray-Curtis similarity index of 77.38% (mostly the result of transcription errors). Biomass audit not conducted (taxa received in single fauna vial).

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1008

Macrobenthos (Training Component)

MB11 - Artificial sample. No taxonomic differences. Two taxa not recorded/extracted (*Fabulina fabula* juv. and *Ampelisca tenuicornis*). Nine individuals not picked/lost from the residue. Bray-Curtis similarity index of 97.84%. Biomass on average 1% heavier than Unicomarine Ltd. Laboratory policy stated nematodes, bryozoans, hydroids, copepods, tunicates, anthozoans and aquatic insects were not extracted.

Ring Test (Training Component)

RT22 – Not participating in this component.
RT23 – Not participating in this component.

Laboratory Reference (Training Component)

LR08 - Not participating in this component.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.
OS25 – Not participating in this component.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1009

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this exercise.
RT23 – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR08 – One generic and two specific differences.

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

OS23 – NMBAQCS sample flag – 'Good'.
Two taxonomic differences. All individuals extracted from residue. Bray-Curtis similarity index of 96.85%. Biomass on average 27.41% lighter than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Acceptable'.
Two taxonomic differences. All individuals extracted from residue. Count variance of one individual. Bray-Curtis similarity index of 90.26%. Biomass on average 16.25% lighter than Unicomarine Ltd.
OS25 – NMBAQCS sample flag – 'Good'.
One taxonomic difference. All individuals extracted from residue. Count variance of two individuals. Bray-Curtis similarity index of 96.55%. Biomass on average 19.22% lighter than Unicomarine Ltd.

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

PS22 – No data supplied for Sorting. NMBAQCS Standards for %silt/clay and IGS(Ski) failed. Median and mean NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'fine sand' prior to analysis; described as fine sand using the Folk triangle.
PS23 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'muddy clay' prior to analysis; described as silt using the Folk triangle.

Laboratory – LB1010

Macrobenthos (Training Component)

MB11 - Artificial sample. Two taxonomic differences. Four taxa not recorded/extracted (*Mediomastus fragilis, Nephtys* sp. juv., *Urothoe elegans* and *Protodorvillea kefersteini*). Twenty-one individuals not picked/lost from the residue. Bray-Curtis similarity index of 93.33%. No biomass data supplied. Residue/fauna stained. Laboratory policy stated all faunal groups extracted.

Ring Test (Training Component)

RT22 – Three generic and nine specific differences. Number of AQC identifications in High group.
RT23 – Seven generic and eight specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR08 – All specimens correctly identified.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.

OS25 – Not participating in this component.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1011

Macrobenthos (Training Component)

MB11 - Artificial sample. No taxonomic differences. All taxa recorded/extracted. Four individuals not picked/lost from the residue. Bray-Curtis similarity index of 99.05%. No biomass data supplied. Laboratory policy stated nematodes, bryozoans, hydroids, copepods, aquatic insects and pips/seeds were not extracted.

Ring Test (Training Component)

RT22 – Three specific differences. Number of AQC identifications in Low group.
RT23 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR08 – Not participating in this exercise.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.
OS25 – Not participating in this component.

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

PS22 – No data supplied for Sorting and IGS(SKi). All remaining NMBAQCS standards passed.
No major differences in size distribution curve. No sediment description provided.
PS23 – No data supplied for Sorting and IGS(SKi). Median standard failed. %silt/clay and Mean NMBAQCS standards passed.
No major differences in size distribution curve. No sediment description provided.

Laboratory – LB1012

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Three generic and ten specific differences. Number of AQC identifications in High group.
RT23 – Two generic and three specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LB08 - Not participating in this component.

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

OS23 – NMBAQCS sample flag – 'Good'.
Sample was subsampled due to high numbers of individuals. Six individuals not picked from residue, including one previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 98.26%. Biomass on average 27.79% lighter than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Good'.
Sample was subsampled due to high numbers of individuals. Fifteen individuals not picked from residue. Count variance of eight individuals. Bray-Curtis similarity index of 96.21%. Biomass on average 56.21% lighter than Unicomarine Ltd.

OS25 – NMBAQCS sample flag – 'Good'.
Six individuals not picked from residue. Count variance of one individual. Bray-Curtis similarity index of 98.72%. Biomass on average 21.56% heavier than Unicomarine Ltd.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1013

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this component.
RT23 – Not participating in this component.

Laboratory Reference (Training Component)

LR08 – Not participating in this component.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.
OS25 – Not participating in this component.

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

PS22 – NMBAQCS standards for median and mean failed. %silt/clay, sorting and IGS(Ski) NMBAQCS standards passed.
Size distribution curve displaced to the left of the other curves. Sediment described as 'sandy' prior to analysis.
PS23 – NMBAQCS standards for mean and IGS(Ski) failed. %silt/clay, median and sorting NMBAQCS standards passed.
Size distribution curve unusual in shape caused by a relatively low 5 – 5.5 phi value and a relatively very high 6 – 7 phi value. Sediment described as 'muddy' prior to analysis.

Laboratory – LB1014

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Two generic and four specific differences. Number of AQC identifications in Low group.
RT23 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR08 – Not participating in this exercise.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.
OS25 – Not participating in this component.

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

PS22 – Not participating in this component.

PS23 – Not participating in this component.

Laboratory – LB1015

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Five generic and eight specific differences. Number of AQC identifications in Mid group.
RT23 – Five generic and five specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR08 – All specimens correctly identified.

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

OS23 – NMBAQCS sample flag – 'Good'.
Four taxonomic differences. Three hundred and forty-five individuals not picked from residue, including six previously unpicked taxa. Bray-Curtis similarity index of 95.23%. Biomass on average 4.14% heavier than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Good'.
Thirty-nine individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 96.92%. Biomass on average 22.10% heavier than Unicomarine Ltd.
OS25 – NMBAQCS sample flag – 'Good'.
Sample was subsampled due to high numbers of individuals. Eighty individuals not picked from residue, including one previously unpicked taxon. Count variance of fifteen individuals. Bray-Curtis similarity index of 95.97%. Biomass on average 42.84% heavier than Unicomarine Ltd.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1016

Macrobenthos (Training Component)

MB11 – Artificial sample. Two taxonomic differences. Five taxa not recorded/extracted (*Mediomastus fragilis, Urothoe elegans, Lanice conchilega, Pholoe inornata* and *Protodorvillea kefersteini*). Thirty individuals not picked/lost from the residue. Bray-Curtis similarity index of 87.56%. Biomass on average 11.4% heavier than Unicomarine Ltd. Laboratory policy stated bryozoans were not extracted.

Ring Test (Training Component)

RT22 – Four generic and eight specific differences. Number of AQC identifications in Mid group.
RT23 – Two specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR08 – Two generic and eight specific differences.

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

OS23 – NMBAQCS sample flag – 'Good'.
One taxonomic error. All individuals extracted from residue. Bray-Curtis similarity index of 95.89%. Biomass reported to five decimal places. Biomass on average 21.14% heavier than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Good'.

Three taxonomic differences. One individual not picked from residue, this was a previously unpicked taxon. Count variance of two individuals. Bray-Curtis similarity index of 95.82%. Biomass reported to five decimal places. Biomass on average 45.46% heavier than Unicomarine Ltd.

OS25 – NMBAQCS sample flag – 'Good'.
Three taxonomic differences. All individuals extracted from residue. Bray-Curtis similarity index of 97.62%. Biomass reported to five decimal places. Biomass on average 22.37% heavier than Unicomarine Ltd.

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

PS22 – NMBAQCS standard for sorting failed. All remaining NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'shelly sand' prior to analysis; described as sand using the Folk triangle.

PS23 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'dark drown sandy mud' prior to analysis; described as gravely sandy mud using the Folk triangle.

Laboratory – LB1017

Macrobenthos (Training Component)

MB11 - Artificial sample. One taxonomic difference. Three taxa not recorded/extracted (*Fabulina* fabula juv., *Mediomastus fragilis* and *Urothoe elegans*). Twenty-three individuals not picked/lost from the residue. Bray-Curtis similarity index of 93.8%. Biomass on average 13.3% lighter than Unicomarine Ltd. Laboratory policy stated copepods were not extracted.

Ring Test (Training Component)

RT22 – Six specific differences. Number of AQC identifications in Mid group.
RT23 – Three specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR08 – Two generic and three specific differences.

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

OS23 – NMBAQCS sample flag – 'Acceptable'.
Six taxonomic differences. Five individuals not picked from residue. Count variance of twenty-three individuals. Bray-Curtis similarity index of 93.29%. Biomass on average 8.59% heavier than Unicomarine Ltd.

OS24 – NMBAQCS sample flag – 'Good'.
Ten taxonomic differences. All individual extracted from residue. Count variance of twenty-seven individuals. Bray-Curtis similarity index of 97.35%. Biomass recorded to five decimal places. Biomass on average 2.15% heavier than Unicomarine Ltd.

OS25 – NMBAQCS sample flag – 'Acceptable'.
Thirty individuals not picked from residue, including two previously unpicked taxa. Count variance of three individuals. Bray-Curtis similarity index of 94.12%. Biomass recorded to five decimal places. Biomass on average 8.85% heavier than Unicomarine Ltd.

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

PS22 – All NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'sand with shell fragments' prior to analysis; described as sand using the Folk triangle.

PS23 – NMBAQCS standards for sorting and IGS(SKi) failed. All remaining NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Incorrect IGS (Ski) figure submitted due to spreadsheet errors. Sediment described as 'black mud' prior to analysis; described as sandy mud using the Folk triangle.

Laboratory – LB1018

Macrobenthos (Training Component)

MB11 – Artificial sample. Five taxonomic differences. One taxon not recorded/extracted (*Protodorvillea kefersteini*). Twenty individuals not picked/lost from the residue. Bray-Curtis similarity index of 81.82%. No biomass data supplied. Laboratory policy stated nematodes, bryozoans, hydroids, copepods, tunicates, anthozoans and aquatic insects were not extracted.

Ring Test (Training Component)

RT22 – Five generic and twelve specific differences. Number of AQC identifications in High group.
RT23 – Six generic and nine specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR08 – Not participating in this component.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.
OS25 – Not participating in this component.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1019

Macrobenthos (Training Component)

MB11 - Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this component.
RT23 – Not participating in this component.

Laboratory Reference (Training Component)

LR08 – Not participating in this component.

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

OS23 – NMBAQCS sample flag – 'Good'.
Two taxonomic differences. Two individuals not picked from residue. Count variance of ten individuals. Bray-Curtis similarity index of 99%. No biomass data supplied.
OS24 – NMBAQCS sample flag – 'Acceptable'.
One taxonomic difference. All individuals extracted from residue. Count variance of three individuals. Bray-Curtis similarity index of 94.6%. No biomass data supplied.
OS25 – NMBAQCS sample flag – 'Poor'.
Four taxonomic differences. One individual not picked from residue, this was a previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 85.1%. No biomass data supplied.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1020

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this exercise.
RT23 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR08 - Not participating in this component.

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

OS23 – NMBAQCS sample flag – 'Poor'.
Two individuals not picked from residue. Count variance of five individuals. Bray-Curtis similarity index of 89.6%. Biomass on average 40.61% heavier than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Fail'.
Twenty-two individuals not picked from residue. Bray-Curtis similarity index of 83.3%. Biomass on average 4.67% heavier than Unicomarine Ltd.
OS25 – NMBAQCS sample flag – 'Fail'.
One taxonomic difference. Seventeen individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 73.8%. Biomass on average 39.81% heavier than Unicomarine Ltd.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1021

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this exercise.
RT23 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR08 – Not participating in this exercise.

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

OS23 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
One individual not picked from residue, this was a previously unpicked taxon. Count variance of twenty-five individuals. Bray-Curtis similarity index of 96.5%. Biomass on average 9.2% heavier than Aquatic Environments.
OS24 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Count variance of three individuals. Bray-Curtis similarity index of 97.9%. Biomass on average 0.5% heavier than Aquatic Environments.
OS25 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Count variance of three individuals. Bray-Curtis similarity index of 99.4%. Biomass audit not conducted due to several dried vials.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1022

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Not participating in this component.
RT23 – Not participating in this component.

Laboratory Reference (Training Component)

LR08 – Not participating in this component.

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

OS23 – NMBAQCS sample flag – 'Good'.
One taxonomic difference. One individual not picked from residue. Count variance of three individuals. Bray-Curtis similarity index of 98.76%. No biomass data supplied.
OS24 – NMBAQCS sample flag – 'Acceptable'.
One individual not picked from residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 92.31%. No biomass data supplied.
OS25 – NMBAQCS sample flag – 'Good'.
All individuals extracted from residue. Count variance of one individual. Bray-Curtis similarity index of 99.5%. No biomass data supplied.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

Laboratory – LB1023

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Two specific differences. Number of AQC identifications in Low group.
RT23 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR08 – Two specific differences.

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

OS23 – NMBAQCS sample flag – 'Acceptable'.
Three taxonomic differences. Six individuals not picked from residue. Count variance of three individuals. Bray-Curtis similarity index of 93.7%. Biomass on average 13.30% heavier than Unicomarine Ltd.
OS24 – NMBAQCS sample flag – 'Fail'. Remedial action has subsequently been successfully performed upon the remaining replicates from this station.
Two taxonomic differences. One individual not picked from residue. Count variance of two hundred and eight-five individuals (mostly nematodes). Bray-Curtis similarity index of 83.9%. Biomass on average 3.59% heavier than Unicomarine Ltd.
OS25 – NMBAQCS sample flag – 'Acceptable'.
Thirty-two individuals not picked from residue, including eleven previously unpicked taxa. Count variance of ten individuals. Bray-Curtis similarity index of 91.2%. Biomass on average 4.03% lighter than Unicomarine Ltd.

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

PS22 – All NMBAQCS standards passed.

No major differences in size distribution curve. Sediment described as 'sand' prior to analysis; described as sand using the Folk triangle.
PS23 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'black mud' prior to analysis; described as sandy mud using the Folk triangle.

Laboratory – LB1024

Macrobenthos (Training Component)

MB11 – Not participating in this component.

Ring Test (Training Component)

RT22 – Four specific differences. Number of AQC identifications in Low group.
RT23 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR08 – Two specific differences.

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

OS23 – Not participating in this component.
OS24 – Not participating in this component.
OS25 – Not participating in this component.

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

PS22 – Not participating in this component.
PS23 – Not participating in this component.

7. Conclusions and Recommendations

A number of observations may be made of 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. The majority of Scheme participants now use e-mail as their primary means of communication. All laboratories participating in Scheme year ten had e-mail capabilities. E-mail capabilities must be made a prerequisite for participation in the Scheme. All primary correspondence for Scheme year eleven 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 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. This deemed "Fail" for no data submission 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. Participating laboratories must take responsibility for ensuring that the level of their participation in the Scheme is communicated to Unicomarine Ltd.
5. There were continued problems associated with the measurement of biomass for individual species. Further consideration needs to be given to the preparation of a standardised protocol and reporting format. Various methods should be subjected to laboratory trials to ascertain a precise and consistent working protocol for NMMP biomass data. 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 submitted permanent or semi-permanent slides of oligochaetes, this rendered re-estimations of biomass impossible. 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.

6. The particle size exercises (PS) once again show differences in the results obtained by different analytical methods (*e.g.* laser, sieve). 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. It is essential that particle size data should be presented with a clear description of the method of analysis used. PS23 highlighted the need for a prescriptive method for laser analysis (including equipment) 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 must be developed for UK NMMP. This should include consultation with 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 correcting future taxonomic developments.

8. Differences in the literature used for identification of invertebrates have been highlighted by the RT, MB and OS exercises. Funding should be made available for the collation of identification literature into a searchable database for use by Scheme participants. Unpublished keys from workshops, *etc.* could be posted on the Scheme's website.

9. There are still some problems of individuals and taxa missed at the sorting stage of macrobenthic sample analysis. The figures for these sorting errors this year still remain a cause for concern. In the MB11 exercise up to 5 taxa (23% of the actual total taxa in the sample) were either not extracted, lost during processing or not distinguished from other extracted taxa. On average 2.4 taxa were not extracted from the residue. None of the participating laboratories extracted all the countable individuals from their residues. In the worst instance 14.1% of total individuals in the sample were not extracted. The situation was worse for the OS samples where a maximum of 11 taxa and up to 27% of the taxa were not extracted. In the worst instance, excluding *in situ* data, 345 individuals were not picked from the residue and up to 28% of the total individuals remained in the residue. On average for the OS exercise 0.84 taxa were not extracted compared with 1.73, 1.98, 2.04, 1.25, 1.48, 0.45 and 1.39 taxa from last seven 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.

10. In Scheme year seven a NMBAQCS Sorting Methods Questionnaire was devised and 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 NMMP samples. A proposal for a standard NMMP approach to oligochaete identification was included in the report. 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. Standard UK NMMP protocols must be developed to standardise the faunal groups to be extracted from NMMP samples, and reasonable levels of identification devised for all taxa likely to be encountered.

11. An improved learning structure to the Scheme through detailed individual exercise reports has been successfully implemented. 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 illustrating the correct identification of the taxa circulated. Participants are encouraged to review their exercise reports and provide feedback concerning content and format wherever appropriate.
12. 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.
13. As greater emphasis is placed upon remedial action there is need for a comprehensive list of taxonomic experts, to be called upon to offer a third party opinion for taxonomic issues. Prior to any third party intervention the disputing laboratory must provide clear reasons for their disagreement and make every effort to resolve the issue within the Scheme.
14. The Scheme's website (www.nmbaqcs.org) is now funded for regular maintenance. Scheme participants are encouraged to visit the site and give suggestions for additional useful content. Provision will be made for accessing online results/reports. A List of Scheme participants should be posted on the site for referencing by contract managers.

8. References

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NMBAQC – Section B: Report from the Contractor - Tables

Table 1. Results from the analysis of Macrobenthic sample MB11 by the participating laboratories.

1	2	3	4	5	6	7	8	9	10	11	12	13	14
LabCode	Number of Taxa				Number of Individuals				Not extracted/lost			Similarity	Taxonomic
LB10xx	PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	Taxa	Ind	%ind	index	errors
LB1001	19	22	-3	13.6	194	213	-19	8.9	3	19	8.9	93.86	4
LB1002	20	22	-2	9.1	191	213	-22	10.3	2	22	10.3	94.55	0
LB1003	20	22	-2	9.1	203	213	-10	4.7	1	9	4.2	97.61	0
LB1005	19	22	-3	13.6	198	213	-15	7.0	3	15	7.0	95.38	2
LB1008	20	22	-2	9.1	204	213	-9	4.2	2	9	4.2	97.84	0
LB1010	19	22	-3	13.6	192	213	-21	9.9	4	21	9.9	93.33	2
LB1011	22	22	0	0.0	209	213	-4	1.9	0	4	1.9	99.05	0
LB1016	22	22	0	0.0	189	213	-24	11.3	5	30	14.1	87.56	2
LB1017	19	22	-3	13.6	190	213	-23	10.8	3	23	10.8	93.80	1
LB1018	19	22	-3	13.6	183	213	-30	14.1	1	20	9.4	81.82	5

Key: PL - participating laboratory.
UM - Unicomarine Ltd.
See Section 6, for further details.

Columns 2 to 9 - Comparison of summary figures supplied (some slight adjustments *i.e.* juveniles).
Columns 10 to 12 - Actual missed taxa / individuals from supplied sample.

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB11.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1001	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	15	-	-	1	1	2	-	19
	%missed	-	26.3	-	-	33.3	4.5	1.5	-	8.9
LB1002	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	14	-	-	0	0	8	-	22
	%missed	-	24.6	-	-	0.0	0.0	6.1	-	10.3
LB1003	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	8	-	-	0	0	2	-	10
	%missed	-	14.0	-	-	0.0	0.0	1.5	-	4.7
LB1005	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	13	-	-	0	0	2	-	15
	%missed	-	22.8	-	-	0.0	0.0	1.5	-	7.0
LB1008	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	4	-	-	1	0	4	-	9
	%missed	-	7.0	-	-	33.3	0.0	3.1	-	4.2
LB1010	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	19	-	-	1	0	1	-	21
	%missed	-	33.3	-	-	33.3	0.0	0.8	-	9.9
LB1011	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	1	-	-	0	0	3	-	4
	%missed	-	1.8	-	-	0.0	0.0	2.3	-	1.9
LB1016	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	17	-	-	1	0	12	-	30
	%missed	-	29.8	-	-	33.3	0.0	9.2	-	14.1
LB1017	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	14	-	-	1	0	8	-	23
	%missed	-	24.6	-	-	33.3	0.0	6.1	-	10.8
LB1018	UM count	-	57	-	-	3	22	131	-	213
	PL missed	-	13	-	-	0	1	6	-	20
	%missed	-	22.8	-	-	0.0	4.5	4.6	-	9.4

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 MB11. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1001	PL	-	4.2112	-	-	0.0094	2.1587	2.313	-	8.6923
	UM	-	3.7055	-	-	0.0047	2.3244	2.2334	-	8.268
	%diff.	-	12.0	-	-	50.0	-7.7	3.4	-	4.9
LB1002	PL	-	1.6456	-	-	0.0025	2.0426	2.0975	-	5.7882
	UM	-	2.6456	-	-	0.0032	2.5048	2.1632	-	7.3168
	%diff.	-	-60.8	-	-	-28.0	-22.6	-3.1	-	-26.4
LB1003	PL	-	4.0465	-	-	0.0086	2.4651	1.339	-	7.8592
	UM	-	3.2976	-	-	0.0068	2.6136	1.6473	-	7.5653
	%diff.	-	18.5	-	-	20.9	-6.0	-23.0	-	3.7
LB1005	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1008	PL	-	2.0791	-	-	0.0077	3.4596	1.84	-	7.3864
	UM	-	2.2384	-	-	0.007	3.2713	1.7935	-	7.3102
	%diff.	-	-7.7	-	-	9.1	5.4	2.5	-	1.0
LB1010	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1011	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1016	PL	-	4.5552	-	-	0.0124	2.2155	2.0404	-	8.8235
	UM	-	3.6314	-	-	0.007	2.1842	1.9924	-	7.815
	%diff.	-	20.3	-	-	43.5	1.4	2.4	-	11.4
LB1017	PL	-	2.23702	-	-	0.00414	2.15906	2.14607	-	6.54629
	UM	-	2.8336	-	-	0.0046	2.5103	2.071	-	7.4195
	%diff.	-	-26.7	-	-	-11.1	-16.3	3.5	-	-13.3
LB1018	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-

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

Table 4. Variation in faunal content reported for the artificial replicate samples distributed as MB11.

Taxa*

LabCode	Polychaeta	Crustacea	Echinodermata	Mollusca	Total taxa
UM data	**11**	**3**	**3**	**5**	**22**
LB1001	9	2	3	5	19
LB1002	9	3	3	5	20
LB1003	9	3	3	5	20
LB1005	8	3	3	5	19
LB1008	11	2	2	5	20
LB1010	8	2	3	6	19
LB1011	11	3	3	5	22
LB1016	11	2	3	6	22
LB1017	10	2	3	4	19
LB1018	11	2	2	4	19
Mean	10	2	3	5	20
Max	11	3	3	6	22
Min	8	2	2	4	19

*UM data = artificial sample circulated

Individuals*

LabCode	Polychaeta	Crustacea	Echinodermata	Mollusca	Total Ind.
UM data	**57**	**3**	**22**	**131**	**213**
LB1001	42	2	21	129	194
LB1002	43	3	22	123	191
LB1003	49	3	22	129	203
LB1005	44	3	22	129	198
LB1008	53	2	22	127	204
LB1010	38	2	22	130	192
LB1011	56	3	22	128	209
LB1016	46	2	22	119	189
LB1017	43	2	22	123	190
LB1018	33	3	21	126	183
Mean	45	3	22	126	195
Max	56	3	22	130	209
Min	33	2	21	119	183

*UM data = artificial sample circulated

Table 5. Results from the analysis of Own Samples (OS23 to OS25) 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
LB1001	OS23	35	38	-3	7.9	166	166	0	0.0	1	2	1.2	2	83.74	5	
LB1001	OS24	27	27	0	0.0	196	181	15	7.7	0	1	0.6	16	90.72	5	
LB1001	OS25	9	10	-1	10.0	15	16	-1	6.3	1	1	6.3	0	96.77	0	
LB1002	OS23	8	8	0	0.0	19	19	0	0.0	0	0	0.0	0	100.00	0	
LB1002	OS24	11	12	-1	8.3	32	33	-1	3.0	1	1	3.0	0	98.46	0	
LB1002	OS25	19	19	0	0.0	50	50	0	0.0	0	0	0.0	0	98.00	1	
LB1003	OS23	85	85	0	0.0	2474	2466	8	0.3	0	6	0.2	14	99.60	0	External audit
LB1003	OS24	37	37	0	0.0	329	315	14	4.3	0	0	0.0	14	97.85	0	External audit
LB1003	OS25	21	21	0	0.0	663	648	15	2.3	0	0	0.0	15	98.86	0	External audit
LB1004	OS23	9	9	0	0.0	26	27	-1	3.7	0	1	3.7	0	98.11	0	External audit
LB1004	OS24	5	5	0	0.0	10	10	0	0.0	0	0	0.0	0	100.00	0	External audit
LB1004	OS25	9	9	0	0.0	15	15	0	0.0	0	0	0.0	0	100.00	0	External audit
LB1005	OS23	17	19	-2	10.5	41	42	-1	2.4	0	1	2.4	0	89.16	3	No biomass data
LB1005	OS24	4	5	-1	20.0	1164	1166	-2	0.2	1	4	0.3	2	99.83	0	No biomass data
LB1005	OS25	36	39	-3	7.7	332	344	-12	3.5	2	11	3.2	-1	96.18	4	No biomass data
LB1006	OS23	40	46	-6	13.0	593	674	-81	12.0	5	59	8.8	-22	92.50	1	Biomass audit not conducted; taxa not split.
LB1006	OS24	12	13	-1	7.7	956	1049	-93	8.9	1	600	57.2	507	92.07	0	Biomass audit not conducted; taxa not split.
LB1006	OS25	5	5	0	0.0	54	54	0	0.0	0	0	0.0	0	100.00	0	Biomass audit not conducted; taxa not split.
LB1007	OS23	7	7	0	0.0	323	339	-16	4.7	0	26	7.7	10	96.68	0	Biomass audit not conducted; taxa not split.
LB1007	OS24	8	11	-3	27.3	226	227	-1	0.4	1	6	2.6	5	92.27	0	Biomass audit not conducted; taxa not split.
LB1007	OS25	32	38	-6	15.8	580	689	-109	15.8	3	11	1.6	-98	77.38	0	Biomass audit not conducted; taxa not split.
LB1009	OS23	33	33	0	0.0	127	127	0	0.0	0	0	0.0	0	96.85	2	
LB1009	OS24	26	26	0	0.0	98	97	1	1.0	0	0	0.0	1	90.26	2	
LB1009	OS25	30	30	0	0.0	88	86	2	2.3	0	0	0.0	2	96.55	1	
LB1012	OS23	3	4	-1	25.0	282	291	-9	3.1	1	6	2.1	-3	98.26	0	Subsampled
LB1012	OS24	5	5	0	0.0	292	315	-23	7.3	0	15	4.8	-8	96.21	0	Subsampled
LB1012	OS25	14	14	0	0.0	267	274	-7	2.6	0	6	2.2	-1	98.72	0	Fauna found in residue dehydrated
LB1015	OS23	91	96	-5	5.2	3968	4313	-345	8.0	6	345	8.0	0	95.23	4	
LB1015	OS24	8	9	-1	11.1	614	653	-39	6.0	1	39	6.0	0	96.92	0	
LB1015	OS25	18	19	-1	5.3	1222	1287	-65	5.1	1	80	6.2	15	95.97	0	
LB1016	OS23	20	19	1	5.0	73	73	0	0.0	0	0	0.0	0	95.89	1	Biomass to 5 dp
LB1016	OS24	26	28	-2	7.1	132	131	1	0.8	1	1	0.8	2	95.82	3	Biomass to 5 dp
LB1016	OS25	29	29	0	0.0	126	126	0	0.0	0	0	0.0	0	97.62	3	Biomass to 5 dp
LB1017	OS23	58	61	-3	4.9	462	490	-28	5.7	0	5	1.0	-23	93.29	6	
LB1017	OS24	87	89	-2	2.2	1273	1246	27	2.1	0	0	0.0	27	97.35	10	Biomass to 5 dp
LB1017	OS25	37	39	-2	5.1	210	237	-27	11.4	2	30	12.7	3	94.12	0	Biomass to 5dp; vial labels & matrix differ
LB1019	OS23	18	18	0	0.0	1486	1498	-12	0.8	0	2	0.1	-10	99.00	2	No biomass data
LB1019	OS24	15	15	0	0.0	437	434	3	0.7	0	0	0.0	3	94.60	1	No biomass data
LB1019	OS25	27	30	-3	10.0	92	96	-4	4.2	1	1	1.0	-3	85.11	4	No biomass data
LB1020	OS23	2	2	0	0.0	30	37	-7	18.9	0	2	5.4	-5	89.55	0	
LB1020	OS24	6	6	0	0.0	55	77	-22	28.6	0	22	28.6	0	83.33	0	
LB1020	OS25	7	8	-1	12.5	72	88	-16	18.2	1	17	19.3	1	73.75	1	
LB1021	OS23	49	50	-1	2.0	465	441	24	5.2	1	1	0.2	25	96.48	0	External audit
LB1021	OS24	43	43	0	0.0	1651	1654	-3	0.2	0	0	0.0	-3	97.92	0	External audit
LB1021	OS25	41	41	0	0.0	710	707	3	0.4	0	0	0.0	3	99.37	0	External audit; Several vials dried
LB1022	OS23	20	20	0	0.0	1130	1128	2	0.2	0	1	0.1	3	98.76	1	No biomass data
LB1022	OS24	5	6	-1	16.7	6	7	-1	14.3	1	1	14.3	0	92.31	0	No biomass data
LB1022	OS25	11	11	0	0.0	101	100	1	1.0	0	0	0.0	1	99.50	0	No biomass data
LB1023	OS23	34	34	0	0.0	178	187	-9	4.8	0	6	3.2	-3	93.70	3	
LB1023	OS24	22	23	-1	4.3	848	1134	-286	25.2	0	1	0.1	-285	83.94	2	
LB1023	OS25	34	45	-11	24.4	217	239	-22	9.2	11	32	13.4	10	91.23	0	

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 (OS23-25).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1001	UM count	6	86	-	-	6	1	67	-	166
OS23	PL missed	0	1	-	-	0	0	1	-	2
	%missed	0.0	1.2	-	-	0.0	0.0	1.5	-	1.2
LB1001	UM count	-	28	-	-	2	107	43	1	181
OS24	PL missed	-	0	-	-	0	0	1	0	1
	%missed	-	0.0	-	-	0.0	0.0	2.3	0.0	0.6
LB1001	UM count	-	11	-	-	1	1	3	-	16
OS25	PL missed	-	0	-	-	0	0	1	-	1
	%missed	-	0.0	-	-	0.0	0.0	33.3	-	6.3
LB1002	UM count	-	9	-	-	9	1	-	-	19
OS23	PL missed	-	0	-	-	0	0	-	-	0
	%missed	-	0.0	-	-	0.0	0.0	-	-	0.0
LB1002	UM count	-	26	-	-	2	1	4	-	33
OS24	PL missed	-	0	-	-	0	0	1	-	1
	%missed	-	0.0	-	-	0.0	0.0	25.0	-	3.0
LB1002	UM count	-	30	-	-	15	1	4	-	50
OS25	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1003	Auditor count	1	972	2	1	374	4	1070	42	2466
OS23	UM missed	0	3	0	0	0	0	3	0	6
	%missed	0.0	0.3	0.0	0.0	0.0	0.0	0.3	0.0	0.2
LB1003	Auditor count	1	20	-	2	14	170	107	1	315
OS24	UM missed	0	0	-	0	0	0	0	0	0
	%missed	0.0	0.0	-	0.0	0.0	0.0	0.0	0.0	0.0
LB1003	Auditor count	-	50	450	-	14	-	133	1	648
OS25	UM missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1004	Auditor count	1	10	13	-	2	-	1	-	27
OS23	UM missed	0	0	1	-	0	-	0	-	1
	%missed	0.0	0.0	7.7	-	0.0	-	0.0	-	3.7
LB1004	Auditor count	1	1	-	-	1	-	7	-	10
OS24	UM missed	0	0	-	-	0	-	0	-	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	-	0.0
LB1004	Auditor count	-	9	-	-	1	-	3	2	15
OS25	UM missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1005	UM count	1	14	-	-	1	15	10	1	42
OS23	PL missed	0	1	-	-	0	0	0	0	1
	%missed	0.0	7.1	-	-	0.0	0.0	0.0	0.0	2.4
LB1005	UM count	-	1161	-	-	-	-	-	5	1166
OS24	PL missed	-	3	-	-	-	-	-	1	4
	%missed	-	0.3	-	-	-	-	-	20.0	0.3
LB1005	UM count	4	267	-	-	-	3	67	3	344
OS25	PL missed	0	0	-	-	-	0	9	2	11
	%missed	0.0	0.0	-	-	-	0.0	13.4	66.7	3.2
LB1006	UM count	2	494	9	10	37	10	112	-	674
OS23	PL missed	0	28	2	3	2	1	23	-	59
	%missed	0.0	5.7	22.2	30.0	5.4	10.0	20.5	-	8.8
LB1006	UM count	-	119	335	-	-	-	595	-	1049
OS24	PL missed	-	14	201	-	-	-	385	-	600
	%missed	-	11.8	60.0	-	-	-	64.7	-	57.2

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS23-25).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1006	UM count	-	3	8	-	40	-	3	-	54
OS25	PL missed	-	0	0	-	0	-	0	-	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1007	UM count	-	101	101	-	137	-	-	-	339
OS23	PL missed	-	19	6	-	1	-	-	-	26
	%missed	-	18.8	5.9	-	0.7	-	-	-	7.7
LB1007	UM count	-	19	207	-	1	-	-	-	227
OS24	PL missed	-	1	4	-	1	-	-	-	6
	%missed	-	5.3	1.9	-	100.0	-	-	-	2.6
LB1007	UM count	-	411	243	-	8	-	27	-	689
OS25	PL missed	-	4	1	-	0	-	6	-	11
	%missed	-	1.0	0.4	-	0.0	-	22.2	-	1.6
LB1009	UM count	-	57	-	-	16	12	42	-	127
OS23	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1009	UM count	1	24	-	-	6	14	52	-	97
OS24	PL missed	0	0	-	-	0	0	0	-	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1009	UM count	-	65	-	-	5	1	15	-	86
OS25	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1012	UM count	-	248	31	-	12	-	-	-	291
OS23	PL missed	-	4	2	-	0	-	-	-	6
	%missed	-	1.6	6.5	-	0.0	-	-	-	2.1
LB1012	UM count	-	142	150	-	23	-	-	-	315
OS24	PL missed	-	5	9	-	1	-	-	-	15
	%missed	-	3.5	6.0	-	4.3	-	-	-	4.8
LB1012	UM count	-	242	19	-	2	-	4	-	267
OS25	PL missed	-	5	0	-	1	-	0	-	6
	%missed	-	2.1	0.0	-	50.0	-	0.0	-	2.2
LB1015	UM count	10	3452	90	32	74	5	43	607	4313
OS23	PL missed	2	249	3	15	6	0	5	65	345
	%missed	20.0	7.2	3.3	46.9	8.1	0.0	11.6	10.7	8.0
LB1015	UM count	-	-	647	-	-	-	1	5	653
OS24	PL missed	-	-	37	-	-	-	1	1	39
	%missed	-	-	5.7	-	-	-	100.0	20.0	6.0
LB1015	UM count	-	867	305	-	10	-	76	29	1287
OS25	PL missed	-	20	11	-	0	-	23	26	80
	%missed	-	2.3	3.6	-	0.0	-	30.3	89.7	6.2
LB1016	UM count	-	28	-	-	7	-	36	2	73
OS23	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1016	UM count	-	69	-	-	3	43	14	2	131
OS24	PL missed	-	0	-	-	0	0	0	1	1
	%missed	-	0.0	-	-	0.0	0.0	0.0	50.0	0.8
LB1016	UM count	5	64	-	-	11	2	44	-	126
OS25	PL missed	0	0	-	-	0	0	0	-	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1017	UM count	14	140	-	-	9	8	43	276	490
OS23	PL missed	0	2	-	-	0	0	0	3	5
	%missed	0.0	1.4	-	-	0.0	0.0	0.0	1.1	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 (OS23-25).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1017	UM count	25	259	-	-	40	19	117	786	1246
OS24	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1017	UM count	-	91	13	-	1	1	87	44	237
OS25	PL missed	-	11	3	-	1	0	12	3	30
	%missed	-	12.1	23.1	-	100.0	0.0	13.8	6.8	12.7
LB1019	UM count	-	1302	-	-	31	1	164	-	1498
OS23	PL missed	-	2	-	-	0	0	0	-	2
	%missed	-	0.2	-	-	0.0	0.0	0.0	-	0.1
LB1019	UM count	2	313	-	-	16	4	92	7	434
OS24	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1019	UM count	-	24	-	-	20	22	24	6	96
OS25	PL missed	-	0	-	-	0	0	1	0	1
	%missed	-	0.0	-	-	0.0	0.0	4.2	0.0	1.0
LB1020	UM count	-	-	2	-	35	-	-	-	37
OS23	PL missed	-	-	1	-	1	-	-	-	2
	%missed	-	-	50.0	-	2.9	-	-	-	5.4
LB1020	UM count	-	17	-	-	23	-	37	-	77
OS24	PL missed	-	3	-	-	9	-	10	-	22
	%missed	-	17.6	-	-	39.1	-	27.0	-	28.6
LB1020	UM count	-	24	19	-	13	-	32	-	88
OS25	PL missed	-	4	6	-	1	-	6	-	17
	%missed	-	16.7	31.6	-	7.7	-	18.8	-	19.3
LB1021	Auditor count	4	383	-	-	4	2	38	10	441
OS23	UM missed	0	0	-	-	0	0	0	1	1
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	10.0	0.2
LB1021	Auditor count	5	933	172	-	35	1	21	487	1654
OS24	UM missed	0	0	0	-	0	0	0	0	0
	%missed	0.0	0.0	0.0	-	0.0	0.0	0.0	0.0	0.0
LB1021	Auditor count	1	150	88	-	49	-	17	402	707
OS25	UM missed	0	0	0	-	0	-	0	0	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1022	UM count	-	538	544	-	1	-	15	30	1128
OS23	PL missed	-	0	1	-	0	-	0	0	1
	%missed	-	0.0	0.2	-	0.0	-	0.0	0.0	0.1
LB1022	UM count	-	2	1	-	3	-	1	-	7
OS24	PL missed	-	0	1	-	0	-	0	-	1
	%missed	-	0.0	100.0	-	0.0	-	0.0	-	14.3
LB1022	UM count	-	77	17	-	2	4	-	-	100
OS25	PL missed	-	0	0	-	0	0	-	-	0
	%missed	-	0.0	0.0	-	0.0	0.0	-	-	0.0
LB1023	UM count	1	103	-	-	20	16	40	7	187
OS23	PL missed	0	2	-	-	0	0	4	0	6
	%missed	0.0	1.9	-	-	0.0	0.0	10.0	0.0	3.2
LB1023	UM count	-	162	30	-	2	-	7	933	1134
OS24	PL missed	-	1	0	-	0	-	0	0	1
	%missed	-	0.6	0.0	-	0.0	-	0.0	0.0	0.1
LB1023	UM count	2	165	5	2	9	2	19	35	239
OS25	PL missed	1	9	2	1	1	2	10	6	32
	%missed	50.0	5.5	40.0	50.0	11.1	100.0	52.6	17.1	13.4

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 OS23-OS25.

		Sample OS23								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1001	PL	0.3198	1.3390	-	-	0.1802	0.0178	2.0748	-	3.9316
	UM	0.2648	1.0063	-	-	0.1452	0.0162	1.6745	-	3.1070
	%diff.	17.2	24.8	-	-	19.4	9.0	19.3	-	21.0
LB1002	PL	-	0.0576	-	-	4.4311	2.5441	-	-	7.0328
	UM	-	0.0798	-	-	4.7385	2.6401	-	-	7.4584
	%diff.	-	-38.5	-	-	-6.9	-3.8	-	-	-6.1
LB1003	UM	0.0014	9.3356	0.0005	0.0002	0.5156	0.0146	3.6539	25.7163	39.2381
	Auditor	0.0014	9.2409	0.0005	0.0002	0.4995	0.0146	3.5603	25.6616	38.9790
	%diff.	0.0	1.0	0.0	0.0	3.1	0.0	2.6	0.2	0.7
LB1004	UM	0.0194	0.0226	0.0004	-	1.0932	-	0.0054	-	1.1410
	Auditor	0.0179	0.0204	0.0004	-	1.0872	-	0.0049	-	1.1308
	%diff.	7.7	9.7	0.0	-	0.5	-	9.3	-	0.9
LB1005	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1006	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1007	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1009	PL	-	0.1490	-	-	0.0031	0.0263	0.2802	-	0.4586
	UM	-	0.2288	-	-	0.0053	0.0314	0.3188	-	0.5843
	%diff.	-	-53.6	-	-	-71.0	-19.4	-13.8	-	-27.4
LB1012	PL	-	0.0463	0.0009	-	0.0021	-	-	-	0.0493
	UM	-	0.0596	0.0016	-	0.0018	-	-	-	0.0630
	%diff.	-	-28.7	-77.8	-	14.3	-	-	-	-27.8
LB1015	PL	0.0031	8.8225	0.0299	0.0049	0.1872	0.0035	76.4893	0.2978	85.8382
	UM	0.0024	5.8281	0.0080	0.0019	0.1298	0.0050	76.1300	0.1757	82.2809
	%diff.	22.6	33.9	73.2	61.2	30.7	-42.9	0.5	41.0	4.1
LB1016	PL	-	0.12195	-	-	0.01453	-	0.65439	0.00310	0.79397
	UM	-	0.0847	-	-	0.0081	-	0.5305	0.0028	0.6261
	%diff.	-	30.5	-	-	44.3	-	18.9	9.7	21.1
LB1017	PL	0.1392	1.0577	-	-	0.0096	0.1382	0.2533	4.2732	5.8712
	UM	0.1274	1.0635	-	-	0.0048	0.1159	0.2111	3.8443	5.3670
	%diff.	8.5	-0.5	-	-	50.0	16.1	16.7	10.0	8.6
LB1019	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1020	PL	-	-	0.0001	-	0.0260	-	-	-	0.0261
	UM	-	-	0.0001	-	0.0154	-	-	-	0.0155
	%diff.	-	-	0.0	-	40.8	-	-	-	40.6
LB1021	UM	0.1378	3.5944	-	-	0.0018	0.6433	12.4132	0.3640	17.1545
	Auditor	0.1359	3.5855	-	-	0.0015	0.6261	10.8564	0.3638	15.5692
	%diff.	1.4	0.2	-	-	16.7	2.7	12.5	0.1	9.2
LB1022	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1023	PL	0.0006	0.8202	-	-	0.0310	0.3942	1.4424	0.0059	2.6943
	UM	0.0002	0.5825	-	-	0.0106	0.3519	1.3899	0.0009	2.3360
	%diff.	66.7	29.0	-	-	65.8	10.7	3.6	84.7	13.3

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - 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 OS23-OS25.

Sample OS24

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1001	PL	-	0.4921	-	-	0.0013	4.1408	0.48881	0.0428	5.16581
	UM	-	0.4931	-	-	0.0013	4.0246	1.0409	0.0416	5.6015
	%diff.	-	-0.2	-	-	0.0	2.8	-112.9	2.8	-8.4
LB1002	PL	-	0.1909	-	-	0.0009	12.7394	0.6877	-	13.6189
	UM	-	0.2685	-	-	0.0014	6.8243	0.6782	-	7.7724
	%diff.	-	-40.6	-	-	-55.6	46.4	1.4	-	42.9
LB1003	UM	0.0007	0.1143	-	0.0003	0.0360	0.0242	0.0785	0.0001	0.2541
	Auditor	0.0007	0.1220	-	0.0001	0.0352	0.0240	0.0734	0.0001	0.2555
	%diff.	0.0	-6.7	-	66.7	2.2	0.8	6.5	0.0	-0.6
LB1004	UM	0.0056	0.0018	-	-	0.8401	-	2.1904	-	3.0379
	Auditor	0.0044	0.0014	-	-	0.7095	-	2.1342	-	2.8495
	%diff.	21.4	22.2	-	-	15.5	-	2.6	-	6.2
LB1005	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1006	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1007	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1009	PL	0.0001	0.0870	-	-	0.0022	0.0654	0.5106	-	0.6653
	UM	0.0001	0.1365	-	-	0.0034	0.0795	0.5539	-	0.7734
	%diff.	0.0	-56.9	-	-	-54.5	-21.6	-8.5	-	-16.2
LB1012	PL	-	0.0242	0.0046	-	0.0034	-	-	-	0.0322
	UM	-	0.0384	0.0084	-	0.0035	-	-	-	0.0503
	%diff.	-	-58.7	-82.6	-	-2.9	-	-	-	-56.2
LB1015	PL	-	-	0.2546	-	-	-	-	0.0002	0.2548
	UM	-	-	0.1974	-	-	-	-	0.0011	0.1985
	%diff.	-	-	22.5	-	-	-	-	-450.0	22.1
LB1016	PL	-	0.42279	-	-	0.01233	20.82219	0.26722	0.02250	21.54703
	UM	-	0.2449	-	-	0.0054	11.2746	0.2090	0.0172	11.7511
	%diff.	-	42.1	-	-	56.2	45.9	21.8	23.6	45.5
LB1017	PL	0.12010	1.37602	-	-	0.00994	0.02768	7.28348	2.54184	11.35906
	UM	0.1269	1.3821	-	-	0.0123	0.0354	7.0775	2.4807	11.1149
	%diff.	-5.7	-0.4	-	-	-23.7	-27.9	2.8	2.4	2.1
LB1019	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1020	PL	-	0.2108	-	-	0.0410	-	27.6853	-	27.9371
	UM	-	0.1296	-	-	0.0295	-	26.4731	-	26.6322
	%diff.	-	38.5	-	-	28.0	-	4.4	-	4.7
LB1021	UM	0.0005	2.6070	0.0268	-	0.0539	0.0070	0.0067	0.1486	2.8505
	Auditor	0.0005	2.6040	0.0238	-	0.0530	0.0070	0.0063	0.1415	2.8361
	%diff.	0.0	0.1	11.2	-	1.7	0.0	6.0	4.8	0.5
LB1022	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1023	PL	-	0.4621	0.0051	-	0.0167	-	40.5262	0.0282	41.0383
	UM	-	0.2673	0.0052	-	0.0164	-	39.2727	0.0023	39.5639
	%diff.	-	42.2	-2.0	-	1.8	-	3.1	91.8	3.6

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - 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 OS23-OS25.

		Sample OS25								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1001	PL	-	0.1929	-	-	0.0020	0.0824	0.7183	-	0.9956
	UM	-	0.1862	-	-	0.0013	0.0862	0.7047	-	0.9784
	%diff.	-	3.5	-	-	35.0	-4.6	1.9	-	1.7
LB1002	PL	-	0.0556	-	-	0.0179	7.2647	0.0325	-	7.3707
	UM	-	0.0710	-	-	0.0261	7.4842	0.0356	-	7.6169
	%diff.	-	-27.7	-	-	-45.8	-3.0	-9.5	-	-3.3
LB1003	UM	-	0.2325	0.0295	-	0.0015	-	0.0873	0.0001	0.3509
	Auditor	-	0.2286	0.0277	-	0.0014	-	0.0865	0.0001	0.3443
	%diff.	-	1.7	6.1	-	6.7	-	0.9	0.0	1.9
LB1004	UM	-	0.1777	-	-	0.7239	-	0.0350	0.0001	0.9367
	Auditor	-	0.1913	-	-	0.7191	-	0.0335	0.0001	0.9440
	%diff.	-	-7.7	-	-	0.7	-	4.3	0.0	-0.8
LB1005	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1006	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1007	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1009	PL	-	0.2445	-	-	0.0016	0.0002	0.0107	-	0.2570
	UM	-	0.2940	-	-	0.0026	0.0002	0.0096	-	0.3064
	%diff.	-	-20.2	-	-	-62.5	0.0	10.3	-	-19.2
LB1012	PL	-	0.1483	0.0037	-	0.0001	-	0.0011	0.0003	0.1535
	UM	-	0.1158	0.0033	-	0.0001	-	0.0010	0.0002	0.1204
	%diff.	-	21.9	10.8	-	0.0	-	9.1	33.3	21.6
LB1015	PL	-	0.5432	0.1407	-	0.0428	-	0.0635	0.0002	0.7904
	UM	-	0.2949	0.0861	-	0.0242	-	0.0464	0.0002	0.4518
	%diff.	-	45.7	38.8	-	43.5	-	26.9	0.0	42.8
LB1016	PL	0.01360	0.19665	-	-	0.01052	0.13945	0.21800	-	0.57822
	UM	0.0110	0.1517	-	-	0.0061	0.0960	0.1841	-	0.4489
	%diff.	19.1	22.9	-	-	42.0	31.2	15.6	-	22.4
LB1017	PL	-	0.47053	0.00042	-	-	0.00001	0.30754	0.01220	0.79070
	UM	-	0.4011	0.0004	-	-	0.0001	0.2701	0.0490	0.7207
	%diff.	-	14.8	4.8	-	-	-900.0	12.2	-301.6	8.9
LB1019	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1020	PL	-	1.3352	0.0035	-	0.0163	-	1.4543	-	2.8093
	UM	-	0.8737	0.0020	-	0.0110	-	0.8043	-	1.6910
	%diff.	-	34.6	42.9	-	32.5	-	44.7	-	39.8
LB1021	UM	-	-	-	-	-	-	-	-	-
	Auditor	Biomass Audit not conducted								-
	%diff.	-	-	-	-	-	-	-	-	-
LB1022	PL	-	-	-	-	-	-	-	-	-
	UM	-	-	-	-	-	-	-	-	-
	%diff.	-	-	-	-	-	-	-	-	-
LB1023	PL	0.0001	1.0351	0.0001	0.0006	0.0043	-	0.2030	3.9491	5.1923
	UM	0.0001	1.2404	0.0001	0.0004	0.0064	-	0.2636	3.8906	5.4016
	%diff.	0.0	-19.8	0.0	33.3	-48.8	-	-29.9	1.5	-4.0

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

Table 8. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS22.

PS22	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS22 - 42 - laser	0.25	1.33	1.29	0.67	-0.110
PS22 - 43 - laser	0.57	1.44	1.40	0.65	-0.100
PS22 - 44 - laser	0.51	1.44	1.41	0.65	-0.100
PS22 - 45 - laser	0.54	1.38	1.34	0.67	-0.100
PS22 - 46 - laser	0.51	1.42	1.38	0.66	-0.100
PS22 - 47 - laser	0.39	1.40	1.35	0.68	-0.120
PS22 - 48 - laser	0.25	1.33	1.28	0.69	-0.110
PS22 - 35 - sieve	0.44	1.51	1.47	0.64	-0.07
PS22 - 36 - sieve	0.49	1.53	1.50	0.64	-0.06
PS22 - 37 - sieve	0.60	1.53	1.48	0.63	-0.08
PS22 - 38 - sieve	0.54	1.53	1.48	0.65	-0.09
PS22 - 39 - sieve	0.49	1.54	1.51	0.64	-0.06
PS22 - 40 - sieve	0.55	1.52	1.48	0.66	-0.07
PS22 - 41 - sieve	0.58	1.53	1.49	0.65	-0.07

Table 9. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS23.

PS23	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS23 - 42 - laser	94.35	6.88	6.95	1.90	0.040
PS23 - 43 - laser	94.36	6.86	6.94	1.89	0.050
PS23 - 44 - laser	94.64	6.89	6.95	1.86	0.040
PS23 - 45 - laser	95.11	6.90	6.97	1.85	0.050
PS23 - 46 - laser	95.88	6.95	7.01	1.80	0.050
PS23 - 47 - laser	95.04	6.89	6.97	1.86	0.060
PS23 - 48 - laser	95.13	6.94	6.97	1.81	0.020
PS23 - 35 - sieve	97.12	8.35	-	-	-
PS23 - 36 - sieve	94.20	8.52	-	-	-
PS23 - 37 - sieve	96.48	8.46	-	-	-
PS23 - 38 - sieve	96.79	8.45	-	-	-
PS23 - 39 - sieve	96.54	8.52	-	-	-
PS23 - 40 - sieve	97.45	8.58	-	-	-
PS23 - 41 - sieve	97.55	8.41	-	-	-

Table 10. Summary of the particle size information received from participating laboratories for the twenty-second particle size distribution - PS22.

Lab	Method	%<63μm	Median	Mean	Sort	IGS (SKi)
LB1001	L	0.00	1.07	1.06	0.68	0.00
LB1002	DS?	0.14	1.54	1.48	0.63	-0.090
LB1003	DS	0.10	1.55	1.55	0.62	-0.010
LB1004	-	-	-	-	-	-
LB1009	L	3.52	1.43	1.56	-	2.35
LB1011	DS/L	0.79	1.24	1.21	-	-
LB1013	L	2.02	1.02	0.92	0.68	0.09
LB1016	WS/DS/L	0	1.25	1.27	0.53	0.10
LB1017*	L	0	1.07	1.06	0.68	0
LB1023	L	1.61	1.34	1.35	0.69	-0.02

Key to methods:

L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette n/c - not calculated
L* - replicated data, only source data included in calculations (see below)
"-" - No data. See Section 6, for details.

Summary	%<63μm	Median	Mean	Sort	IGS (SKi)
Number of values	8	8	8	6	7
Mean of laboratories	1.02	1.31	1.30	0.64	0.35
Mean of 7 replicates (laser)	0.43	1.39	1.35	0.67	-0.11
Mean of 7 replicates (sieve)	0.53	1.53	1.49	0.64	-0.07
Laboratory minimum	0.00	1.02	0.92	0.53	-0.09
Laboratory maximum	3.52	1.55	1.56	0.69	2.35

Table 11. Summary of the particle size information received from participating laboratories for the twenty-third particle size distribution - PS23.

Lab	Method	% < 63μm	Median	Mean	Sort	IGS (SKi)
LB1001	L	87.62	6.36	6.19	0.74	3.22
LB1002	L	75.52	5.93	5.81	2.06	-0.130
LB1003	L	83.98	5.70	5.87	1.94	0.140
LB1004	-	-	-	-	-	-
LB1009	L	96.31	6.53	5.75	1.74	0.133
LB1011	L	84.55	4.9	5.63	-	-
LB1013	L	79.53	6.09	3.76	1.58	-0.736
LB1016	L	86.60	6.22	6.30	2.02	0.08
LB1017*	L	87.62	6.36	6.19	0.74	3.22
LB1023	L	96.23	6.94	6.89	1.51	0.05

Key to methods:

L - Laser analysis	DS - Dry sieve	CC - Coulter counter
S - Sieve	WS - Wet sieve	FD - Freeze dried
P - Pipette		n/c - not calculated

L* - replicated data, only source data included in calculations (see below)

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

Summary	% < 63μm	Median	Mean	Sort	IGS (SKi)
Number of values	8	8	8	7	7
Mean of laboratories	86.29	6.08	5.78	1.66	0.39
Mean of 7 replicates (laser)	94.93	6.90	6.97	1.85	0.04
Mean of 7 replicates (sieve)	96.59	8.47	-	-	-
Laboratory minimum	75.52	4.90	3.76	0.74	-0.74
Laboratory maximum	96.31	6.94	6.89	2.06	3.22

Table 12. The identifications of the fauna made by participating laboratories for RT22. Names are given only where different from the AQC identification.

RT22	Taxon	LB1001	LB1003	LB1005	LB1010	LB1012
RT2201	Pseudarachna hirsuta	--	0 0	Gnathia juvenile	Idotea pelagica	ISOPODA(Gnathiidae?) 0
RT2202	Potamopyrgus antipodarum	--	0 0	--	- [jenkinsi]	--
RT2203	Paradoneis lyra	--	0 0	--	--	--
RT2204	Saxicavella jeffreysi	--	0 0	--	--	Thracia phaseolina
RT2205	Sphaerosyllis tetralix	--	0 0	--	--	--
RT2206	Aora gracilis	--	0 0	--	- typica	- typica
RT2207	Tanaopsis graciloides	--	0 0	--	Leptognathia breviremis	--
RT2208	Anaitides mucosa	--	0 0	--	[Phyllodoce] -	[Phyllodoce] -
RT2209	Lysianassa ceratina	--	0 0	--	--	--
RT2210	Gibbula cineraria	- umbilicus	0 0	- tumida	- umbilicalus	- umbilicalis
RT2211	Nephtys kersivalensis	- cirrosa	0 0	- hombergii	- hombergii	- hombergii
RT2212	Pholoe baltica	--	0 0	- [inornata]	- [inornata]	- [minuta]
RT2213	Asclerocheilus intermedius	[Asclerocheirus] -	0 0	Polyphysia crassa	--	Paradoneis eliasoni
RT2214	Onoba semicostata	--	0 0	--	--	- aculeus
RT2215	Parvicardium scabrum	- minimum	0 0	- ovale	- minimum	- ovale
RT2216	Pseudoprotella phasma	--	0 0	--	--	- [phasma (var. typica)]
RT2217	Abra alba	--	0 0	--	--	--
RT2218	Cerastoderma edule	--	0 0	Parvicardium exiguum	--	--
RT2219	Corophium lacustre	- acutum	0 0	--	- acutum	--
RT2220	Sphaeroma hookeri	- rugicauda?	0 0	- rugicaudata	Cirolana cranchii	- monodi
RT2221	Edwardsia claparedii	--	0 0	--	--	--
RT2222	Levinsenia gracilis	--	0 0	--	--	--
RT2223	Protodorvillea kefersteini	- [keferstenii]	0 0	--	--	--
RT2224	Ampelisca tenuicornis	--	0 0	--	- eschrichtii	- aequicornis
RT2225	Orchomene nanus	- [nana]	0 0	--	- [nana]	- [nana]

RT22	Taxon	LB1002	LB1004	LB1009	LB1011	LB1014
RT2201	Pseudarachna hirsuta	Pleurogonium rubicundum	0 0	0 0	--	--
RT2202	Potamopyrgus antipodarum	--	0 0	0 0	--	--
RT2203	Paradoneis lyra	--	0 0	0 0	--	--
RT2204	Saxicavella jeffreysi	--	0 0	0 0	--	--
RT2205	Sphaerosyllis tetralix	--	0 0	0 0	--	--
RT2206	Aora gracilis	--	0 0	0 0	--	--
RT2207	Tanaopsis graciloides	--	0 0	0 0	--	Leptognathia gracilis
RT2208	Anaitides mucosa	--	0 0	0 0	--	--
RT2209	Lysianassa ceratina	--	0 0	0 0	--	--
RT2210	Gibbula cineraria	[Gibbula (Steromphala)] -	0 0	0 0	- sp. juv.	--
RT2211	Nephtys kersivalensis	- hombergii	0 0	0 0	- [?kersivalensis]	- hombergii
RT2212	Pholoe baltica	--	0 0	0 0	- assimilis	- [inornata]
RT2213	Asclerocheilus intermedius	--	0 0	0 0	--	Sclerocheilus minutus
RT2214	Onoba semicostata	[Onoba (Onoba)] -	0 0	0 0	--	--
RT2215	Parvicardium scabrum	--	0 0	0 0	--	--
RT2216	Pseudoprotella phasma	--	0 0	0 0	--	--
RT2217	Abra alba	--	0 0	0 0	--	--
RT2218	Cerastoderma edule	--	0 0	0 0	--	--
RT2219	Corophium lacustre	- acutum	0 0	0 0	--	--
RT2220	Sphaeroma hookeri	- rugicauda	0 0	0 0	- rugicaudata	- rugicaudata
RT2221	Edwardsia claparedii	--	0 0	0 0	--	- [claparedi]
RT2222	Levinsenia gracilis	--	0 0	0 0	--	--
RT2223	Protodorvillea kefersteini	--	0 0	0 0	--	--
RT2224	Ampelisca tenuicornis	--	0 0	0 0	--	--
RT2225	Orchomene nanus	--	0 0	0 0	--	--

Table 12. The identifications of the fauna made by participating laboratories for RT22. Names are given only where different from the AQC identification.

RT22	Taxon	LB1015	LB1017	LB1020	LB1023
RT2201	Pseudarachna hirsuta	Munna kroyeri	- -	0 0	- -
RT2202	Potamopyrgus antipodarum	- -	- -	0 0	- -
RT2203	Paradoneis lyra	Levinsenia gracilis	- -	0 0	- -
RT2204	Saxicavella jeffreysi	- -	- -	0 0	- -
RT2205	Sphaerosyllis tetralix	- -	- taylori	0 0	- -
RT2206	Aora gracilis	- -	- -	0 0	- -
RT2207	Tanaopsis graciloides	Leptochelia dubia	- -	0 0	- -
RT2208	Anaitides mucosa	[Phyllodoce] -	- -	0 0	- -
RT2209	Lysianassa ceratina	- -	- -	0 0	- -
RT2210	Gibbula cineraria	- -	- umbilicalis	0 0	- -
RT2211	Nephtys kersivalensis	- -	- hombergii	0 0	- caeca
RT2212	Pholoe baltica	- synophthalmica	- -	0 0	- -
RT2213	Asclerocheilus intermedius	Lipobranchus jeffreysii	- -	0 0	- -
RT2214	Onoba semicostata	- -	- -	0 0	- -
RT2215	Parvicardium scabrum	- ovale	- ovale	0 0	- -
RT2216	Pseudoprotella phasma	- [pharma]	- -	0 0	- -
RT2217	Abra alba	- -	- -	0 0	- -
RT2218	Cerastoderma edule	- -	- glaucum	0 0	- glaucum
RT2219	Corophium lacustre	- -	- -	0 0	- -
RT2220	Sphaeroma hookeri	[Sphearoma] rugicauda	- rugicauda	0 0	- -
RT2221	Edwardsia claparedii	Aslia lefevrei	- -	0 0	- -
RT2222	Levinsenia gracilis	- -	- -	0 0	- -
RT2223	Protodorvillea kefersteini	- -	- -	0 0	- -
RT2224	Ampelisca tenuicornis	- -	- -	0 0	- -
RT2225	Orchomene nanus	- [nana]	- -	0 0	- -

RT22	Taxon	LB1016	LB1018	LB1021	LB1024
RT2201	Pseudarachna hirsuta	0 0	Munna sp.	0 0	- -
RT2202	Potamopyrgus antipodarum	- [jenkinsi]	- -	0 0	- -
RT2203	Paradoneis lyra	- -	[Cirrophorus] -	0 0	- -
RT2204	Saxicavella jeffreysi	Mya truncata	- -	0 0	- -
RT2205	Sphaerosyllis tetralix	- -	- sp.	0 0	- -
RT2206	Aora gracilis	- -	- typica	0 0	- -
RT2207	Tanaopsis graciloides	Leptognathia gracilis	0 0	0 0	- -
RT2208	Anaitides mucosa	[Phyllodoce] -	[Phyllodoce] -	0 0	- -
RT2209	Lysianassa ceratina	[Lyssianassa] -	0 0	0 0	- -
RT2210	Gibbula cineraria	- tumida	- sp.	0 0	- -
RT2211	Nephtys kersivalensis	- hombergii	- sp. juv.	0 0	- hombergii
RT2212	Pholoe baltica	- [inornata]	- -	0 0	- [inornata]
RT2213	Asclerocheilus intermedius	- -	- -	0 0	- -
RT2214	Onoba semicostata	- -	- -	0 0	- -
RT2215	Parvicardium scabrum	- -	- ovale	0 0	- exiguum
RT2216	Pseudoprotella phasma	- -	- -	0 0	- -
RT2217	Abra alba	- -	- nitida	0 0	- -
RT2218	Cerastoderma edule	- -	- -	0 0	- -
RT2219	Corophium lacustre	- acherusicum	- -	0 0	- acutum
RT2220	Sphaeroma hookeri	- rugicauda	- rugicauda	0 0	- rugicauda
RT2221	Edwardsia claparedii	- -	0 0	0 0	- -
RT2222	Levinsenia gracilis	- -	- -	0 0	- -
RT2223	Protodorvillea kefersteini	- -	- -	0 0	- -
RT2224	Ampelisca tenuicornis	- -	- -	0 0	- -
RT2225	Orchomene nanus	Lyssianassa ceratina	0 0	0 0	- -

Table 13. The identifications of the fauna made by participating laboratories for RT23. Names are given only where different from the AQC identification.

RT23	Taxon	LB0901	LB0903	LB0905	LB0910	LB0912	LB0915
RT2301	Sabellaria spinulosa	--	Lagis koreni	--	--	--	--
RT2302	Lepidonotus squamatus	--	--	--	--	--	- [squamata]
RT2303	Pomatoceros lamarcki	- [lamarckii]	--	--	--	- [lamarki]	--
RT2304	Aonides paucibranchiata	--	--	--	--	--	Paraonis fulgens
RT2305	Ehlersia cornuta agg.	Syllis amica	Syllis/Trypanosyllis -	- [cornuta]	[Syllis] [cornuta]	[Syllis] [cornuta]	[Syllis] [cornuta]
RT2306	Crepidula fornicata	--	--	- [fornicata juv.]	Acmaea virginea	--	--
RT2307	Pomatoceros triqueter	--	--	--	--	--	--
RT2308	Crangon allmanni	- [allmani]	--	--	- [allmani]	--	--
RT2309	Gnathia oxyuraea	--	--	--	- [oxyurea]	--	--
RT2310	Unciola crenatipalma	--	Corophium volutator	--	Aora typica	Aoridae 0	--
RT2311	Lacuna vincta	--	- parva	--	Barleeia unifasciata	- parva	Cingulopsis fulgida
RT2312	Echinocyamus pusillus	--	--	--	--	--	[Echiocyamus] -
RT2313	Nucula nucleus	--	--	--	- sulcata	--	--
RT2314	Mysella bidentata	--	--	--	--	--	--
RT2315	Atylus falcatus	--	--	--	--	--	--
RT2316	Exogone verugera	--	- hebes	--	--	--	--
RT2317	Anoplodactylus petiolatus	--	--	--	Nymphon gracile	--	--
RT2318	Glycera lapidum agg.	- [lapidum]	- [lapidum]	--	- [lapidum (complex)]	- [mimica]	- [lapidum]
RT2319	Chamelea striatula	Circumphalus casina	Circomplalus casina	- gallina	Astarte elliptica	[Venus] -	Circomphalus casina
RT2320	Lumbrineris gracilis	--	--	--	--	--	--
RT2321	Microprotopus maculatus	--	--	--	Stenothoidae 0	--	--
RT2322	Mytilus edulis	--	Modiolula phaseolina	- [edulis juv.]	--	--	Modiolus modiolus
RT2323	Iphimedia minuta	--	--	- obesa	Epimera cornugera	[Panoploea] -	--
RT2324	Timoclea ovata	Arctica islandica	--	--	--	Nucula nucleus	Gouldia minimum
RT2325	Asterias rubens	--	--	--	--	--	--

RT23	Taxon	LB0902	LB0904	LB0909	LB0911	LB0914	LB0916
RT2301	Sabellaria spinulosa	--	0 0	--	- alveolata	--	--
RT2302	Lepidonotus squamatus	--	0 0	--	--	--	--
RT2303	Pomatoceros lamarcki	--	0 0	--	- triqueter	--	--
RT2304	Aonides paucibranchiata	--	0 0	Paradoneis armata	--	--	--
RT2305	Ehlersia cornuta agg.	- [cornuta]	0 0	- [cornuta]	- [cornuta]	- [cornuta]	- [cornuta]
RT2306	Crepidula fornicata	--	0 0	--	--	--	--
RT2307	Pomatoceros triqueter	--	0 0	--	- lamarcki	--	--
RT2308	Crangon allmanni	--	0 0	--	- [allmani]	--	--
RT2309	Gnathia oxyuraea	--	0 0	--	--	--	--
RT2310	Unciola crenatipalma	--	0 0	--	--	--	--
RT2311	Lacuna vincta	--	0 0	Eatonina fulgida	--	--	- parva
RT2312	Echinocyamus pusillus	--	0 0	--	--	--	--
RT2313	Nucula nucleus	- hanleyi	0 0	--	--	--	--
RT2314	Mysella bidentata	--	0 0	--	--	--	--
RT2315	Atylus falcatus	--	0 0	--	--	--	--
RT2316	Exogone verugera	--	0 0	[Exogene] -	--	--	--
RT2317	Anoplodactylus petiolatus	--	0 0	--	--	--	--
RT2318	Glycera lapidum agg.	- [lapidum]	0 0	- [lapidum (complex)]	- [lapidum]	- [lapidum]	- [lapidum]
RT2319	Chamelea striatula	--	0 0	- gallina	Circomphalus casina	- gallina	--
RT2320	Lumbrineris gracilis	--	0 0	--	--	--	--
RT2321	Microprotopus maculatus	--	0 0	--	--	--	--
RT2322	Mytilus edulis	--	0 0	--	--	--	--
RT2323	Iphimedia minuta	--	0 0	--	--	--	- obesa
RT2324	Timoclea ovata	Crenella decussata	0 0	Laevicardium crassum	--	--	--
RT2325	Asterias rubens	--	0 0	--	--	--	--

Table 13. The identifications of the fauna made by participating laboratories for RT23. Names are given only where different from the AQC identification.

RT23	Taxon	LB0917	LB0920	LB0923
RT2301	Sabellaria spinulosa	- -	0 0	- -
RT2302	Lepidonotus squamatus	- -	0 0	- -
RT2303	Pomatoceros lamarcki	- -	0 0	- -
RT2304	Aonides paucibranchiata	- -	0 0	- -
RT2305	Ehlersia cornuta agg.	[Syllis] [cornuta]	0 0	- [cornuta]
RT2306	Crepidula fornicata	- -	0 0	- -
RT2307	Pomatoceros triqueter	- -	0 0	- -
RT2308	Crangon allmanni	- -	0 0	- -
RT2309	Gnathia oxyuraea	- -	0 0	- -
RT2310	Unciola crenatipalma	- -	0 0	- -
RT2311	Lacuna vincta	- -	0 0	- -
RT2312	Echinocyamus pusillus	- -	0 0	- -
RT2313	Nucula nucleus	- sulcata	0 0	- -
RT2314	Mysella bidentata	- -	0 0	- -
RT2315	Atylus falcatus	- -	0 0	- -
RT2316	Exogone verugera	- -	0 0	- -
RT2317	Anoplodactylus petiolatus	- -	0 0	- -
RT2318	Glycera lapidum agg.	- [lapidum]	0 0	- [lapidum]
RT2319	Chamelea striatula	- gallina	0 0	- gallina
RT2320	Lumbrineris gracilis	- -	0 0	- -
RT2321	Microprotopus maculatus	- longimanus	0 0	- -
RT2322	Mytilus edulis	- -	0 0	Modiolus modiolus
RT2323	Iphimedia minuta	- -	0 0	- -
RT2324	Timoclea ovata	- -	0 0	- -
RT2325	Asterias rubens	- -	0 0	- -

RT23	Taxon	LB0918	LB0921	LB0924
RT2301	Sabellaria spinulosa	- -	0 0	- -
RT2302	Lepidonotus squamatus	- -	0 0	- -
RT2303	Pomatoceros lamarcki	- -	0 0	- -
RT2304	Aonides paucibranchiata	[Anoides] -	0 0	- -
RT2305	Ehlersia cornuta agg.	- [cornuta]	0 0	- [cornuta]
RT2306	Crepidula fornicata	- -	0 0	- -
RT2307	Pomatoceros triqueter	- -	0 0	- -
RT2308	Crangon allmanni	- -	0 0	- -
RT2309	Gnathia oxyuraea	- maxillaris	0 0	- -
RT2310	Unciola crenatipalma	Ischyrocerus anguipes	0 0	- -
RT2311	Lacuna vincta	Littorina obtusata	0 0	- -
RT2312	Echinocyamus pusillus	- -	0 0	- -
RT2313	Nucula nucleus	- nitidosa	0 0	- -
RT2314	Mysella bidentata	- -	0 0	- -
RT2315	Atylus falcatus	- -	0 0	- -
RT2316	Exogone verugera	- -	0 0	- -
RT2317	Anoplodactylus petiolatus	Pycnogonum littorale	0 0	- -
RT2318	Glycera lapidum agg.	- tesselata	0 0	- [lapidum]
RT2319	Chamelea striatula	Veneridae 0	0 0	- gallina
RT2320	Lumbrineris gracilis	- -	0 0	- -
RT2321	Microprotopus maculatus	icrodeutopus cf. anomal	0 0	- -
RT2322	Mytilus edulis	- -	0 0	- -
RT2323	Iphimedia minuta	- -	0 0	- -
RT2324	Timoclea ovata	Veneridae 0	0 0	Cerastoderma edule
RT2325	Asterias rubens	- -	0 0	- -

Table 14. Summary of the results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR08.

	Differences		
LabCode	**Generic**	**Specific**	**name changes**
LB1001	0	3	0
LB1002	0	1	0
LB1003	0	0	2
LB1004	np	np	np
LB1005	8	11	0
LB1009	1	2	1
LB1010	3	4	0
LB1011	np	np	np
LB1014	np	np	np
LB1015	0	0	1
LB1016	2	8	2
LB1017	2	3	0
LB1021	np	np	np
LB1023	0	2	0
LB1024	0	2	0

Key: "-" - No data.
np - Not participating.
See Section 6, for details.

Table 15. Results from the Own Samples (OS23-25) 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 Sample Flag
LabCode	Lab.	Target	Flag	Missed	% Missed	Remedial Action	Lab.	%	Remedial Action	Lab.	Target	Flag	Missed	% Missed	Remedial Action	Lab.	Target	Flag	Target	Lab.	Flag	
LB1001 OS23	35	34.2 - 41.8	PASS	1	2.6	-	5	13.5	Reprocess	166	149.4 - 182.6	PASS	2	1.2	-	3.9316	2.4856 - 3.7284	*Fail*	90.0	83.74	Fail	Fail
LB1001 OS24	27	24.3 - 29.7	PASS	0	0.0	-	5	18.5	-	196	162.9 - 199.1	PASS	1	0.6	-	5.1658	4.4812 - 6.7218	*PASS*	90.0	90.72	PASS	Acceptable
LB1001 OS25	9	8.0 - 12.0	PASS	1	10.0	-	0	0.0	-	15	14.0 - 18.0	PASS	1	6.3	-	0.9956	0.7827 - 1.1741	*PASS*	90.0	96.77	PASS	Good
LB1002 OS23	8	6.0 - 10.0	PASS	0	0.0	-	0	0.0	-	19	17.0 - 21.0	PASS	0	0.0	-	7.0328	5.9667 - 8.9501	*PASS*	90.0	100.00	PASS	Excellent
LB1002 OS24	11	10.0 - 14.0	PASS	1	8.3	-	0	0.0	-	32	29.7 - 36.3	PASS	1	3.0	-	13.6189	6.2179 - 9.3269	*Fail*	90.0	98.46	PASS	Good
LB1002 OS25	19	17.0 - 21.0	PASS	0	0.0	-	1	5.3	-	50	45.0 - 55.0	PASS	0	0.0	-	7.3707	6.0935 - 9.1403	*PASS*	90.0	98.00	PASS	Good
LB1003 OS23	85	76.5 - 93.5	PASS	0	0.0	-	0	0.0	-	2474	2219.4 - 2712.6	PASS	6	0.2	-	39.2381	31.1832 - 46.7748	*PASS*	90.0	99.60	PASS	Good
LB1003 OS24	37	33.3 - 40.7	PASS	0	0.0	-	0	0.0	-	329	283.5 - 346.5	PASS	0	0.0	-	0.2541	0.2044 - 0.3066	*PASS*	90.0	97.85	PASS	Good
LB1003 OS25	21	18.9 - 23.1	PASS	0	0.0	-	0	0.0	-	663	583.2 - 712.8	PASS	0	0.0	-	0.3509	0.2754 - 0.4132	*PASS*	90.0	98.86	PASS	Good
LB1004 OS23	9	7.0 - 11.0	PASS	0	0.0	-	0	0.0	-	26	24.3 - 29.7	PASS	1	3.7	-	1.1410	0.9046 - 1.3570	*PASS*	90.0	98.11	PASS	Good
LB1004 OS24	5	3.0 - 7.0	PASS	0	0.0	-	0	0.0	-	10	8.0 - 12.0	PASS	0	0.0	-	3.0379	2.2796 - 3.4194	*PASS*	90.0	100.00	PASS	Excellent
LB1004 OS25	9	7.0 - 11.0	PASS	0	0.0	-	0	0.0	-	15	13.0 - 17.0	PASS	0	0.0	-	0.9367	0.7552 - 1.1328	*PASS*	90.0	100.00	PASS	Excellent
LB1005 OS23	17	17.0 - 21.0	PASS	0	0.0	-	3	15.8	Reprocess	41	37.8 - 46.2	PASS	1	2.4	-	-	-	-	90.0	89.16	Fail	Poor
LB1005 OS24	4	3.0 - 7.0	PASS	1	20.0	-	0	0.0	-	1164	1049.4 - 1282.6	PASS	4	0.3	-	-	-	-	90.0	99.83	PASS	Good
LB1005 OS25	36	35.1 - 42.9	PASS	2	5.1	-	4	10.8	-	332	309.6 - 378.4	PASS	11	3.2	-	-	-	-	90.0	96.18	PASS	Good
LB1006 OS23	40	41.4 - 50.6	Fail	5	10.9	-	1	2.4	-	593	606.6 - 741.4	Fail	59	8.8	-	-	-	-	90.0	92.50	PASS	Acceptable
LB1006 OS24	12	11.0 - 15.0	PASS	1	7.7	-	0	0.0	-	956	944.1 - 1153.9	PASS	600	57.2	-	-	-	-	90.0	92.07	PASS	Acceptable
LB1006 OS25	5	3.0 - 7.0	PASS	0	0.0	-	0	0.0	-	54	48.6 - 59.4	PASS	0	0.0	-	-	-	-	90.0	100.00	PASS	Excellent
LB1007 OS23	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	323	305.1 - 372.9	PASS	26	7.7	-	-	-	-	90.0	96.68	PASS	Good
LB1007 OS24	8	9.0 - 13.0	Fail	1	9.1	-	0	0.0	-	226	204.3 - 249.7	PASS	6	2.6	-	-	-	-	90.0	92.27	PASS	Acceptable
LB1007 OS25	32	34.2 - 41.8	Fail	3	7.9	Review	0	0.0	-	580	620.1 - 757.9	Fail	11	1.6	-	-	-	-	90.0	77.38	Fail	Fail
LB1009 OS23	33	29.7 - 36.3	PASS	0	0.0	-	2	6.1	-	127	114.3 - 139.7	PASS	0	0.0	-	0.4586	0.4674 - 0.7012	*Fail*	90.0	96.85	PASS	Good
LB1009 OS24	26	23.4 - 28.6	PASS	0	0.0	-	2	7.7	-	98	87.3 - 106.7	PASS	0	0.0	-	0.6653	0.6187 - 0.9281	*PASS*	90.0	90.26	PASS	Acceptable
LB1009 OS25	30	27.0 - 33.0	PASS	0	0.0	-	1	3.3	-	88	77.4 - 94.6	PASS	0	0.0	-	0.2570	0.2451 - 0.3677	*PASS*	90.0	96.55	PASS	Good
LB1012 OS23	3	2.0 - 6.0	PASS	1	25.0	-	0	0.0	-	282	261.9 - 320.1	PASS	6	2.1	-	0.0493	0.0504 - 0.0756	*Fail*	90.0	98.26	PASS	Good
LB1012 OS24	5	3.0 - 7.0	PASS	0	0.0	-	0	0.0	-	292	283.5 - 346.5	PASS	15	4.8	-	0.0322	0.0402 - 0.0604	*Fail*	90.0	96.21	PASS	Good
LB1012 OS25	14	12.0 - 16.0	PASS	0	0.0	-	0	0.0	-	267	246.6 - 301.4	PASS	6	2.2	-	0.1535	0.0963 - 0.1445	*Fail*	90.0	98.72	PASS	Good
LB1015 OS23	91	86.4 - 105.6	PASS	6	6.3	-	4	4.4	-	3968	3881.7 - 4744.3	PASS	345	8.0	-	85.8382	65.8247 - 98.7371	*PASS*	90.0	95.23	PASS	Good
LB1015 OS24	8	7.0 - 11.0	PASS	1	11.1	-	0	0.0	-	614	587.7 - 718.3	PASS	39	6.0	-	0.2548	0.1588 - 0.2382	*Fail*	90.0	96.92	PASS	Good
LB1015 OS25	18	17.0 - 21.0	PASS	1	5.3	-	0	0.0	-	1222	1158.3 - 1415.7	PASS	80	6.2	-	0.7904	0.3614 - 0.5422	*Fail*	90.0	95.97	PASS	Good
LB1016 OS23	20	17.0 - 21.0	PASS	0	0.0	-	1	5.3	-	73	65.7 - 80.3	PASS	0	0.0	-	0.7940	0.5009 - 0.7513	*Fail*	90.0	95.89	PASS	Good
LB1016 OS24	26	25.2 - 30.8	PASS	1	3.6	-	3	11.1	-	132	117.9 - 144.1	PASS	1	0.8	-	21.5470	9.4009 - 14.1013	*Fail*	90.0	95.82	PASS	Good
LB1016 OS25	29	26.1 - 31.9	PASS	0	0.0	-	3	10.3	-	126	113.4 - 138.6	PASS	0	0.0	-	0.5782	0.3591 - 0.5387	*Fail*	90.0	97.62	PASS	Good
LB1017 OS23	58	54.9 - 67.1	PASS	0	0.0	-	6	9.8	-	462	441.0 - 539.0	PASS	5	1.0	-	5.8712	4.2936 - 6.4404	*PASS*	90.0	93.29	PASS	Acceptable
LB1017 OS24	87	80.1 - 97.9	PASS	0	0.0	-	10	11.2	-	1273	1121.4 - 1370.6	PASS	0	0.0	-	11.3591	8.8919 - 13.3379	*PASS*	90.0	97.35	PASS	Good
LB1017 OS25	37	35.1 - 42.9	PASS	2	5.1	-	0	0.0	-	210	213.3 - 260.7	Fail	30	12.7	-	0.7907	0.5766 - 0.8648	*PASS*	90.0	94.12	PASS	Acceptable
LB1019 OS23	18	16.0 - 20.0	PASS	0	0.0	-	2	11.1	-	1486	1348.2 - 1647.8	PASS	2	0.1	-	-	-	-	90.0	99.00	PASS	Good
LB1019 OS24	15	13.0 - 17.0	PASS	0	0.0	-	1	6.7	-	437	390.6 - 477.4	PASS	0	0.0	-	-	-	-	90.0	94.60	PASS	Acceptable
LB1019 OS25	27	27.0 - 33.0	PASS	1	3.3	-	4	13.8	Reprocess	92	86.4 - 105.6	PASS	1	1.0	-	-	-	-	90.0	85.11	Fail	Poor
LB1020 OS23	2	.0 - 4.0	PASS	0	0.0	-	0	0.0	-	30	33.3 - 40.7	Fail	2	5.4	Review	0.0261	0.0124 - 0.0186	*Fail*	90.0	89.55	Fail	Poor
LB1020 OS24	6	4.0 - 8.0	PASS	0	0.0	-	0	0.0	-	55	69.3 - 84.7	Fail	22	28.6	Reprocess	27.9371	21.3058 - 31.9586	*PASS*	90.0	83.33	Fail	Fail
LB1020 OS25	7	6.0 - 10.0	PASS	1	12.5	Review	1	14.3	Review	72	79.2 - 96.8	Fail	17	19.3	Reprocess	2.8093	1.3528 - 2.0292	*Fail*	90.0	73.75	Fail	Fail
LB1021 OS23	49	45.0 - 55.0	PASS	1	2.0	-	0	0.0	-	465	396.9 - 485.1	PASS	1	0.2	-	17.1545	12.4554 - 18.6830	*PASS*	90.0	96.48	PASS	Good
LB1021 OS24	43	38.7 - 47.3	PASS	0	0.0	-	0	0.0	-	1651	1488.6 - 1819.4	PASS	0	0.0	-	2.8505	2.2689 - 3.4033	*PASS*	90.0	97.92	PASS	Good
LB1021 OS25	41	36.9 - 45.1	PASS	0	0.0	-	0	0.0	-	710	636.3 - 777.7	PASS	0	0.0	-	-	-	-	90.0	99.37	PASS	Good
LB1022 OS23	20	18.0 - 22.0	PASS	0	0.0	-	1	5.0	-	1130	1015.2 - 1240.8	PASS	1	0.1	-	-	-	-	90.0	98.76	PASS	Good
LB1022 OS24	5	4.0 - 8.0	PASS	1	16.7	-	0	0.0	-	6	5.0 - 9.0	PASS	1	14.3	-	-	-	-	90.0	92.31	PASS	Acceptable
LB1022 OS25	11	9.0 - 13.0	PASS	0	0.0	-	0	0.0	-	101	90.0 - 110.0	PASS	0	0.0	-	-	-	-	90.0	99.50	PASS	Good
LB1023 OS23	34	30.6 - 37.4	PASS	0	0.0	-	3	8.8	-	178	168.3 - 205.7	PASS	6	3.2	-	2.6943	1.8688 - 2.8032	*PASS*	90.0	93.70	PASS	Acceptable
LB1023 OS24	22	20.7 - 25.3	PASS	0	0.0	-	2	8.7	Review	848	1020.6 - 1247.4	Fail	1	0.1	-	41.0383	31.6511 - 47.4767	*PASS*	90.0	83.94	Fail	Fail
LB1023 OS25	34	40.5 - 49.5	Fail	11	24.4	-	0	0.0	-	217	215.1 - 262.9	PASS	32	13.4	-	5.1923	4.3213 - 6.4819	*PASS*	90.0	91.23	PASS	Acceptable

Table 16. Z-score results for the derived statistics supplied by participating laboratories for the particle size (PS) exercises - PS22 and PS23 - NMBAQC / UK NMMP standards applied.

PS22																
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
LaserRepAv	0.43	-0.37	PASS	1.39	0.27	PASS	1.35	0.03	PASS	0.67	0.52	PASS	-0.106	-1.44	PASS	-
SieveRepAv	0.53	-0.24	PASS	1.53	1.13	PASS	1.49	0.88	PASS	0.64	-0.36	PASS	-0.071	-0.97	PASS	-
LB1001	0.00	-0.95	PASS	1.07	-1.76	PASS	1.06	-1.75	PASS	0.68	1.02	PASS	0.000	0.00	PASS	Sand with shell frags/Sand
LB1002	0.14	-0.76	PASS	1.54	1.21	PASS	1.48	0.83	PASS	0.63	-0.91	PASS	-0.090	-1.23	PASS	Sand/Sand
LB1003	0.1	-0.81	PASS	1.55	1.27	PASS	1.55	1.26	PASS	0.62	-1.30	PASS	-0.010	-0.14	PASS	Medium-coarse sand/Sand
LB1004	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1009	3.52	3.80	Fail	1.43	0.51	PASS	1.56	1.32	PASS	-	-	Deemed Fail	2.35	31.91	Fail	Fine Sand / Fine Sand
LB1011	0.79	0.12	PASS	1.24	-0.68	PASS	1.21	-0.83	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1013	2.02	1.78	PASS	1.02	-2.07	Fail	0.92	-2.61	Fail	0.68	1.02	PASS	0.094	1.27	PASS	Sandy/-
LB1016	0	-0.95	PASS	1.25	-0.62	PASS	1.27	-0.46	PASS	0.53	-4.77	Fail	0.100	1.35	PASS	Shelly sand/Sand
LB1017*	0	-0.95	PASS	1.07	-1.76	PASS	1.06	-1.75	PASS	0.68	1.02	PASS	0	0.00	PASS	Sand with shell frags/Sand
LB1023	1.61	1.22	PASS	1.34	-0.05	PASS	1.35	0.03	PASS	0.69	1.41	PASS	-0.020	-0.28	PASS	Sand/Sand

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

PS23																
Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description
LaserRepAv	94.93	0.98	PASS	6.90	1.28	PASS	6.97	2.08	Fail	1.85	0.39	PASS	0.044	-0.09	PASS	Mud/-
SieveRepAv	96.59	1.24	PASS	8.47	4.84	Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1001	87.62	-0.17	PASS	6.36	0.06	PASS	6.19	0.29	PASS	0.74	-5.13	Fail	3.22	32.23	Fail	Black Mud/Sandy Mud
LB1002	75.52	-2.08	Fail	5.93	-0.91	PASS	5.81	-0.58	PASS	2.06	1.42	PASS	-0.130	-1.86	PASS	Mud/Sandy Mud
LB1003	83.98	-0.75	PASS	5.70	-1.44	PASS	5.87	-0.44	PASS	1.94	0.83	PASS	0.140	0.89	PASS	Muddy Sand/Sandy Mud
LB1004	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1009	96.31	1.19	PASS	6.53	0.44	PASS	5.75	-0.72	PASS	1.74	-0.17	PASS	0.133	0.82	PASS	Muddy Clay/Silt
LB1011	84.55	-0.66	PASS	4.9	-3.25	Fail	5.63	-0.99	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1013	79.53	-1.45	PASS	6.09	-0.55	PASS	3.76	-5.28	Fail	1.58	-0.96	PASS	-0.736	-8.03	Fail	Muddy/-
LB1016	86.60	-0.33	PASS	6.22	-0.26	PASS	6.30	0.54	PASS	2.02	1.22	PASS	0.080	0.28	PASS	D.brown sandy mud/gravelly sandy mud
LB1017*	87.62	-0.17	PASS	6.36	0.06	PASS	6.19	0.29	PASS	0.74	-5.13	Fail	3.22	32.23	Fail	Black Mud/Sandy Mud
LB1023	96.23	1.18	PASS	6.94	1.37	PASS	6.89	1.90	PASS	1.51	-1.31	PASS	0.050	-0.03	PASS	-

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

Table17. Comparison of the overall performance of laboratories from 1995/96 to 2003/04 with respect to the NMBAQC / UK NMMP standards.

Scheme Year	Exercise	Pass (>90% BCSI)	Fail (<90% BCSI)	% Pass
02 (1995/96)	01	10	0	100
03 (1996/97)	02, 03, 04	21	6	78
04 (1997/98)	05, 06, 07	27	7	79
05 (1998/99)	08, 09, 10	24	9	73
06 (1999/00)	11, 12, 13	29	13	69
07 (2000/01)	14, 15, 16	26	13	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

Key: * - Own Samples selected from completed data matrices
BCSI - Bray Curtis similarity index (untransformed)

Table 18. Comparison of each laboratory's Bray-Curtis similarity performance in the Own Sample exercises from Scheme year 02 (1995/96) to Scheme year 10 (2003/04).

	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		
	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**
LB1001	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
LB1002	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.68	91.36	93.63	98.66	96.44	92.46	100	98.46	98
LB1003	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
LB1004	-	-	-	-	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
LB1005	-	-	-	-	-	-	-	-	-	-	-	-	-	92.09	96.52	82.22	91.5	99.34	97.22	84.94	76.92	80.46	89.16	99.83	96.18
LB1006	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.5	92.07	100
LB1007	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
LB1008	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1009	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
LB1010	93.55	92.8	-	98.76	-	-	-	-	-	-	97.81	92.89	97.8	89.73	95.06	98.87	93.19	97.65	95.95	95.08	93.15	84.05	-	-	-
LB1011	-	-	-	-	95.75	92.56	96.37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1012	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
LB1013	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1014	-	-	-	-	-	-	-	-	-	-	97.92	84.85	97.29	-	-	-	-	-	-	-	-	-	-	-	-
LB1015		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
LB1016	-	-	-	-	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
LB1017	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
LB1018	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1019	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	88.89	43.32	83.72	99	94.6	85.11
LB1020	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
LB1021	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
LB1022	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
LB1023	-	-	-	-	-	-	-	95.08	53.66	60.42	-	-	-	-	-	-	84.32	100	80.31	-	-	-	93.7	83.94	91.23
LB1024	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	96.89	72.07	56.22	-	-	-	-	-	-

Key: **Shaded cells** = 'Fail' flag irrespective of subsequent remedial action.
- = no data / not participating

NMBAQC – Section B: Report from the Contractor - Figures

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS22. Seven samples analysed by sieve and seven samples analysed by Laser.

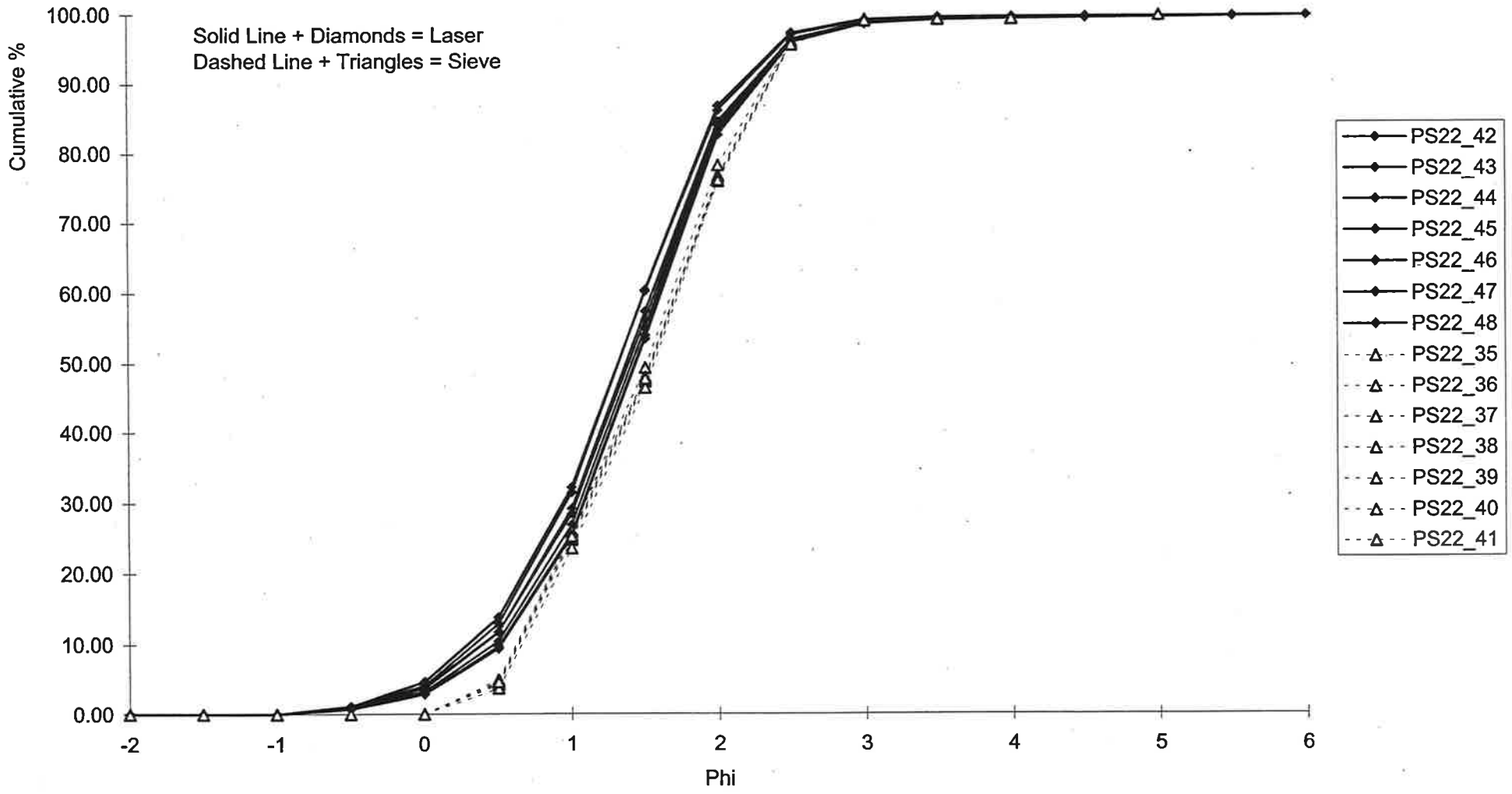


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS23. Seven samples analysed by sieve and seven samples analysed by Laser.

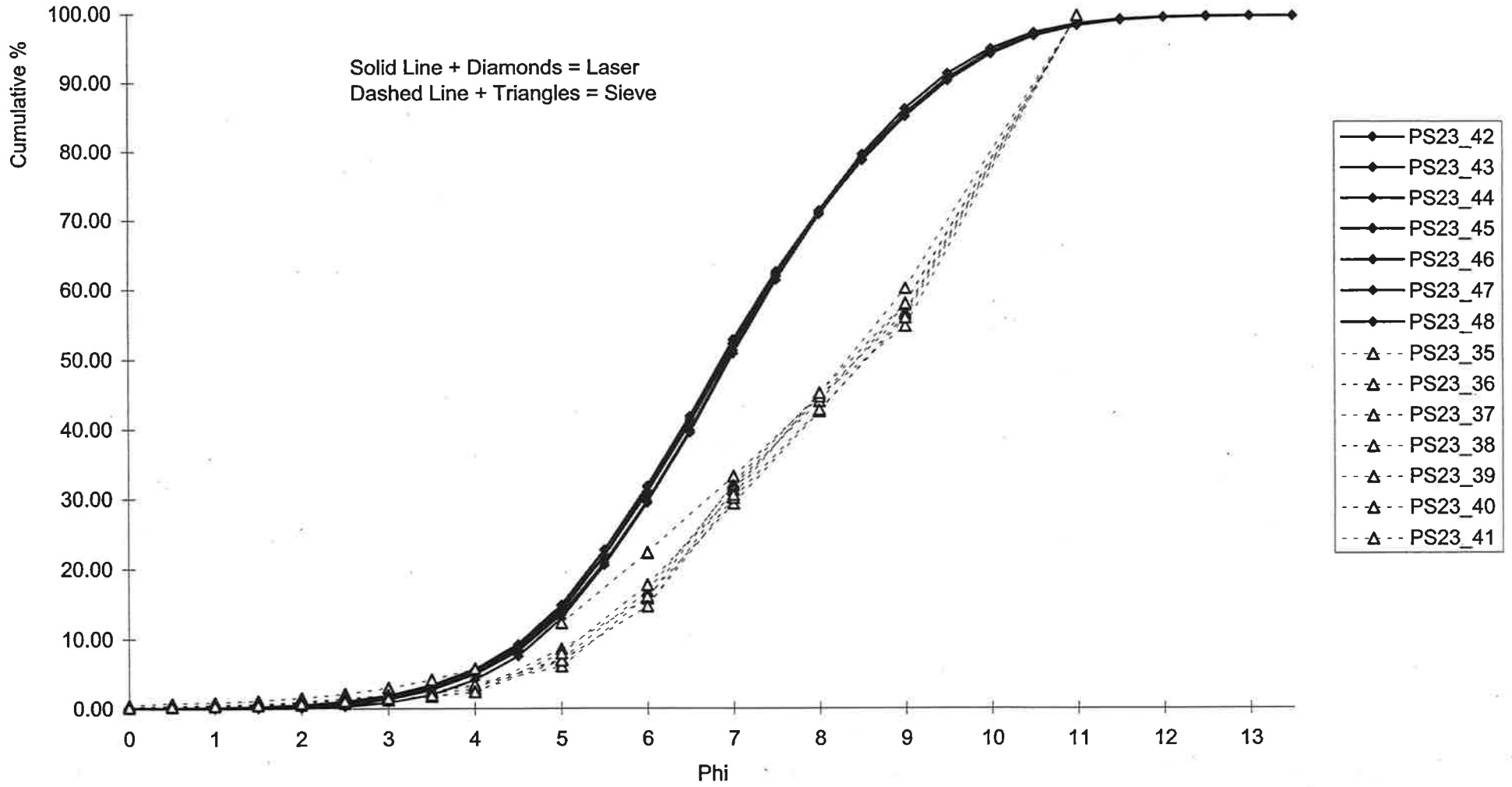


Figure 3. Particle size distribution curves resulting from analysis of sediment sample PS22 by the participating laboratories.

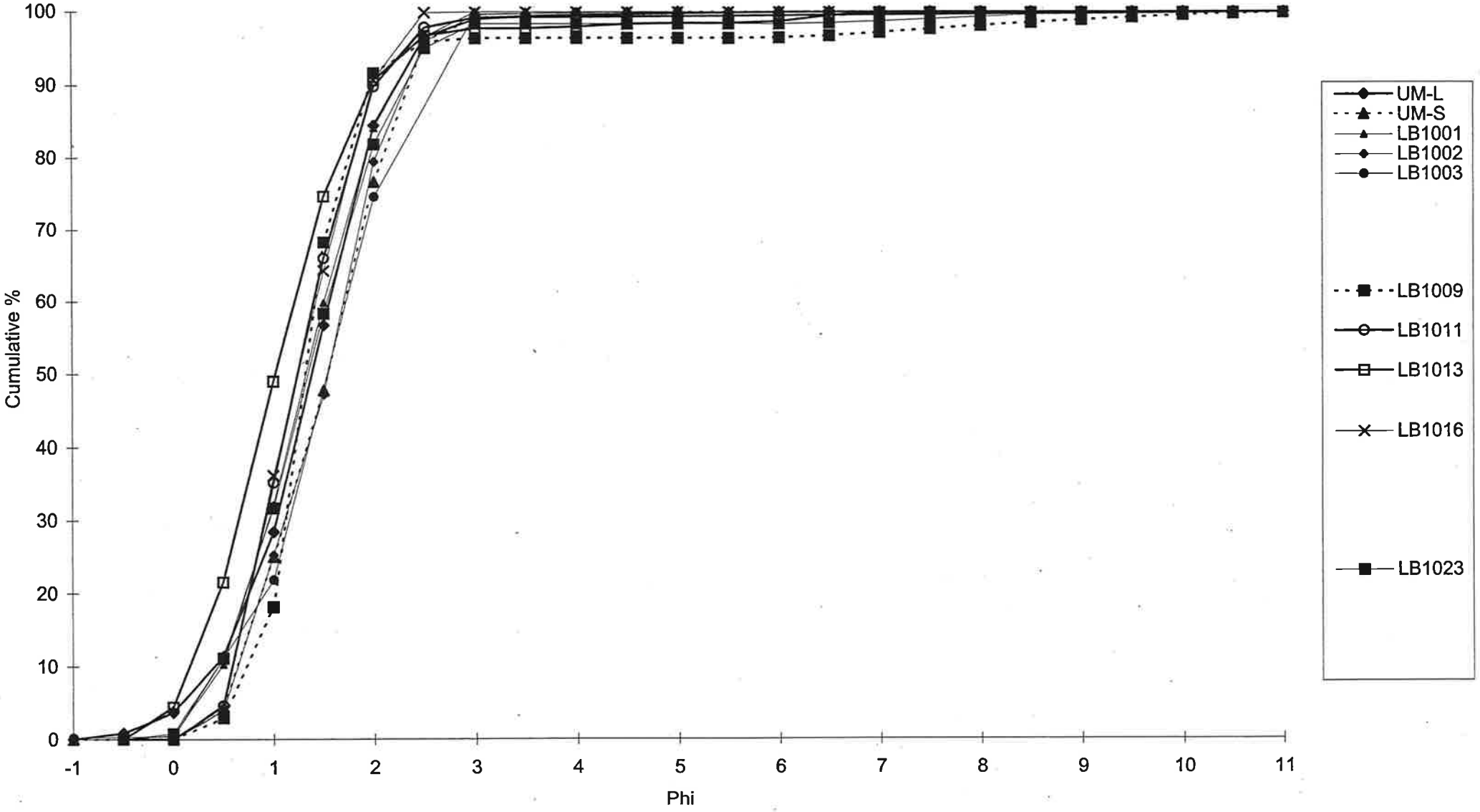


Figure 4. Particle size distribution curves resulting from analysis of sediment sample PS23 by the participating laboratories.

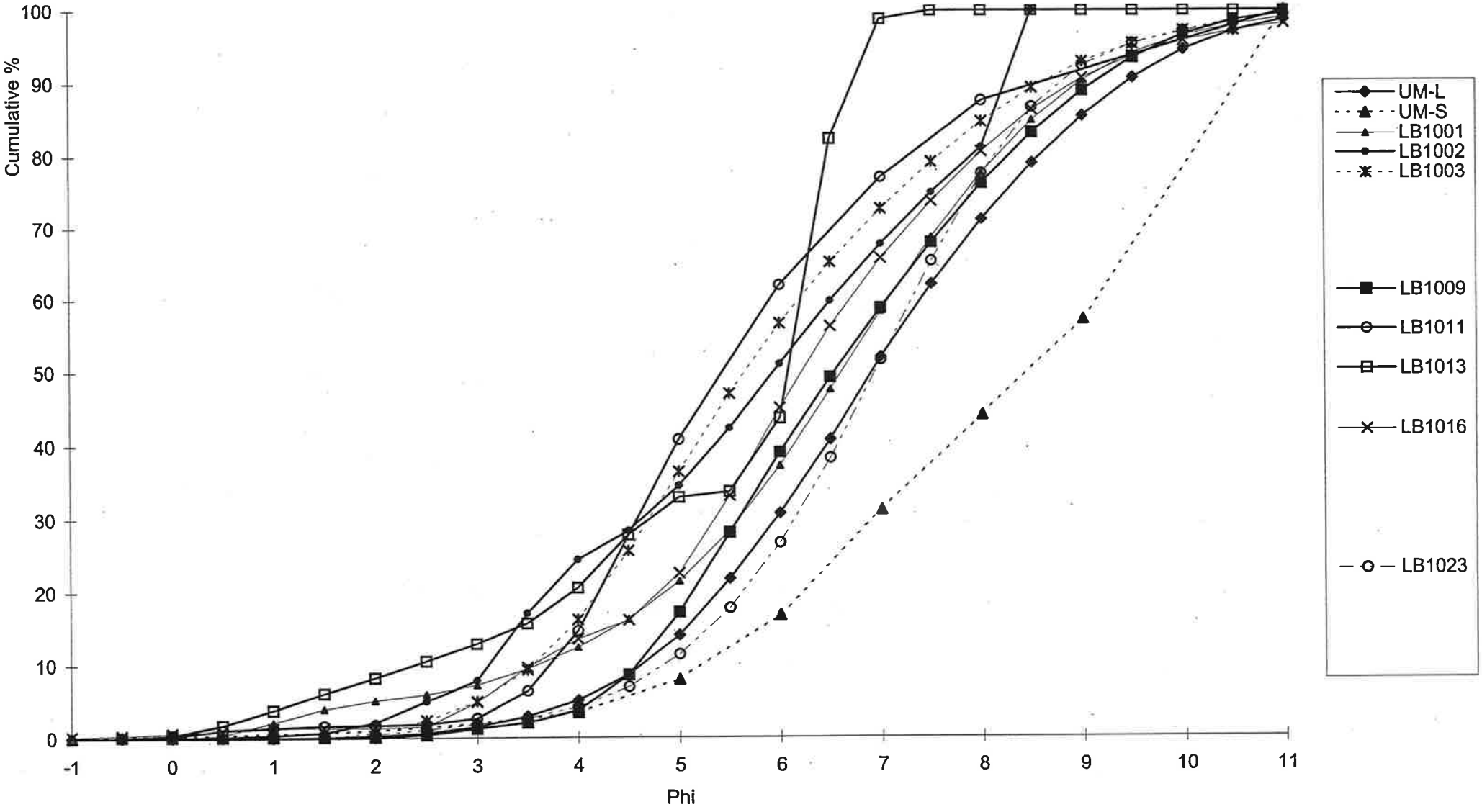


Figure 5. Z-scores for PS22 derived statistics (replicated data not displayed).

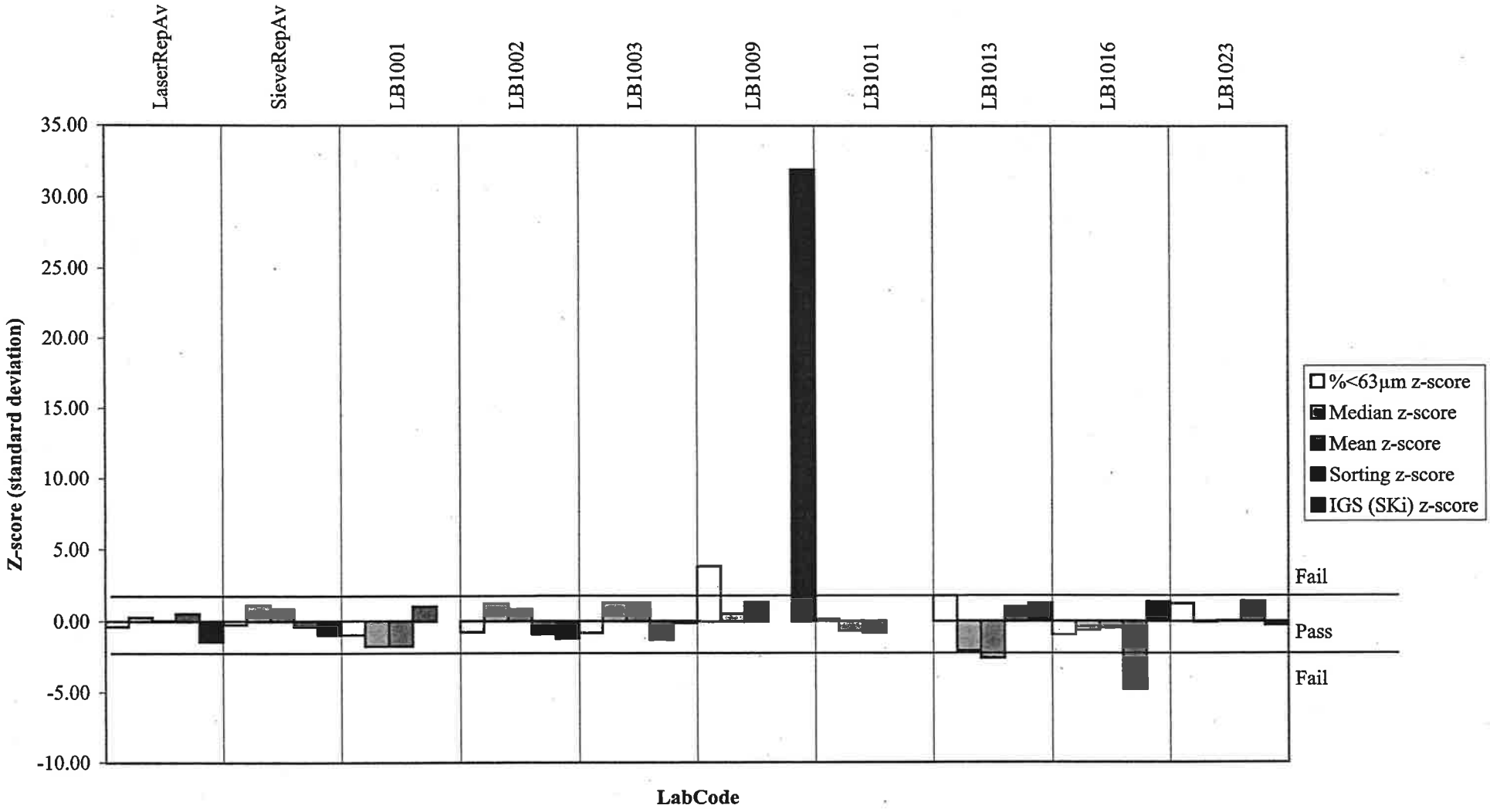


Figure 6. Z-scores for PS23 derived statistics (replicated data not displayed).

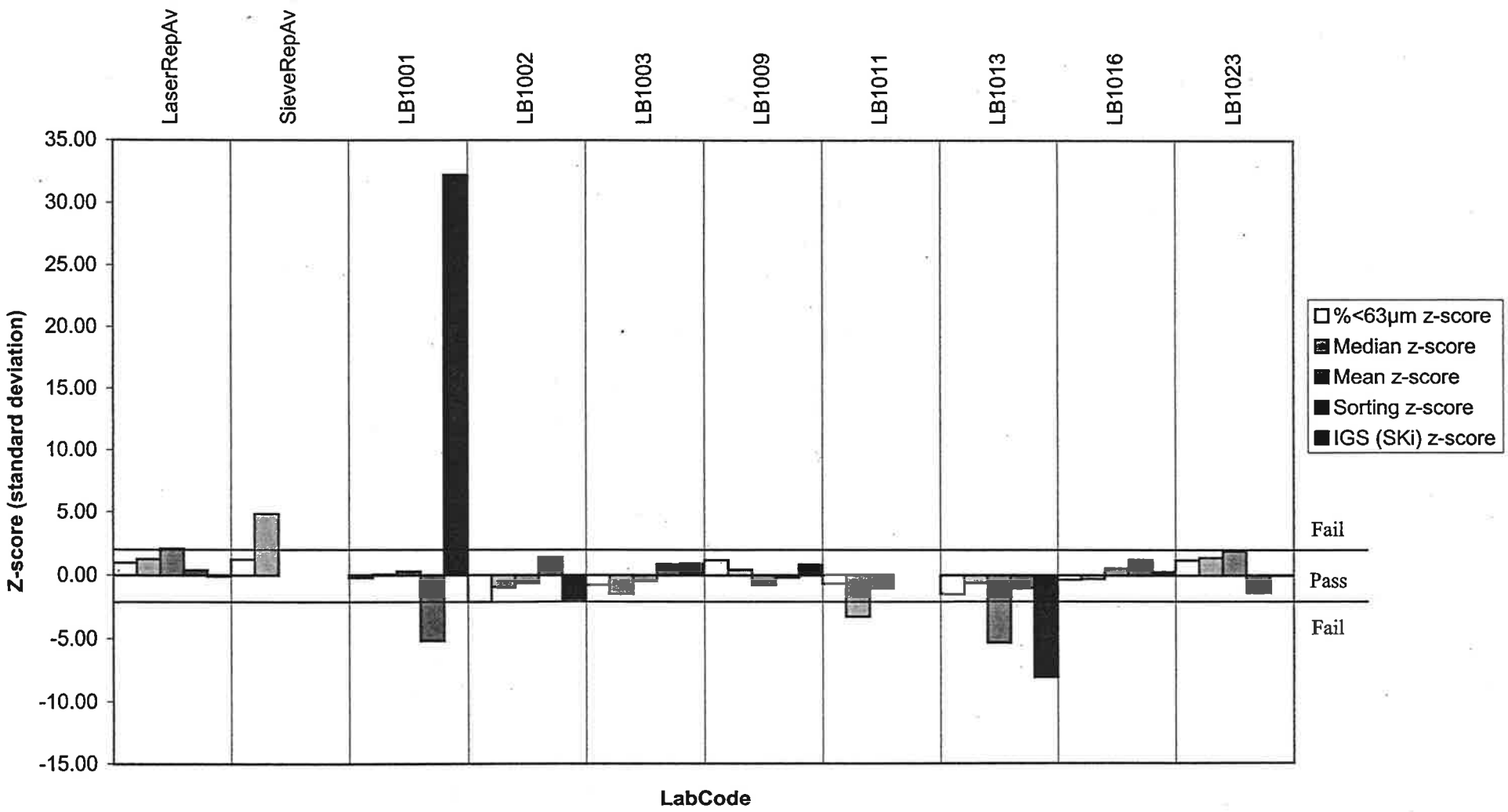


Figure 7. The number of differences from the AQC identification of specimens distributed in RT22 for each of the participating laboratories. Arranged in order of increasing number of differences.

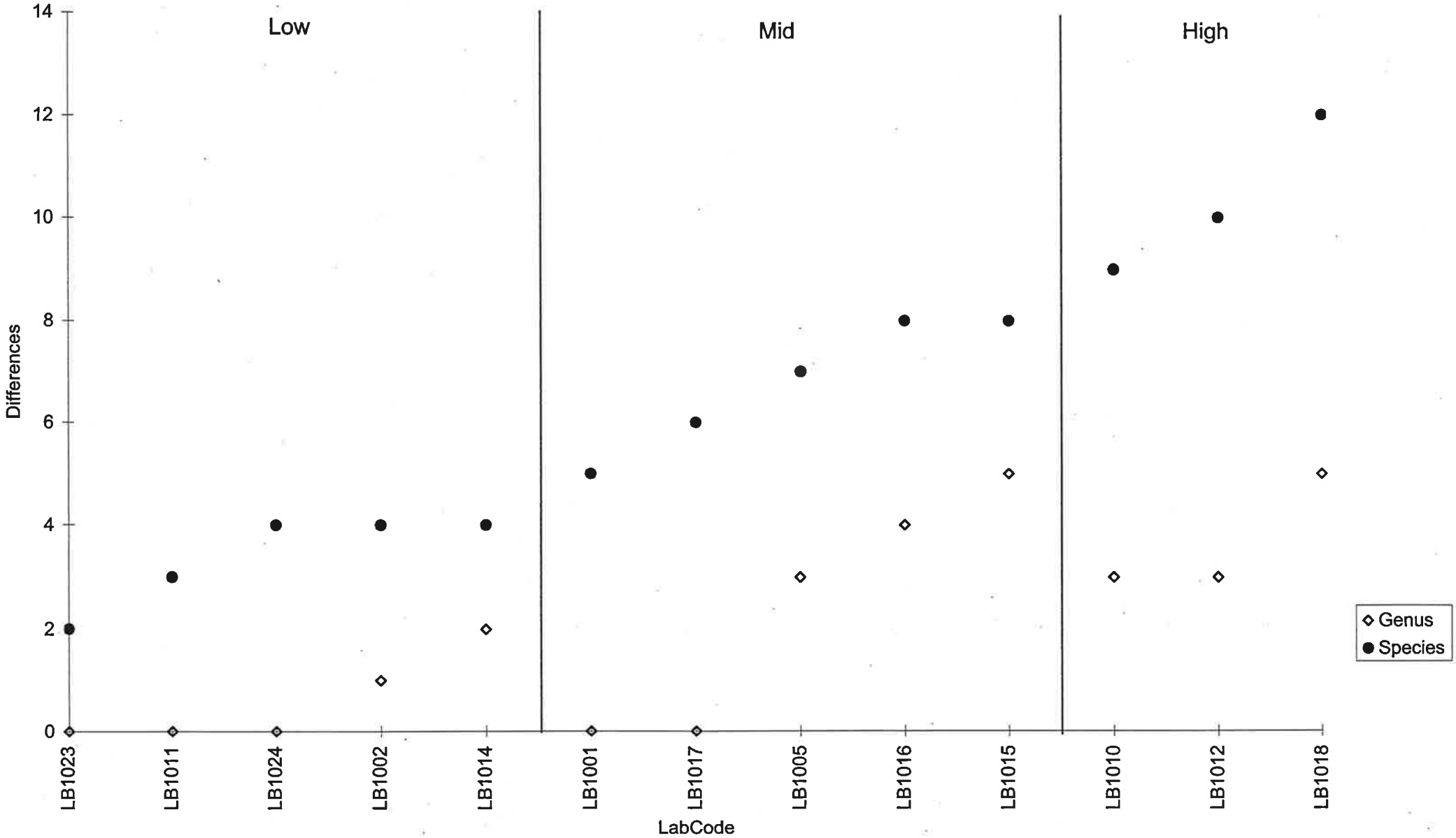
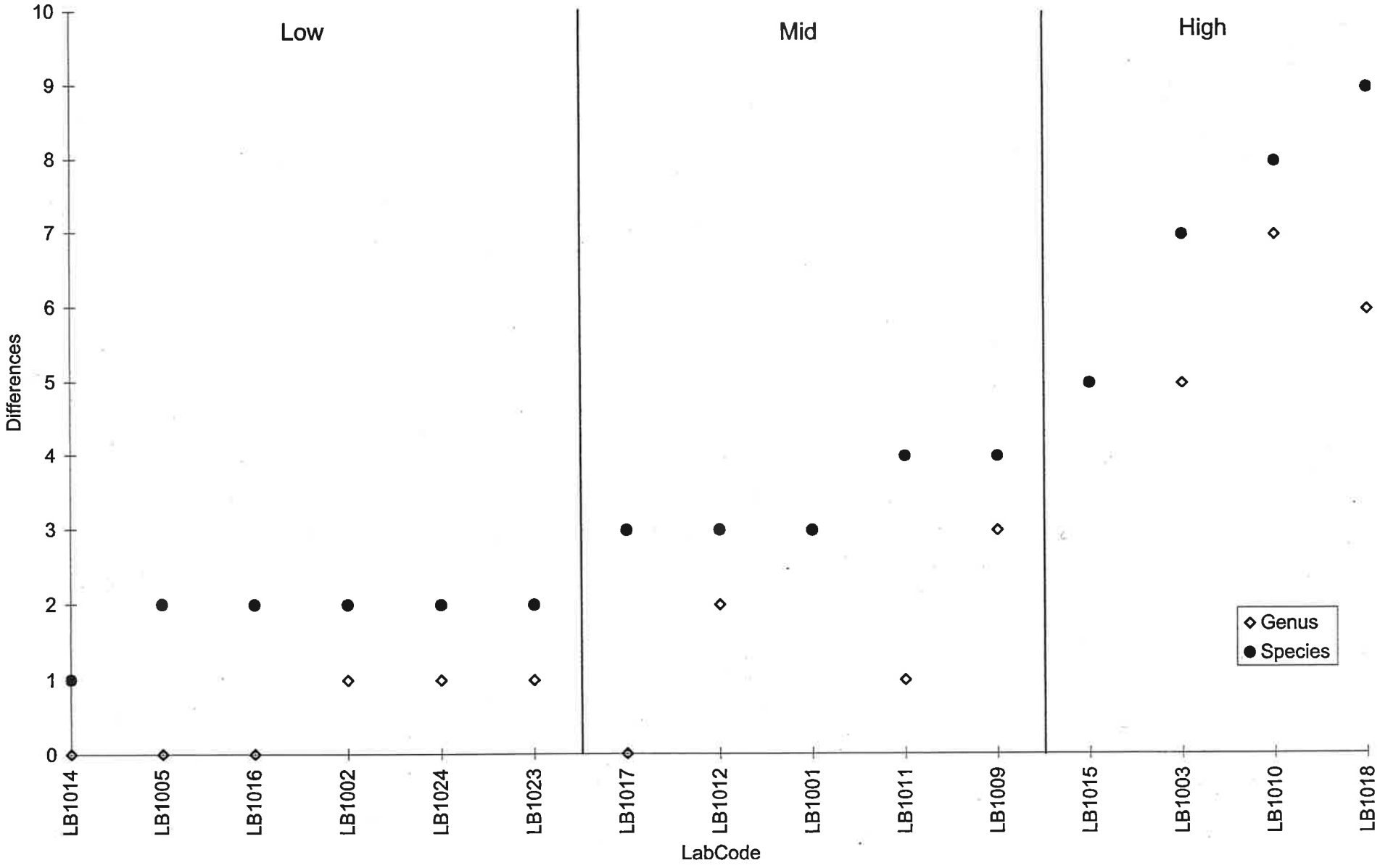


Figure 8. The number of differences from the AQC identification of specimens distributed in RT23 for each of the participating laboratories. Arranged in order of increasing number of differences.



NMBAQC – Section B: Report from the Contractor - Appendices

Section B: 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. Specifically, to consider the fauna recorded in the NMMP samples. To encourage the assemblage and use of collections of reference specimens for NMMP stations. This exercise will be scored. However, the results are **not** used in the assignment of overall laboratory pass / fail flags.

Protocol:

Please provide twenty-five identified specimens from your laboratory reference material. For NMMP laboratories this should be from samples collected as part of the NMMP programme. Participating laboratories are given **free choice** of taxa they wish to submit for this exercise. All fauna selected should be from waters around the British Isles. If possible, the species selected should differ from those you sent as part of a previous circulation. If you are unable to supply specimens as specified then alternative specimens can be substituted. Duplicate examples of species can be submitted for the purpose of establishing growth series. Two of the twenty-five specimens requested 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 is still disagreement after return of the specimens we will provide full explanations for our identification on request 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.

Origin of specimens:

Where possible specimens should be selected from samples taken at stations forming part of the NMMP programme, or from the same area. If this is not possible then select from samples which represent your normal area of operation or a particular survey.

Preparation

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

Timescale:

Please send specimens to Unicomarine Ltd. by 7th November 2003. Results and specimens will be returned as soon after receipt as practicable.

Problems

Please call if you have any queries about this exercise.

List of groups from which specimens should be selected

	Major Group	Group	Note
1	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
2	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
3	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
4	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
5	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
6	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
7	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
8	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
9	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
10	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
11	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
12	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
13	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
14	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
15	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
16	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
17	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
18	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
19	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
20	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
21	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
22	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
23	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
24	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
25	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)

Section B: 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	**Poor – Remedial Action Suggested**
<85	**Fail – 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.