BEQUALM - NMBAQC

Biological Effects Quality Assurance in Monitoring

National Marine Biological Analytical Quality Control

Annual Report

Year 11 - 2004/2005

National Marine Biological AQC Coordinating Committee – August 2006

BEQUALM

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report - Year 11 - 2004/2005

Section A – Report from the NMBAQC Co-ordinating Committee

Section B – Report from the Contractor.

1. SCHEME REVIEW AND FUTURE ROLE.

The BEQUALM / NMBAQC scheme completed Year 11 in 2004/05. While the scope of the scheme outlined below remained similar to previous years it is likely to change significantly with the forthcoming European Water Framework Directive (WFD). The WFD states that international analytical standards be applied and that there will a requirement for competent monitoring authorities to provide some quality assurance for data submissions. It is expected that in addition to its role for the UK NMMP benthic programme the NMBAQC group will be required to lead on quality assurance for all the WFD marine biological quality elements: invertebrates, transitional water fish, phytoplankton, macroalgae, and angiosperms. A workshop on fish and epibiota sampling took place in Year 11 and ring test components on transitional water fish, and phytoplankton are included in NMBAQC plans for Year 12.

The Year 11 scheme remained focussed on macrobenthic invertebrates. The results for Year 11 showed improvement on previous years, though many of the same quality issues have arisen again (see Section 3). These included incomplete exercises and failure to carry out remedial action on NMMP samples. Labs that do not manage to complete exercises and return data fail to take full advantage of the training opportunity presented. It needs to be emphasized that the aim of the scheme is to assist all labs to maintain and improve their quality standards. The exercises provide valuable training for participants and sharing information on problems and pitfalls via bulletins and feedback to the scheme contractor is of benefit to all. It is remiss of labs to undertake all the expense and effort of sampling, analysis, and quality control only to fall at the last hurdle by not completing remedial action. Data that remains flagged is effectively of no value and serves no purpose.

The scheme has demonstrated that minor variations in sample processing procedures may have significant quality effects and that even very experienced ecologists may be mislead by identification keys which are ambiguous, erroneous, out of date, or simply not comprehensive. The Year 11 results re-iterate the need for the production of standardised marine species lists, guides to standard taxonomic literature, and the development of detailed sample processing protocols for benthos (and particle size) samples as well as a taxonomic discrimination protocol outlining the levels of identification expected for various taxonomic groups. In addition the provision of taxonomic workshops at both “beginner” and “expert” is still required to assist with the development of both new and experienced ecologists. The scheme will also aim to support the production of new or revised identification keys on various groups with the aim of making these more widely available via publication. The scheme plans to address the above issues as funds become available in Years 12 and 13.

It is envisaged that the new NMMP database, MERMAN, planned for 2006, may archive sample data collected by UK government agencies for both NMMP and WFD. This data will subsequently be available to ICES/OSPAR (International Council for Exploration of the Sea/ Oslo-Paris Commission). The addition of WFD data to the NMMP database may require some revision of the proportion of samples audited for individual labs. Moreover the remedial action and flagging procedure for samples being submitted to the database may require clarification. A preliminary guide note for post audit data amendments prior to re-submission to the NMMP database has now been provided (Appendix 6.4).

The scheme remains entirely UK based and there is little support to expand the scheme into Europe. This issue has been raised with the ICES/OSPAR Steering Group on Quality Assurance of Biological Measurements in the Northeast Atlantic (SGQAE) in Denmark in February 2005 (see Section 4).

2. SCOPE OF THE SCHEME

The eleventh 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 eighteen 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 for Year 11:

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 of 25 marine decapod taxa.

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 operation of the scheme for Year 11 and its results is contained in the contractors report in Section B. Only the main issues arising are discussed below.

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 6.1). 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.

The MB12 sample originated in the Medway Estuary. Only 3 of the 9 participating labs achieved the "Acceptable" level (90% similarity) for analysis. The main reason for the poor results was the mis-identification of cirratulids. Although cirratulids have frequently featured in ring tests and workshops, and a provisional identification key has been produced through the scheme, it is clear that they remain a challenge for many participants. The outcome of the MB12 exercise demonstrates the value of this component for highlighting problem areas and emphasizes the need for further training on problematical taxonomic groups.

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 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 10, there are still some problems with some labs regarding their extraction efficiency. In addition some labs appear to be repeating taxonomic errors and are failing to address taxonomic errors raised in "pass" samples. The aim of the scheme is not simply to achieve "pass" levels but to improve standards overall and to encourage labs to investigate and minimise all errors arising through appropriate training.

The Committee recognises the need to develop a **processing requirements protocol and taxonomic discrimination 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 is planned for Year 13)

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.

Almost all labs provided a pre and post analysis description, the latter based on the Folk triangle. Some of the descriptions were clearly inconsistent with the supplied sample. It is again suspected that different equipment or processing methodology may be producing highly variable data. **A more detailed particle size sample processing protocol may help eliminate some of these discrepancies.**

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. The first ring tests comprised a mixture of various taxa and the second test focused on decapod crustaceans. Minor issues were once again raised in relation to literature used for identification. **The provision of a standard NMBAQC 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 were permitted to include up to 2 uncertain taxa in Year 10 and up to 5 problematic taxa in Year 11.

Although the LR exercise is not assigned a pass / fail standard**, it would be beneficial if participants were required to indicate the status of their submitted specimens. This would help distinguish mis-identification of assigned reference specimens from that of recognised problematical**

material. Both the verification of reference specimens and the provision of a second opinion on problematical specimens are valuable services for participants.

3.2 Participation

The number of participating labs in Year 11 was 24 and did not change from Year 10, although the level of participation is quite variable (See Appendix 6.2). The participants comprised private contractors, university labs and Government labs in Scotland, Northern Ireland, England and Wales. The one European lab, from Germany, which joined the scheme in Year 10 dropped out in Year 11. It seems that the imperative driving participation in AQC schemes is not yet as strong in continental Europe despite the forthcoming Water Framework Directive. 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, laboratories submitting data to the NMMP database should endeavour to undertake all relevant training exercises and are required to carry out any required remedial actions on submitted Own Samples.**

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 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" are not participating in, or not completing, all relevant 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 with data feedback due to late or non- returns. **Laboratories that miss data or sample return deadlines will be deemed to have failed**.

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 6.3). 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 has been some confusion among NMMP labs about procedural details of amending data of audited samples prior to re-submission to the NMMP database. This should apply both to initial Pass samples and Fail samples (and there associated replicates) once remedial action has been completed. **A guidance note on this process has now been produced** (see Appendix 6.4)**.**

Eighteen labs participated in the OS exercise, submitting fifty-four samples for audit. The grading of the samples in Year 11 was improved on Years 8, 9, or 10 with only three samples failing to achieve acceptable standards. The percentage of samples achieving Pass level in Year 11 is 94%, the highest pass rate since Year 02 (see Section B, Table 17).

Status	Year .8	Year .9	Year .10	Year 11
Excellent	3	2	4	10
Good	17	23	28	29
Acceptable	15	8	11	11
Poor	1	2	3	0
Fail	9	9	5	3
Total	**45**	**44**	**51**	**54**

3.6 Flagging of data submitted to the NMMP database.

a) Benthos 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 6.5. Most of the data is derived from the year 2003 except one lab which submitted 2004 data. The data presented covers 58 numbered NMMP sites, although the NMMP Green Book (v.9, Dec.2005 – see www.sepa.org.uk) cites 76 sites for benthos analysis. However, 6 sites shown here (39, 255, 265, 275, 389, and 755) do not match sites in the Green Book. It is evident that some sites may have been renumbered (275 & 389 as 276 & 390) but the status of other sites still remains unclear. **Clarification of the current site status should be provided by the monitoring authorities and the Green Book to be updated. There is a need for the NMMP database to be able to track changes to site names or numbers.**

Of the Year 11 NMMP samples, two were originally graded as less then acceptable. To date remedial action has not been carried out on these samples and the sites and their associated replicates remain flagged. It is of concern that one of these sites also remains flagged from Year 10, and remedial action also remains outstanding for another 3 sites from Year 10.
It is imperative that all labs submitting data to the NMMP database complete the required remedial actions in order to validate their samples.

There has been some discussion about the attachment of flags to NMMP benthic samples. The chemistry AQC scheme applies a one out/all out flag based on post analysis AQC. This assumes that all the samples are similar and the principal source of error lies with the analysis. Hence if the AQC

analysis fails then it is probable that the actual analyses are also of unacceptable quality. However with macrobenthos the situation is different. Samples from different sites may vary quite significantly and these differences may have a major influence on the analytical error. Moreover the AQC process is applied directly on a selection of the NMMP samples. Hence, at present the data flagging and remedial action is applied on a sample/site basis and non-audited samples are deemed valid by default.

However, this procedure may raise anomalies especially as only 3 samples are selected for auditing per lab irrespective of how many sites the lab monitors. For example if one of the labs fails on all 3 audited samples and does not undertake remedial action then the audited sample sites remain flagged all 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.**

b) Particle Size data

Two PS exercises (PS24 & PS25) were distributed in Year 11. 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. 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 has been 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 has been no AQC flagging mechanism operating for sediment data or cross-referencing of sediment data and benthos data held on the NMMP database system. **With the planned introduction of the new MERMAN database in 2006, clarification is needed to ensure all the relevant PSA data is submitted and that an effective AQC flagging system is introduced as soon as possible.**

4. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

The membership of the committee is shown in Appendix 6.6.

The committee has supported a study aimed at producing a predictive model of benthic invertebrate communities based on the NMMP dataset. The investigation was funded by SNIFFER (Scotland and Northern Ireland Forum for Environmental Research) and carried out by IECS (Institute of Estuarine & Coastal Studies). The long awaited report has now been produced (Allen, 2004) and an outline summary of the project and the "MARINPACS" model is presented in Appendix 6.7.

The expanding role of the NMBAQC scheme commenced with a workshop on Fish and Epibenthos sampling held at the Millport marine lab in Scotland in November 2004. The workshop programme (see Appendix 6.8) attracted a whole new swathe of participants from the UK monitoring authorities (EA, SEPA, EHS, DARDNI) as well as from the Marine Institute of the Republic of Ireland, and a number of consultancies. As a follow-up, plans were set in motion for a ring test on identification of preserved marine and estuarine fish (including juvenile specimens) in Scheme year 12 (2005-06).

As in previous years committee members have been directly involved in the development of assessment tools for biological quality elements of the Water Framework Directive (WFD). This includes Task Teams working on both transitional water fish communities and marine invertebrates. Reports on phases 1& 2 of these projects were published in 2004 (Coates *et al.*2004, Prior *et al.*2004). These initiatives continued throughout 2005 and progress reports for phase 3 of the task teams are provided in Appendix 6.9. In September 2004, the Marine Invertebrate Task Team (MBITT) attended the WFD North East Atlantic Geographical Implementation Group (NEAGIG) workshop at the Kristineberg Research Station, Sweden, with the aim of intercalibrating the UK marine invertebrate assessment tool with comparable tools being developed for the WFD in other North-East Atlantic countries. The investigations of the MBITT have considerable relevance to the current benthic invertebrate focus of the NMBAQC scheme. The requirements of the WFD has resulted in the production of several related reports examining seabed indicator taxa (Hiscock *et al*., 2004), hard substratum communities (Hiscock *et al*.,2005) and lagoon communities (Milner, 2006).

The committee was represented at the ICES/OSPAR Steering Group on Quality Assurance of Biological Measurements in the Northeast Atlantic (SGQAE) held in Denmark in Feb. 2005 (see ICES 2005). A report on the operation of the BEQUALM/NMBAQC scheme was presented. It was noted that there are no participants outside the UK. A German institute participated in 2004 but encountered difficulties due to regional differences in fauna and their lab did not have the appropriate experience/literature to identify UK fauna. This highlights the difficulty in trying to operate an international ring test with little financial support or direction from the BEQUALM secretariat. SGQAE expressed concern over the promotion of the BEQUALM scheme at an international level and yet there is no support for the UK's NMBQAC group to enable it to extend to international laboratories. At present, labs in other Contracting Parties who are submitting data to OSPAR are not in BEQUALM and therefore it is not possible to assess their QA performance. This will affect the quality assurance of the data. SGQAE/SGQAB recommended that OSPAR/ICES highlight the lack of international participation in BEQUALM, and how that will affect an assessment of the QA of data for international assessments.

References

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ICES (2005). ICES/OSPAR Steering Group on Quality Assurance of Biological Measurements in the Northeast Atlantic, ICES headquarters 22-25 February 2005.
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Environment Agency R & D Technical Report E1-116, E1-132, pp.1-83, App. I-VII.

5. FINANCIAL SUMMARY 2004/2005

The administration of the financial component of the scheme continued to the carried out by the Environment Agency (National Marine Service, Peterborough) following transfer from SEPA at the commencement of Year 10 in April 2003.

Although the cost for participating in the full Scheme was kept at the same level as for 2003/2004, fees in 2004/2005 were restructured to provide consistency for those laboratories participating in only certain modules. Scheme participation costs were set as:

Full Scheme (membership and 5 modules)	£2690.00
Scheme membership and single module	£1395.00
Scheme membership and two modules	£1718.75
Scheme membership and three modules	£2042.50
Scheme membership and four modules	£2366.25
Information only	£795.00

(A 10% reduction was offered for laboratories new to the Scheme.)

The table below shows that income exceeded expenditure for Year 11. Of the Year 11 scheme income, 62% was from Government laboratories and 38% from external contractors. Annual scheme expenditure costs fluctuate considerably from year to year, as the number and level of participation of different labs varies. This makes budget forecasting, and hence fee setting, very difficult. Scheme fees need to be set to ensure that the scheme is self-funding and does not fall into deficit. In Year 9, the Scheme made a loss of -£8699.34, while in Year 10 there was a surplus of +£2281.54. In Year 11 the surplus had increased to +£12069.11 providing a good financial buffer for future expenditure.

The committee decided to freeze fees for as long as possible (Yr12 and Yr13 to date) and to use the excess financial income from Yr 11 to subsidise the production of a taxonomic literature database, taxonomic keys, additional ring tests and workshops for scheme participants.

The benthic scheme contract continues to be administered by Unicomarine on the basis of their experience, good management and reasonable cost having won the contract in a competitive tendering exercise at the end of 1997/98. The Contract is up for renewal at the end of Year 12 (2005/2006)

Financial Summary 2004/2005

	INCOME	***EXPENDITURE***
Core Scheme Components	*59845.00*	*47147.39*
Fish & Epifauna Workshop	*4650.00*	*5157.00*
Travel/Admin etc.		*121.50*
TOTAL	*64495.00*	*52425.89*
Initial Balance	*12069.11*	
Balance carried from 03/04	*8277.20*	
Balance at year-end, April 05	***£20,346.31***	

6. APPENDICES

Appendix 6.1 - 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 6.2 - NMBAQC Participants - Scheme Year 11 - 2004/2005

a) Laboratories

AstraZeneca Ltd., (Brixham Environmental Laboratory)

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

CMACS (Centre for Marine & Coastal Studies, Port Erin Marine Lab., Isle of Man)

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

Ecomaris Ltd. (Huntingdon, Cambridgeshire)

Environment Agency (North East, Newcastle)

Environment Agency (North West, Warrington)*

Environment Agency (Anglian, Lincoln)

Environment Agency (South East -Thames, Camberley)

Environment Agency (Southern, West Malling)

Environment Agency (South West, Blandford Forum)

Environment Agency (Wales – Cardiff)

Environment Agency (Wales – Llanelli)

Environment Agency (EMAP-Marine-Environmental Monitoring & Assessment Process)*

EHS (Environment & Heritage Service, Lisburn, Northern Ireland.)

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

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

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

Fugro Survey Ltd. (Environmental Division, Great Yarmouth)

Hebog Environmental (Gwynedd, Wales)

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

MES Ltd. (Marine Ecological Surveys Ltd., Bath)

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

Scottish Environment Protection Agency (North Area, Dingwall)

Scottish Environment Protection Agency (South East Area, Edinburgh/Aberdeen)

Scottish Environment Protection Agency (South West Area, Glasgow)

* Results for these labs not included in Section B report.

Appendix 6.2 Contd. - NMBAQC Participants - Scheme Year 11 -

b) Laboratory Participation Levels

Year 11 (2004/05) Labs.	MB	OS	PS	RT	LR
AstraZeneca, Brixham Environmental Lab	0	1	1	1	1
CEFAS - Burnham	1	1	1	1	1
CMACS (Port Erin Marine Lab.)	1	0	0	0	1
DARDNI - Belfast	1	1	1	1	1
Ecomaris Ltd.	0	1	0	0	0
EA NE - Newcastle	0	1	0	0	0
EA NW – Warrington*	0	1	0	1	
EA Anglian - Lincoln	0	1	0	0	0
EA SE Thames - Camberley	0	1	0	1	0
EA Southern - West Malling	0	1	0	1	0
EA SW - Blandford	0	1	0	1	0
EA Wales - Cardiff	0	1	0	1	0
EA Wales - Llanelli	0	0	1	0	0
EA EMAP-Marine – Peterborough*	1	1	0	1	1
EHS (Environment & Heritage Service)	1	1	1	1	1
Emu Ltd.	0	1	0	1	1
ERT (Scotland) Ltd.	1	1	1	1	1
Environmental Services (Inst. of Aquaculture)	0	0	0	1	1
Fugro Survey Ltd.	0	1	0	1	0
Hebog Environmental	1	1	1	1	1
IECS - University of Hull	0	1	1	1	1
Marine Ecological Surveys Ltd.	0	1	0	0	0
SAMS Research Services Ltd.	1	0	0	1	1
SEPA North Area, Dingwall	1	1	0	1	1
SEPA Southeast Area – Edinburgh/Aberdeen	1	1	1	1	1
SEPA Southwest Area - Glasgow	1	1	1	1	1
Totals.	11	22	10	20	15

MB – Macrobenthos exercise
OS – Own Sample exercise.
PS – Particle Size exercise.
RT – Ring Test exercise
LR – Laboratory Reference exercise.
* Results for these labs not included in Section B report.

c) Other Participating Organisations

Other organisations contribute funding to the scheme but only participate at a representation level for information exchange. These include:

English Nature (EN)
Scottish Natural Heritage (SNH)
Countryside Commission for Wales (CCW)
Joint Nature Conservation Committee (JNCC)
FRS / SEERAD (Fisheries Research Services, Scottish Executive Environment & Rural Affairs Department)

Appendix 6.3 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 6.3 (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 6.4 Guide to amending data for AQC'ed NMMP Benthos samples

Benthic invertebrate data for the UK NMMP programme is submitted annually by the relevant competent monitoring authority to the NMMP database (from Yr13 data will be submitted to MERMAN). Data for each calendar year is submitted by June of the following year. As NMBAQC results for "Own Samples" are generally not available at the time of the initial submission, amended data is subsequently resubmitted once the AQC process and any remedial action is completed.

1. Own Samples achieving overall "Pass" flag – (ie. Acceptable, Good, or Excellent)

Taxon Names – amend taxonomic errors
amend name changes or mis-spellings.

Taxon Numbers – amend miscounts.

Biomass – amend biomass data where taxa have been mis-identified in part, or misplaced in taxon vials with other taxa.

Biomass – do not amend other biomass data unless a "fail" flag has been applied to the estimation of biomass. If biomass error is related to 1 or 2 large taxa then only these need amended (assuming this brings revised biomass within target).

Specimens found in residue – amend taxon names, numbers, and biomass to include all fauna recovered from the re-sort.

No changes required to associated replicates.

2. Samples achieving overall "Fail" flag – (*i.e.* Poor or Bad)

Amend Own Sample data as shown in part 1, above. Undertake required remedial action on associated replicate samples from batch (*i.e.* same NMMP site/stratum for the same year). Inform NMBAQC contractor/contract manager of completion of remedial action.

Amend relevant data of associated replicate samples resulting from remedial action:

Taxon Names – amend taxonomic errors.
Taxon Numbers – amend miscounts.

Biomass – amend biomass data where taxa have been mis-identified in part, or misplaced in taxon vials with other taxa.

Biomass – do not amend other biomass data.

Specimens found in residue – amend taxon names, numbers, and biomass to include all fauna recovered from the remedial re-sorts.

Appendix 6.5 - NMMP Sample and Site Flagging - Year 11

Lab	Data Matrices Submitted	Own Samples Selected	Grade	Flag Status
	Year Site - Location			
A	2003_45 CMT5	RepE (OS26)	Excellent	Validated
	2003_55 CMT7	RepE (OS27)	Good	Validated
	2003_70 STN H Irvine Bay	-		deemed validated
	2003_76 L.Linnhe	RepE (OS28)	Acceptable	Validated
B	2003_175 Kingston Hudds	RepC (OS27)	Acceptable	Validated
	2003_208 Kincardine	RepC (OS28)	Acceptable	Validated
	2003_NMMP trial site Cromarty Firth	RepC (OS26)	Good	Validated
B1	2003_(255B) N. Sea	RepB (OS26)	Good	Validated
	2003_(39B) N. Sea	RepB (OS27)	Good	Validated
C	2003_210 Yarrow Slake	-		deemed validated
	2003_220 Budle Bay	RepC (OS26)	Fail	Flagged
	2003_225 Hebburn	-		deemed validated
	2003_235 Ferry Crossing	-		deemed validated
	2003_265 Alex. Bridge	-		deemed validated
	2003_270 Off Seaham	RepC (OS27)	Good	Validated
	2003_275 Sandy Point	-		deemed validated
	2003_305 Bamlett's Bight	-		deemed validated
	2003_315 No23 Buoy	RepC (OS28)	Fail	Flagged
	2003_325 Phillips Buoy	-		deemed validated
	2003_755 Seacombe Ferry	-		deemed validated
	2003_765 Ch. C1 Buoy	-		deemed validated
	2003_766 u/s 11 mile post	-		deemed validated
	2003_767 North Bay	-		deemed validated
	2003_768 St. Bees	-		deemed validated
D	2003_356 Inside Spurn	RepE (OS26)	Good	Validated
	2003_357 Grimsby Roads	-		deemed validated
	2003_358 Sunk Island	RepE (OS27)	Excellent	Validated
	2003_388 WW19 off Boston	RepE (OS28)	Good	Validated
E	2003_389 Cork Hole	RepC (OS26)	Good	Validated
E1	2003_390 Blackwater	Rep5 (OS26)	Acceptable	Validated
F	2003_435 Woolwich	Rep1 (OS26)	Good	Validated
	2003_455 Mucking	Rep1 (OS27)	Good	Validated
	2003_455 Mucking	Rep5 (OS28)	Good	Validated
G	2003_505 Dock Head	RepD (OS28)	Good	Validated
	2003_526 Burham	RepB (OS26)	Good	Validated
	2003_527 Sun Pier	RepB (OS27)	Good	Validated
H	2003_245 NSTF14	RepC (OS26)	Excellent	Validated
	2003_345 NSTF53	RepC (OS27)	Good	Validated
	2003_536 Lyme Bay	RepC (OS28)	Good	Validated

Appendix 6.5 Contd. - NMMP Sample and Site Flagging - Year 11

Lab	Data Matrices Submitted	Own Samples Selected	Grade	Flag Status
	Year Site - Location			
I	2003_555 Warren Point	-		deemed validated
	2003_565 Hamoaze	RepC (OS26)	Good	Validated
	2003_566 Upper South Deep	-		deemed validated
	2003_567 Wytch	RepE (OS27)	Excellent	Validated
	2003_576 Jennycliffe	RepA (OS28)	Good	Validated
J	2003_625 Purton	-		deemed validated
	2003_635 Bedwin	-		deemed validated
	2003_645 Peterstone	-		deemed validated
	2003_646 Cosheston Point	RepE (OS27)	Excellent	Validated
	2003_647 Ynys-hir	-		deemed validated
	2003_648 Bontddu	RepE (OS28)	Acceptable	Validated
	2003_690 Mostyn Bank	RepE (OS26)	Acceptable	Validated
K	2004_845 BL5	RepD (OS26)	Good	Validated
	2004_820 BR3	-		deemed validated
	2004_880 Kilderry	RepE (OS28)	Good	Validated
	2004_825 IS1	RepA (OS27)	Excellent	Validated
L	2003_806 NMP4	RepA (OS26)	Excellent	Validated
	2003_807 NMP5	-		deemed validated
	2003_808 Buoy(NMP6)	-		deemed validated
	2003_865 NC2(NMP2)	RepB (OS27)	Excellent	Validated
	2003_875 NC1(NMP1)	RepE (OS28)	Good	Validated

Appendix 6.6

NATIONAL MARINE BIOLOGICAL AQC COORDINATING COMMITTEE
Membership - Scheme Year 11 (2004/05)

Matt Service (Chair)	DARD(NI) - (Department of Agriculture & Rural Development (Northern Ireland), Agriculture, Food and Environmental Science Division.
Elaine Hamilton (Contract Manager - resigned Sept .04)	SEPA South East (Scottish Environment Protection Agency)
Myles O'Reilly (Contract Manager from Sept.04)	SEPA South West
Tim Mackie (Secretary)	EHS, DOENI (Environment & Heritage Service, Department of Environment, Northern Ireland)
Chris Ashcroft (Finance Manager) (Replaced by Alison Miles Sept. 04)	Environment Agency (National Marine Service)
Nigel Proctor*	IECS (Institute of Estuarine & Coastal Studies. University of Hull)
Mike Robertson (Replaced by Clare Greathead Sept.04)	FRS / SEERAD (Fisheries Research Services, Scottish Executive Environment & Rural Affairs Department)
Keith Cooper	CEFAS (Centre for Environment, Fisheries and Aquaculture Science)
Jon Davies** (Replaced by Jenny Hill, Jun.04)	JNCC (Joint Nature Conservation Committee, Peterborough)
Carol Milner (Replaced Elaine Hamilton Jan.05)	SEPA North Area, Dingwall

* Nominated representative for non-agency labs/independent consultancies.
**Represents the nature conservation agencies (JNCC, EN, SNH, CCW, EHSNI)

Appendix 6.7 – Summary of SNIFFER "MARINPACS" Report

DERIVATION OF NUMERICAL PREDICTIVE MODELS FROM THE NMP DATASET

Background

There is a growing need for the application of reference condition models for marine macro-invertebrate benthic communities which may used to assist the derivation of Ecological Quality Standards/Objectives. Such models would benefit existing monitoring and surveillance programmes of marine habitats and may also help fulfil the requirements of European legislation such as the Water Framework Directive.

Objectives and approach

This study utilised data from the UK National Monitoring Programme (NMP) from 1992 to 1995 and aimed to characterise the benthic invertebrate community structure at the NMP sampling stations. The results of the analyses were used to derive a number of numerical models of the benthos. The models then used environmental variables to predict species composition (similar to the RIVPACS model for river systems) and to predict biological parameters (such as number of species, abundance, and diversity). Analysis of the species/abundance dataset included the calculation at each site of biological parameters: number of species, total abundance, mean abundance per species, abundance evenness per species, faunal diversity, and a trophic index which classifies fauna into feeding groups.

Key findings

In general, coastal sites (intermediate/offshore areas) tended to show moderate to high numbers of species and diversity, whilst the majority of estuarine sites had lower diversities and the highest total abundances. Sites with an impoverished benthic fauna tended to be estuarine sites subject to strong tidal currents. Trophic index values were higher in the coastal sites indicating minimal anthropogenic impact, and lower in the estuarine sites suggesting some disturbance e.g. due to organic enrichment. Similarity analysis of the species/abundance data was used to define 10 site groups (communities) for the estuarine sites and 13 groups for the coastal sites. Analysis incorporating environmental data indicated that tidal current speed, silt content and depth were of primary importance for explaining species distribution in coastal sites, whilst salinity and silt content were the most important environmental factors for estuarine sites.

The species composition prediction models appeared to give moderately good results. The model for coastal data incorporated maximum tidal current speed, median particle size, silt content, depth, latitude and longitude and correctly predicted 76% of sites to their respective site groups (communities). A cross-validated model for which each site in turn is removed from the analysis correctly predicted 49%. The estuarine model utilised median particle size, silt content, depth, salinity, latitude and longitude and correctly predicted 76.5% of sites for the full model and 44.5% of sites for the cross-validated model. The lower predictive success of the cross-validated model was due in part to the small sample size of many of the groups. Validation and refinement of the models is ongoing with the sites currently validated showing between up to 89% of species occurrence correctly predicted and up to 100% of the top 70% most abundant species in the validation sites correctly predicted. The predictive ability of the model was limited by the relatively small dataset, the low number of environmental variables used in model construction, the lack of biological explanatory variables and the relatively limited range of benthic communities used in model development. Cases where the model failed to work well were those where the environmental parameters or the species assemblages in the validation sites had changed significantly from those initially used for the model development.

Appendix 6.7 – Contd. Summary of SNIFFER "MARINPACS" Report

The models produced to predict the biological parameters were based on linear regression techniques and showed significant correlation coefficient (R) values ranging from 0.43 to 0.85. The total proportion of variance explained by the models ranged from 19% to 72%. For validation purposes the predicted and observed values of the biological parameters from the regression models were compared and 95% confidence limits calculated for the predicted values. Whilst the majority of validation sites fell within expected ranges (i.e. had not changed significantly from predicted values) a number of sites had observed values outside the confidence limits indicating a departure from the reference condition.

The suite of modelling routines to accompany this report has been provided in Excel™ format. These routines are provided in a stand alone excel workbook (Excel™ 97 or XP compatible) called MARINPACS (MARine INvertebrate Prediction And Classification System). This system comprises two model types which run on a range of environmental parameters entered by the operator. The Invertebrate Prediction Models predict the species composition and the Biotic Index Models predict the biological parameters (number of species, total abundance, mean abundance, abundance evenness, faunal diversity, and trophic index value). Further work is required on the validation and development of these models ideally utilising larger data sets and a greater number environmental variables. It would also be useful to employ other modelling techniques.

KEY WORDS

Marine, coastal, estuarine, benthic, community, modelling, reference condition, Multiple Discriminant Analysis, cluster analysis, diversity, trophic status, MARINPACS

Appendix 6.8 - FISH & EPIBENTHOS WORKSHOP PROGRAMME

NMBAQC Scheme Fish & Epibenthos Workshop 15th-19th November 2004
University Marine Biological Station, Millport, Isle of Cumbrae, Scotland

Day	Session	Programme	Leader
Mon. 15th Nov 2004	pm	**15:00 Welcome** Workshop Aims and Objectives Survey Design and Gear Selection Allocation of groups for Field Activities	Steve Coates Steve Coates Steve Coates Tim Mackie
Tues. 16th Nov 2004	am	**Field Exercise** Otter trawls/beam trawls Implications of deck sorting of catch/ sub-sampling / volumetric comparison	Michael McAliskey
	pm	BEQUALM Fish Disease Principles of fish aging. Practical fish aging and dissection of liver and muscle Fish Identification	Steve Feist Willy McCurdy Willy McCurdy Willy McCurdy
		Includes Open Forum session	
Wed. 17th Nov 2004	am	**Water Framework Directive Requirements** Quality Assurance – draft QA protocol Standard Lists, Use of UNICORN database.	Steve Coates
	pm	**Epifaunal Analysis from trawl and video** Quantifying video ID, quantitative, visual fast count, SACFOR and other quantitative scales Sediment descriptors (Possible boat trip for epifauna by-catch sampling)	 James Strong James Strong James Strong
	evening	Workshop Dinner	-
Thur. 18th Nov 2004	am	Fyke netting , beach seining Equipment demonstrations – electronic fish measuring boards, scales Comparison of camera data vs trawl data	Steve Coates James Strong
	pm	Position Fixing Risk Assessments SOP review Data Analysis	Tbd
Fri. 19th Nov 2004	am	Wrap up Session Departure	Steve Coates Tim Mackie

Appendix 6.9 – Progress Reports on WFD Task teams

a) Transitional Waters Fish Task Team – Progress Report Jan.05

During 2004 the Project team has been involved with collating data from as many transitional sites as possible as part of classification tool development. This along with progression of the biannual monitoring strategy (as recommended within R&D Technical Report E1-131/TR) has included a series of new fisheries surveys within 33 transitional waters of England & Wales.

Data Evaluation: Continued progress is being made with populating the UNICORN V4 database with new and archive fisheries datasets. Data from England & Wales is now being transferred into the Environment Agency's BIOSYS database, with UK & Irish data remaining on UNICORN V4 as part of the UK-ROI Intercalibration process. The team now has over 150 'Transitional Fish' data sets from the UK & Ireland, which are currently being evaluated by the project team. Invaluable support was received from Dr Trevor Harrison (who developed the South African classification scheme), Julian Ellis of WRc and Plymouth Marine Laboratory.

Database Development: The team has been involved with the development of the transitional fish component of the Environment Agency's new biological database, BIOSYS, working closely with the BIOSYS development team, ensuring that the required functionality has been carried over from UNICORN V4. Recently, the team has been heavily involved with data migration testing, ensuring adequate QA of migrated data.

Current and Future Monitoring: A considerable amount of time has been spent establishing where the data gaps lie and with providing technical support for the EU WFD intercalibration exercise. Output from the Newcastle workshop has developed a provisional list of 'transitional types' that is to be surveyed using the multi-method biannual monitoring strategy.

Discussions with CEFAS and Sea Fisheries Committees (SFC) have been held to develop collaborative work within 'transitional waters' of England & Wales. Exploratory survey programmes are still to be agreed but it is hoped that joint workloads can be established further during 2005 in order to maximise both Agency.

Proposed Phase 4 Transitional Fish Task Team work Programme:

Period	***Activity***
Jan – Mar 2005	Analysis of collated datasets in order to test estuarine classification scheme. Support WFD Intercalibration process.
April 2005	Preparation of survey workloads within Intercalibration and Reference estuaries followed by bi-annual fieldwork.
May – July 2005	Monitoring within Intercalibration & Reference estuaries
August 2005	Analysis of collated datasets in order to test estuarine classification scheme
Sept – Nov 2005	Monitoring within Intercalibration & Reference estuaries
Dec 05 – Mar 06	Refinement of classification tools and classification scheme

R&D Report - as part of the Phase 3 deliverables a joint Transitional & Coastal (TraC) R&D Report is due to be published in April 2005. This will include all the biological quality element tool development for angiosperms, phytoplankton, macro-algae, benthic invertebrates and fish. This will also include all current fisheries development work to date, reference datasets, and refinement of the metrics and statistical analysis. It will also provide a series of case studies within the UK as part of the development of assessing ecological status.

Appendix 6.9 – Contd. - Progress Reports on WFD Task teams

b) Marine Benthic Invertebrate Task Team – Progress Report April 05

Classification Tool Development:

Assessment of Biological Quality Element: benthic invertebrate
Within a water body the assessment of the benthic invertebrate element could consist of the following parts (not all will necessarily be required for each water body)

- Soft substratum sample assessment (Multimetric developed)
- Hard substratum sample assessment (Developing under contract with MBA)
- Loss of habitat (spatial extent) (Link to Hydromorph. Project)
- Imposex (NMMP methodology)
- Alien taxa (Link to Alien Species Group)
- Megafauna ?????

Soft Substratum

(1) Coastal Waters

Work to date has focused on the subtidal, soft sediment habitats. A multimetric has been proposed to assess the status of a sample, this includes weighted metrics -AMBI, Simpsons, abundance, and no. of taxa. (It should be stressed that the multimetric is a sample assessment tool, not a water body assessment.)

The multimetric has been presented as an Excel workbook template in order to automate the calculations. Current ecological class boundaries are set using the Garroch Head (sewage sludge disposal site) pressure gradient dataset. These class boundaries are under review following a wider analysis of data and feedback from the Project Board.

The multimetric template was circulated to the Project Board members for testing with local datasets prior to the last Project Board (Edinburgh, Mar 05). Feedback to date has been incorporated but it is essential that the multimetric is trialed more widely to ensure that it meets the requirements of all the UK and Republic of Ireland (ROI) WFD Agencies.

(2) Transitional Waters

Sample assessment from transitional waters is being progressed along three lines:
higher salinity, subtidal transitional waters – transitional embayments
reduced salinity, subtidal transitional waters
reduced salinity, intertidal transitional waters

Focus is on the mud and muddy sand habitats. As for the coastal water tool, confidence in the proposed ecological status classes and ability to detect anthropogenic impact can only be achieved if suitable datasets are available on which to base assessments. Status assessments are being progressed for polyhaline (salinity 18 to 30) and mesohaline (salinity 5 to 18) transitional zones but we insufficient data available in the low salinity, oligohaline (salinity 0.5 to 5) zone to establish suitable assessment methods.

Initially the coastal multimetric is being used, recognising that the boundaries need to be shifted to take account of the more naturally stressed environment. Weighting of the individual metrics within the multimetric may also need to be altered in order to detect anthropogenic impact over natural stress.

Appendix 6.9 – Contd. - Progress Reports on WFD Task teams

Testing now needs to focus on data from (i) pressure gradients and (ii) dominant habitats.

(i) *Pressure Gradients*: Requests have gone out to all Project contacts to identify and provide further pressure gradient datasets. In particular, contacts have been asked to identify which are the main pressures acting on the benthic invertebrate communities in their water bodies. There is a need to ensure that the multimetric responds to these 'priority' pressures and to identify the confidence in detecting the impact of these pressures.

Specific Pressure Gradient being tested:

Dataset	***Pressure***	***Notes***
Garroch Head	Sewage Sludge disposal	Used to set initial class boundaries of subtidal status classes
Crouch Estuary	TBT	Salinity gradient
Cleveland Potash	Potash- smothering	Smothering pressure of particulates
Milford Haven – Sea Empress Spill	Total Hydrocarbon Concentrations	Coastal waters in and adjacent to Milford Haven
Loch Aline	Silica mine	
Fish Farm (numerous - SEPA)	Organics	Grab size only 0.015m2
Loch Leven	PAH	Grab size only 0.015m2
Enteromorpha - numerous	Nutrient Enrichment	Intertidal cores
Comprehensive Studies – HNDA - numerous	Sewage discharge	
Tees Estuary	Titanium Dioxide	
Liverpool Bay	Dredge disposal	

Suzanne Ware (CEFAS) is also looking to identify any aggregate extraction data that could be used (generally commercially confidential). A full list of the Pressures assessed will be documented in the R & D report.

(ii) *Habitats*: It will not be possible to establish tools/boundaries for every habitat type. The current multimetric has been established for coastal, sublittoral fine sands and muds (EUNIS type A4.2 and 4.3) as assessment of these stable depositional sediments provides the greatest potential for identifying anthropogenic impact on the benthic invertebrate community. They also represent the habitats for which the most comprehensive data is available.
Project board members have been asked to identify 'priority' habitats from their water bodies. This list will be used to target effort to decide which other habitats need class boundary testing.

*Habitats currently being assessed**:***

Type	***Habitat***	***EUNIS (old)***
CW	Sublittoral sands and muddy sands	A4.25
CW	Sublittoral muds	A4.31
TW	Polyhaline/Mesohaline – Sublittoral muddy sands	A4.26
TW	Polyhaline/Mesohaline – Sublittoral muds	A4.32
TW	Polyhaline/Mesohaline – Littoral sands and muddy sands	A2.21-2.25
TW	Polyhaline/Mesohaline – Littoral muds	A2.31-2.37

Data have also been identified for marine and transitional water lagoons, although this has not yet been worked up.

Actions for MTT representatives:
Ensure benthic task team representatives have resource (time) to:

- Identify priority habitats
- Identify priority pressures
- Test multimetric on range of data and report findings back to Project Board
- Provide pressure/habitat data to Project

Hard Substratum

The report of the scoping study and initial work on the development of a hard substratum classification has been drafted (MarLIN and MBA). The report has reviewed species that appear characteristic of unperturbed and perturbed situations on hard substratum. Assessment would be assisted by a 'Shore scoring system' that corresponds to the Macroalgal tool.
However, Hiscock *et al.*(2005) felt that there is an insufficient number of 'disturbance sensitive' or 'disturbance favoured' taxa to produce an equivalent of the AMBI index for hard substratum. The project team will meet with the contractors to review progress but it appears unlikely that a robust hard substratum classification tool will be ready by November 2005.

Loss of habitat (spatial extent)

The loss of habitat for benthic invertebrates, e.g. removal of intertidal mudflat, needs to be included in the water body assessment of the biological quality element. Closer links need to be set up with the Hydromorphology project to establish how this will be done.

Imposex

In Water Bodies where TBT pressure has been identified and, where target organisms exist, Imposex measurements will be incorporated. Methodology will follow that for NMMP.

Alien Species

MBITT is seeking further guidance from UK TAG and the Alien Species Group (ASG) with regard to assessment of the ecological status of a water body in terms of alien taxa.
In agreement with the alien taxa guidance it is suggested that if there are any alien taxa from the high-impact or unknown-impact list present, then status can not be High, despite the outcome of the classification metric. The ecological status would be downgraded to Good. However, if the current marine taxa on the Alien taxa list are not revised this could mean that in the marine environment, there will be no or very few water bodies at High status. An alien taxon would only drop the water body assessment from Good to Moderate if the functioning of the ecosystem is significantly altered.

Megafauna

No decision has been reached on how to include the presence/absence of megafauna (e.g. Sea Fans, Sea Pens). The issue will be discussed at the next Project Board. The difficulty will be in establishing (non-destructive).monitoring to incorporate this component.

Appendix 6.9 – Contd. - Progress Reports on WFD Task teams

Confidence/Risk of Misclassification

This work now has a high priority. For each habitat to be assessed, a risk of misclassification needs to be calculated. The Project will continue to work with Julian Ellis (WRc) in establishing the best method in assessing certainty.

B.) North East Atlantic Geographical Implementation Group(NEAGIG) Intercalibration

At the Bordeaux meeting, it was agreed that the UK would collate a range of sample data from Member States (MS) for NEA types 1 and 26. These data would be loaded to the MBITT UNICORN database and then data exported in a common matrix (to standardise taxa, sample size etc). This common matrix would then be circulated to all participants so that each MS could assign a status to each sample using their national assessment methods. Sample results could then be ranked for a first step 'intercalibration' of methods.
Agreement at the sample level is required as a first step. (Water body assessment requires a spatial assessment/monitoring design that has not been decided on yet).

Deadline for the submission of data was the end of March 2005. Julia Haythornthwaite (SEPA) and Graham Phillips (EA) have worked on processing the data for the week commencing the 4th April. They are now awaiting the results of some taxon name queries but hope to extract the common data matrix by mid April 2005.

Response to the call for data has been good. The number of samples submitted per Member State is: Germany 64, Belgium 137, Republic of Ireland 36, Spain (Basque Region) 45, Denmark 71, United Kingdom 135.
No data have been received yet from Norway, France, the Netherlands, or Portugal.

Due to the high number of samples submitted, the data will be extracted in two ways:

(i) '*Core'* matrix: this will be a reduced sample matrix that will include samples from a perceived range of ecological status' from different MS (pre- and post- data truncation).
(ii) '*Full*' matrix: all samples that have been submitted (pre- and post- truncation).

MSs will be asked to use their national assessment methods to give an ecological class status assessment of the 'core' matrix ('full' matrix if resource allows) and rank samples by the 3rd June 2005. MBITT will then collate and disseminate results to the participants by the end of June. This timescale will allow a second phase to be carried out prior to the next NEAGIG meeting in September 2005.

SECTION B - REPORT FROM THE CONTRACTOR

SCHEME OPERATION – YEAR 11 – 2004-05

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 eleventh year of operation of the National Marine Biological Analytical Quality Control (NMBAQC) Scheme.

The Scheme consisted of five components:

- Analysis of a single marine macrobenthic sample.
- Re-analysis by Unicomarine Ltd. of three own samples supplied by each of the participating laboratories.
- Analysis of two sediment samples for physical description.
- Identification of two sets of twenty-five animal specimens.
- 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 tenth 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. Overall agreement between the laboratories and Unicomarine Ltd. was generally poor with results markedly lower than those achieved in previous MB exercises. The samples posed problems associated with the identifications of the more abundant taxa. Extraction efficiency, irrespective of sorting, was on average 97%; however two 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 approximately 48.8% and 100% and was better than 90% in just 33% of comparisons and better than 95% in only 22% of comparisons.

The Scheme year nine protocols for 'blind' **Own Sample (OS)** audits were continued in this Scheme year. Laboratories were to submit full completed data matrices from their previous year's UK National Marine Monitoring Programme (UK NMMP 2003) samples or alternative sampling programmes (if not responsible for UK NMMP samples). The OS 'pass/fail' flagging system, introduced in Scheme year eight, was continued (See Appendix 2: Description of the Scheme standards for each component). The results for the Own Samples were much 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 87% of comparisons and better than 95% in 83% of all comparisons. The Bray-Curtis similarity index ranged from 71% to 100% with an average figure of 96%. The Bray-Curtis similarity index was greater than 95% in 74% of comparisons and in most cases (94%) 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. 'Pass/fail' criteria were applied based upon z-scores from the major derived statistics with an acceptable range of ±2 standard deviations (See Appendix 2: Description of the Scheme standards for each component). The influence of analytical technique on the results returned for the PS exercises was evident, as found in previous exercises. In most cases there was good agreement between laboratories. The first particle size exercise of the Scheme year (PS24) received nine data returns (including replicated data) that resulted in seven 'fail' flags and one 'deemed fail' flags (no statistic/data supplied). The second particle size exercise of the Scheme year (PS25) received seven data returns (including replicated data) that resulted in six 'fail flags' and two 'deemed fail' flags.

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' 'Decapoda' specimens. For the general set of fauna (RT24) 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 1.9 generic errors and 2.8 specific errors; this specific error figure is much lower than that (6.3) of the general ring test from the previous Scheme year. The majority of the generic errors can be attributed to three mollusc taxa. The 'targeted' ring test (RT25 – 'Decapoda') posed far fewer problems for species identification. On average each participating laboratory recorded 1.2 generic errors and 1.8 specific errors. Four specimens were responsible for the bulk of these errors (73% of all generic and 65% of 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., was 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 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 eleventh year of the Scheme (2004/05) followed the format of the tenth 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. Thirteen laboratories were government laboratories; eleven 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 of the Scheme.

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 can 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 2003 format for storage and analysis. In this and previous Scheme years slow or missing returns for exercises lead to delays in processing the data and resulted in difficulties with reporting and rapid feedback of results to laboratories. Reminders were distributed shortly before each exercise deadline.

2.1.3 Confidentiality

To preserve the confidentiality of participating laboratories, each are identified by a four-digit Laboratory Code. Each Scheme year eleven participant was given a confidential LabCode in July 2004, these codes were randomly assigned. These new codes are prefixed with the Scheme year to reduce the

possibility of obsolete codes being used inadvertently by laboratories, *e.g.* Laboratory number four in Scheme year eleven will be recorded as LB1104.

In the present report all references to Laboratory Codes are the post-July 2004 codes (Scheme year eleven).

2.2 Macrobenthic Samples (MB)

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

2.2.1 Preparation of the Samples

Sample MB12 was collected from the Medway Estuary; in an area of muddy substrate. A set of samples was collected using a 0.1m² Day Grab. Sampling was carried out while at anchor and samples for distribution were collected within a five hour period. All grabs taken were equal in size. Sieving was carried out on-board using a mesh of 0.5mm, followed by fixing in buffered formaldehyde solution. Samples were mixed after a week in the fixative. Prior to distribution to the participating laboratories the samples were washed over a 0.5mm sieve and transferred to 70% IMS (Industrial Methylated Spirits).

2.2.2 Analysis required

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

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

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.* 2003 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 examined the production of derived statistics from the particle size analysis of replicate sediment samples. Two samples of sediment, one coarse the other much finer, were distributed in 2004/05. Both samples were derived from natural sediments and prepared as described below. In each case a random subsample of the prepared replicates were divided for analysis using either laser diffraction or sieve analysis techniques to ensure sample replicate consistency and illustrate variations between these 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 (1 mm) to remove gravel, shell and large faunal content. Following sieving, the sediment for each PS circulation was well mixed in a large tray and allowed to settle for a week. Each sediment was sub-sampled by coring in pairs. One core of a pair was stored as the 'A' component, the other as the 'B'. To ensure sufficient weight for analysis, and to further reduce variation between distributed PS samples, this process was repeated three times for each sample replicate, *i.e.* each distributed sample was a composite of three cores.

The numbering of the replicate samples was random. All of the odd-numbered 'B' components (a total of 14) were sent for particle size analysis to assess the degree of inter-sample variation. Half the replicates were analysed using 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 conduct particle size analysis on the samples using their normal technique (either in-house or using a subcontractor) and to return basic statistics on the sample including %<63µm, mean, median, sorting and skewness. A written description of the sediment characteristics was to be recorded (pre-processing and post-processing using the Folk Triangle) along with an indication of any peroxide treatment. Also requested was a breakdown of the particle size distribution of the sediment, to be expressed as a weight of sediment in half-phi (ϕ) intervals. 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 2004/05. The first of the year's RT circulations (RT24) 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 molluscs, 28% were polychaete worms and 4% were echinoderms. The second circulation (RT 25) 'targeted' specimens of decapods and similar fauna. Details of substratum, salinity, depth and geographical location were provided for all ring test specimens to assist identification.

2.5.1 Preparation of the Samples

The specimens distributed were obtained from a range of surveys from around the UK. 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 (RT24) and the 'targeted' RT (RT25), 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 encourages laboratories to build extensive, verified reference collections to improve identification consistency. The creation and use of reference collections are viewed as best practice. The participants were required to submit a reference collection of twenty-five specimens for re-examination by Unicomarine Ltd. Labs are also permitted to use this exercise to verify identifications of taxa including difficult or problematic taxa about which they are unsure.

2.6.1 Selection of fauna

The different geographical distributions of species meant that a request for a uniform set of species from all laboratories was unlikely to be successful. Accordingly a list of instructions was distributed to participating laboratories (Appendix 1). The specimens were to broadly represent the faunal groups circulated in the general Ring Tests, *i.e.* mixed phyla. Each laboratory was invited to include, if they wished, five 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 2004/05 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 macrobenthic sample (MB12) was from an estuarine station in the Medway Estuary. The samples comprised approximately half a litre of mud with some vegetation taken from a depth of approximately five metres. The samples contained on average ten species and one hundred and sixteen individuals, covering a variety of phyla. The composite list from all samples was thirty species. Four out of the nine samples returned had been stained with Rose Bengal during sample processing. None of the laboratories subsampled their residues. Nine of the ten laboratories participating in this exercise returned samples and data. Detailed results have been reported to the participating laboratories (Hall, 2005), additional comments are added below.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB12, 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 considerable variation between laboratories in the percentage of taxa identified in the samples. Up to two taxa (and 25% of the total taxa in the sample) were either not extracted or not recognised within the picked material. On average Unicomarine Ltd. recorded one more taxon than the participating laboratories.

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

3.1.2.2 Number of Individuals

Re-sorting of the sample residues by Unicomarine Ltd. retrieved varied numbers of individuals from all samples except LB1107 and LB1116. These data are presented in columns 11 and 12 of Table 1. The number of individuals not extracted from the sample (column 11) is given as a percentage of the total number in the sample (including those missed) in column 12 (*i.e.* column 12 = column 11 / column 7 %). The proportion of missed individuals in 78% of the samples was less than 5% of the true total number in the sample. In the worst instance thirteen individuals, 13.5% of the total number of

individuals, were not extracted during the initial sample processing. The average number of missed individuals found upon re-sorting the residue was less than three. A breakdown of the missed individuals by taxonomic group is presented in Table 2.

3.1.2.3 *Uniformity of identification*

Most of the species in the distributed sample were identified correctly by the participating laboratories. One of the participating laboratories had no taxonomic differences (Table 1, column 15). In the worst instances three taxonomic differences were recorded. On average fewer than one and a half taxonomic differences were encountered per sample. The fauna commonly misidentified were *Corophium volutator*, cirratulids and oligochaetes.

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

The fauna list for each sample obtained by the participating laboratory was compared with the list obtained for the same sample following its re-examination by Unicomarine Ltd. The comparison was made by calculating the Bray-Curtis similarity index for the pair of samples using non-transformed data. The results of this calculation are presented in Table 1 (column 14). There was variation among laboratories in the values calculated for the index, from 48.8% to 100%, with an average value of 77.4%. The index for the majority of laboratories (6 of 9) was below 90% and five of the participating laboratories would have achieved 'fail' sample flags if the NMBAQC/UK NMMP standards were applied. The primary reason for these theoretical 'fail' flags is the misidentification of cirratulids. 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 MB12 circulation is presented in Table 3. Four laboratories did not supply biomass data or supplied data in an unsuitable format. The average difference between the two weight values was 2.2%, with the measurement made by Unicomarine Ltd. typically being less (*i.e.* lighter) than that made by the participating laboratory. There was great variation in biomass estimations between participating laboratories and between taxonomic groups. The range of overall biomass percentage difference results, between participating laboratories and Unicomarine Ltd., was from –5.3% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +13% (measurements by laboratory were greater than those made by Unicomarine Ltd.). The average difference between estimations varied greatly between faunal groups, ranging from –100% to +7.1% (from crustaceans to oligochaetes, respectively)

3.1.5 *Uniformity of samples*

The faunal content of the samples distributed as MB12 is shown in Table 4. Data received from the participating laboratories were fairly similar showing natural variation often encountered in subtidal estuarine samples.

3.2 Own Sample (OS)

3.2.1 *General comments*

Following the request to participating laboratories to submit data of suitable samples for re-analysis, fifty-four selected samples were received from eighteen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS26, OS27 and OS28 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 4 to 90, and the number of individuals from 3 to 2332. All eighteen laboratories participating in this exercise returned all three Own Samples; ten 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 thirty-eight samples (70% of all samples) the number of taxa recorded by the participating laboratories was identical to that obtained by Unicomarine Ltd. (column 4). In the sixteen exceptions, the difference was at most five taxa and the average difference was less than 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 44%. The average difference was 4.1% (fourteen samples exceeded this average). Twenty-two of the fifty-four samples received 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 eighteen samples contained taxa in the residue which were not previously extracted, the worst example being four new taxa found in the residue (column 10). In the worst instance residue was found to contain fifty-nine individuals. A breakdown of the missed individuals by taxonomic group is presented in Table 6. The average number of missed individuals found upon re-sorting the residue was eight, and the average number of missed taxa was less than one.

3.2.3 *Uniformity of identification*

Taxonomic differences between Unicomarine Ltd. and participating laboratories' results were found in twenty-one (39%) of the fifty-four samples received. An average of just over one taxonomic difference per laboratory were recorded; in the worst instance twelve 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 71% to 100%, with an average figure of 96%. Three samples from two different laboratories achieved a similarity figure of less than 85%. Eleven samples gave a similarity figure of 100%; these were submitted by nine different laboratories (LB1101, LB1102, LB1111, LB1112, LB1113, LB1114, LB1115, LB1117 and LB1123). The best overall results were achieved by laboratory LB1101, whose results comprised 99.70%, 100% and 98.92%. The worst overall results were achieved by laboratory LB1110, whose results comprised 82.37%, 98.44% and 71.38%. It should be noted that a small number of differences between samples can result in a large difference in the Bray-Curtis index. This difference does not necessarily reflect the laboratory's interpretative ability.

3.2.5 *Biomass determinations*

It was not possible to make an accurate comparison of the biomass determination in all cases; four laboratories did not supply biomass data; three samples were reported to either five or six decimal places; one laboratory provided biomass data to species but combined all fauna in one vial. Table 7 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. Thirty-nine of the fifty-four 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 +8.7% difference between the two sets of results (*i.e.* heavier than Unicomarine Ltd.), the range was from –24.8% to +56.2%. 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 +8.5% for polychaetes, +19.5% for oligochaetes, -13.1% for nemerteans, +4.5% for crustaceans, -10% for Chelicerata, +3.6% for echinoderms, -6.2% for molluscs and –11.3% for all remaining faunal groups. These figures are different to those produced by this same exercise in each of the previous years, this emphasises the variability caused by not only duration and method of drying but also the consistency of results within each major taxonomic group. The Unicomarine Ltd. biomass data was achieved using a non-pressure drying procedure as specified in the Green Book.

3.3 Particle Size Analysis (PS)

3.3.1 General comments

Most participating laboratories now provide data in the requested format, though some variations remain. As previously reported, it should be remembered that the results presented are for a more limited number of analytical laboratories than is immediately apparent since this component of the Scheme is often sub-contracted by participants to one of a limited number of specialist laboratories. For PS24, nine out of ten participating laboratories returned data (including laboratories with grouped results); one laboratory did not provide data. For PS25, seven out of the ten participating laboratories returned data; three laboratories did not provide data, one of which notified non-participation.

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 within analysis techniques from the sandy sediment circulated as PS24; the shape of the distribution curves was similar for the two analytical techniques and they were closely grouped with the sieve curves displaced half phi to the right of the laser curves. This sample had a low percentage of sediment in the fine fraction (average of 2.27% <63µm). The figures for %<63µm varied considerably between the two techniques with laser analysis producing an average figure of 1.19% and sieve and pipette producing approximately 2.8 times this figure (3.34%). Consequently, the derived statistic for median particle size (ϕ) were markedly different between the two techniques. The average median particle size from laser analyses was 1.64ϕ, compared with 2.12ϕ from sieve and pipette analyses. Similar differences were noted for mean, sorting and skewness statistics. Results for the individual *replicates* are provided in Table 8 and are displayed in Figure 1.

Sample PS25 was of a muddy sediment (average of 80.42% <63µm) and the cumulative distribution curves differed between the two techniques, particularly for the composition of silt/clay particles. The figures for % <63µm produced by two techniques were extremely similar; laser analysis produced an average of 80.20% and sieve and pipette produced 80.65%. The derived statistic for median particle size varied by just 0.61ϕ between the two techniques. No other statistical comparisons were possible due to the limitations of the pipette analysis with samples of this nature. 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 (see below) removed from the mean estimations of each of the major derived statistics.

It should be noted that one laboratory which normally sub-contract their particle size analysis to another laboratory (also participating), elected to utilise the results from this laboratory for PS24 and PS25; this laboratory's data are regarded as replicated data and are not included in the calculation of z-scores. This laboratory is indicated in Tables 10 and 11 by an asterisk against their LabCode. Accordingly the results from the sub-contracting laboratory have been used in the Figures and Tables as appropriate. In Figures 3, 4, 5 and 6 only data from the sub-contracting laboratory are displayed, although it also applies to the contracting laboratory. In Tables 10 and 11, which present the summary statistics for PS24 and PS25 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-fourth distribution – PS24*

There was generally good agreement for PS24 between the results from the analysis of *replicates* and those from the majority of participating laboratories. The results for a single laboratory (LB1117) 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). Only one participating laboratory (LB1116) used a sieve and pipette methodology; their cumulative curve followed that of the *replicate* data.

3.3.3.2 *Twenty-fifth distribution – PS25*

There was 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 variation in data received from the participating laboratories. The derived statistic for %silt/clay ranged from 66.45% to 81.56%, with the majority of laboratories producing figures slightly lower than the *replicate* analyses produced by Unicomarine Ltd.

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 laboratories 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 RT24 the species were from a variety of Phyla while for RT25 twenty-five specimens of 'Decapoda' 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 RT24 specimens and eighteen laboratories received RT25 specimens. For RT24, fourteen laboratories returned data; two laboratories specified non-participation for this exercise; two did not supply data or indicate non-participation. For RT25, thirteen laboratories returned data; three laboratories 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. Pectinaria auricoma* for *Amphictene auricoma*.
- Simple mis-spelling of a name*, e.g. Peresiella chymencides* for *Peresiella clymenoides*.

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 RT24 and RT25. 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 2003/04 as there was only a single 'standard' exercise (RT24). RT25 was targeted on 'Decapoda' fauna. 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 (RTB24 and RTB25), 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-fourth distribution – RT24*

Table 12 presents the results for the RT24. Nine of the twenty-five specimens circulated were crustaceans; eight were molluscs; seven were polychaetes; and one was an echinoderm specimen. The agreement at the generic level was relatively good; twenty-seven errors (from a potential three hundred and fifty) were recorded from the fourteen participating laboratories. Agreement at the specific level was also relatively good; thirty-nine errors were recorded. For over three quarters 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.

Approximately one third of the ring test comprised mollusc taxa and these caused problems for several laboratories; specifically *Ovatella myosotis* (medium immature specimens), *Nuculoma tenuis* (small juvenile specimens) and *Tragula fenestrata* (small juvenile specimens). The molluscs accounted for 59% of the generic and 41% of the specific differences recorded. Six of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Amphictene auricoma, Abra alba, Magelona alleni, Ampelisca brevicornis, Corbula gibba* and *Eusyllis blomstrandi*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB24 - Hall & Worsfold, 2004) which was circulated to each laboratory that supplied results for this exercise.

3.4.3.2 *Twenty-fifth distribution – RT25*

RT25 contained twenty-five 'Decapoda' specimens. Four of the specimens were donated by Sammy De Grave (Oxford University Museum of Natural History); he also verified the remaining specimens circulated. The results from the circulation are presented in Table 13 in the same manner as for the other circulations. The agreement at the generic level was very good; just fifteen errors (from a potential three hundred and twenty-five) were recorded from the thirteen participating laboratories. Agreement at the specific level was also very good; only twenty-three errors were recorded. Only a few of the taxa were responsible for the majority of differences and these are described briefly below.

The bulk of the errors recorded could be attributed to four specimens. *Palaemon macrodactylus, Pilumnus hirtellus* (juvenile specimen without appendages), *Thoralus cranchii* and *Gastrosaccus*

spinifera accounted for a total of 73% of all generic and 65% of all the specific differences recorded. The *Gastrosaccus spinifer* specimens were included to assess any 'presumed decapod' errors that may occur; two errors were recorded, both *Nyctiphanes couchi*, which is also not a decapod. Thirteen of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Pisidia longicornis, Pandalus borealis, Crangon allmanni, Galathea intermedia, Carcinus maenas, Palaemon elegans, Palaemon longirostris, Liocarcinus holsatus, Pontophilus norvegicus, Pandalus montagui, Philocheras trispinosus, Hippolyte varians* and *Pandalina brevirostris*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB25 – Hall & Worsfold, 2005) 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 RT24 and RT25 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 RT24 were of molluscs. Mollusc specimens (eight specimens in total) were responsible for 63% of generic differences and 44% of the total number of specific differences. Nine of the twenty-five specimens circulated were crustaceans and these produced 19% of the generic and 31% of the specific differences recorded. Polychaetes, despite only seven specimens being circulated, accounted for 15% of the total number of generic differences and 23% of specific differences. The single echinoderm specimen circulated produced 4% of the generic and 3% 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. This component assesses the ability of participating laboratories to identify material from their own area, or with which they are familiar. Of the fourteen laboratories participating in this exercise, twelve laboratories supplied specimens for verification; two 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 MB12 comprised a typical estuarine mud sample. The extraction of fauna from the sediment was relatively straightforward. The dominant taxa recorded in the majority of samples were *Streblospio shrubsolii* and *Tharyx* Type A. Two of the participating laboratories extracted all the countable material from the residue, however generally few individuals were not extracted from the residues. Identification caused various problems for the majority of laboratories, only one laboratory (LB1116) correctly identified all their extracted fauna. Some taxonomic mistakes were noted particularly *Tharyx* Type A and *Corophium voluator*. Six of the nine returning laboratories attained a Bray-Curtis similarity index less than 90%. The highest Bray-Curtis similarity index achieved was 100% (LB1116). The average Bray-Curtis figure of 77% is somewhat poor for these typical estuarine

samples. It represents the lowest figure for the MB component, to date; the average for MB11 (an artificial sample) was 93%, MB10 was 88%, MB09 was 93%, MB08 was 95%, MB07 was 88%, MB06 was 91%, MB05 was 85% and MB04 was 82%.

Table 4 shows the variation, by major Phyla, between those samples circulated for the macrobenthic exercise (MB12). The area sampled was relatively uniformed in its faunal composition. The samples were typical of the area and showed some natural variation. All samples were of relatively equal volume and sediment characteristics.

The 'blot-drying' procedure employed by Unicomarine Ltd. for the determination of biomass was as specified in the Green Book, *i.e.* avoiding excessive pressure when blotting specimens dry. However, there remains a considerable variation between the estimates of total biomass made by the participating laboratories and Unicomarine Ltd. Five laboratories provided biomass data; three provided data that was lighter in total than Unicomarine Ltd.; two supplied data that was heavier than Unicomarine Ltd. estimations. The extremes recorded were 5.3% lighter (LB1117) and 13% heavier (LB1116) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories and Unicomarine Ltd. was 2.2% (*i.e.* laboratory measurements were heavier 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 –3.1% (MB11). It seems likely that the main reasons for the observed differences between the measurements are more thorough, or less consistent, drying by participating laboratories prior to weighing. A similar observation was made in previous years of the Scheme. The average percentage difference between Unicomarine Ltd. and participating laboratories biomass figures for MB11 was -3.1%, MB10 was -13.3%, MB09 was –14.6%, MB08 it was +4.9%, MB07 it was –1.67%, MB06 it was +26%, MB05 it was +32% and for MB04 it was +20%. There are likely to be several reasons for the differences between years, though the nature of the fauna in the distributed samples is likely to of particular importance.

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

4.2 Own Sample Analyses

Considering just the Bray-Curtis index, as a measure of similarity between the results obtained by the participating laboratories and those obtained from re-analysis, participating laboratories performed much better in the OS exercises and the MB12 exercise. The average value of the index was 96% for the OS, compared with 77% for MB12. This is probably due to the lack of familiarity with the samples circulated for MB12; several participants do not routinely process estuarine samples. In previous years the most apparent difference between these exercises was the far better extraction of individuals and taxa from the residue in the Own Samples, however this year due to the nature MB12 the OS results are only slightly better. The marked difference between the average Bray-Curtis similarity figures for OS and MB components this year is primarily due to more significant taxonomic errors recorded in the MB samples.

There were fifty-four samples submitted for this component. This was facilitated by the distribution of timely reminders. Approximately 94% of fifty-four samples received exceeded the 90% Bray-Curtis pass mark and approximately 74% of the samples exceeded 95% Bray-Curtis similarity. The average Bray-Curtis similarity index achieved was 96%. These figures show an improvement upon the good results from previous OS exercises. In the 2003/04 Scheme year ten (OS 23, 24 and 25) the average Bray-Curtis figure was 94%, and 80% (of the fifty-one samples received) achieved more than 90% Bray-Curtis results. In the 2002/03 Scheme year nine (OS 20, 21 and 22) the average Bray-Curtis figure was 92%, and 75% (of the forty-four samples received) achieved more than 90% Bray-Curtis results. In the 2001/02 Scheme year eight (OS 17, 18 and 19) the average Bray-Curtis figure was 90.5% and 78%

(of the forty-five samples received) achieved more than 90% Bray-Curtis results. In the 2000/01 Scheme year seven (OS 14, 15 and 16) the average Bray-Curtis figure was 90.8% and 67% (of the forty-five samples received) achieved more than 90% Bray-Curtis results. In the 1999/2000 Scheme year six (OS 11, 12 and 13) the average Bray-Curtis figure was 91.4% and 73% (of the fifty-one samples received) achieved more than 90% Bray-Curtis results. In the 1998/99 Scheme year five (OS 08, 09 and 10) the average Bray-Curtis figure was 89.3% and 71% (of the forty-two samples received) achieved more than 90%. In the 1997/98 Scheme year four (OS 05, 06 and 07) the average Bray-Curtis figure was 93.6% and 83% (of the forty samples received) achieved more than 90%.

Since the beginning of the OS component four hundred and twenty-three samples have been received (OS01-28). The average Bray-Curtis similarity figure is 92.45%. Ninety-one samples have fallen below the 90% pass mark (22%). Forty-seven samples have achieved a similarity figure of 100% (11% 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.

Some instances of repeated taxonomic errors in Own Samples from previous Scheme years have been noted. Taxonomic errors should be investigated by participating laboratories even if the 'whole sample' has achieved a 'pass' flag. If a participating laboratory disagrees with any recorded taxonomic errors they should contact Unicomarine Ltd for further information (as they are invited to do so upon receipt of their Own Sample Interim Report).

4.3 Particle Size Analyses

The difference between the two main techniques employed for analysis of the samples (laser and sieve) was again evident in the results from the analysis of the replicates samples. The sample distributed as PS24 appeared from an analysis of *replicates* (Figure 1) to be very uniform and the results from participating laboratories (Figure 3) were relatively closely grouped. Figure 5 shows the z-scores for each of the major statistics supplied by the participating laboratories. Data received from LB1109 indicated much higher proportions of silt/clay than the other data returns for PS24 and LB1117 recorded a much larger coarse sand fraction hence these two sets of results are displaced in the cumulative curve figure (Figure 3).

There was a significant amount of scatter in the results for PS25 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 lower silt-clay fraction compared to the *replicate* sample data produced prior to the exercise. In last year's mud circulation (PS23) 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 PS24 and PS25 samples prior to analysis. The results varied considerable and some were extremely descriptive (Table 16, final column). Participating laboratories were also instructed to describe the sediment using the Folk triangle after analysis. Data were provided by six laboratories for PS24 and five laboratories for PS25. Half of the laboratories (3) described PS24, using the Folk triangle, as 'sand'; one recorded 'fine sand'; one recorded 'medium sand'; and one described 'light brown very slightly muddy mixed sand'. All the laboratories (5) providing sediment descriptions described PS25, using the Folk triangle, as 'sandy mud'; although one laboratory recorded 'slightly gravely sandy mud'. All PS samples are pre-sieved at either 1 or 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 participating laboratories used laser analysis. However, as demonstrated in these and previous PS exercises, 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. RT24 identified discrepancies with literature used by some participating laboratories for their identification of the *Magelona johnstoni* specimens. RT25 identified discrepancies with literature used by some participating laboratories for their identification of the *Palaemon macrodactylus, Crangon allmanni* and *Philochera trispinosus* specimens, the latter two specimens highlighted inconsistencies with nomenclature. All participating laboratories have been made aware of this via the ring test bulletins (RTB24 & RTB25).

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 1.4, and in half of the returns (6 of 12) 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 four differences in identification (8 of 12 laboratories). The average number of specific differences was 3.5. 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 96% of the comparisons were considered to have passed the enumeration of taxa standard; 89% exceeded the enumeration of individuals standard and 94% 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); three of the fifty-four samples are flagged as 'Fail'; eleven are flagged as 'Acceptable'; twenty-nine are flagged as 'Good'; and eleven 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 77% 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 Scheme year nine, (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 PS24 exercise. One participating laboratory did not submit all five requested statistics; these statistics have been flagged as 'Deemed Fail'. One laboratory (LB1109), which submitted data for %<63µm, failed to meet the standard for this statistic; two laboratories (LB1104 and LB1115) failed to meet the standard for median (ϕ); all participating laboratories passed the standard for mean (ϕ); three laboratories (LB1109, LB1116 and LB1117) failed to meet the standard for sorting; one laboratory (LB1109) failed to meet the standard for IGS(Ski). Four of the participating laboratories passed all standards. The lower section of Table 16 shows the results for the PS25 exercise. One participating laboratory did not submit all five requested statistics; these statistics have been flagged as 'Deemed Fail'. One laboratory (LB1107), which submitted data for %<63µm, failed to meet the standard for this statistic; one laboratory (LB1107) failed to meet the standard for median (ϕ); one laboratory (LB1107) failed to meet the standard for mean (ϕ); all participating laboratories passed the standard for sorting; three laboratories (LB1104, LB1107 and LB1115) failed to meet the standard for IGS(Ski). Four laboratories passed all standards.

5.2 Statement of Performance

Each participating laboratory has received a 'Statement of Performance', which includes a summary of results for each of the Schemes 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 ten years based upon the current NMBAQC Scheme standards (See Appendix 2: Description of the Scheme standards for each component). This year's fifty-four Own Samples resulted in the second highest percentage pass rate, 94% (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 ten 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 with an overall increase in data quality, *i.e.* fewer failing samples and a higher average Bray-Curtis similarity score. Monitoring the situation over a longer period is required before a firm statement about changes in laboratory standards could be made. However, the introduction of 'blind' audits in Scheme year eight have not caused an increase in the number of failures, as initially expected.

5.4 Remedial Action

It is imperative that failing UK NMMP samples, audited through the Own Sample exercise, are addressed. Remedial action should be conducted upon the remaining UK NMMP station replicates to emend and validate the flagged data. The revised NMBAQC Scheme OS standards, introduced in Scheme year eight, give clear guidance 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 a Bray-Curtis similarity index of <90% Three samples 'failed' in this Scheme year (including two 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 monitored by the NMBAQC committee. The participating laboratories are expected to initiate remedial action and notify the NMBAQC Scheme Contract Manager when this has been completed. Any remedial action undertaken should be audited externally where required. The NMBAQC committee will provide clarification on specific details of remedial action or consider appeals relating to the remedial action process. For Year 11, remedial action, outlined below, was required for associated replicates of the following Own Samples:

NMMP samples

LB1110 OS26- Review *Fabricia stellaris / Manayunkia aestuarina* identifications;
Resort residue for remaining replicates and re-audit.

LB1110 OS28- Review *Tubificoides* cf. *galiciensis* identifications.

Non-NMMP samples

LB1120 OS28- Review policy for recording *in-situ* records;
Review identification of live verses dead *Hydrobia ulvae.*

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 RT24 and RT25 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 uses 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 – LB1101

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – Eight generic and ten specific differences. Number of AQC identifications in High group.
RT25 – Six generic and six specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Count variance of four individuals. Bray-Curtis similarity index of 99.7%. Biomass on average 5.05% heavier than Aquatic Environments.
OS27 – NMBAQCS sample flag – 'Excellent'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 9.88% heavier than Aquatic Environments.
OS28 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Count variance of six individuals. Bray-Curtis similarity index of 98.9%. Biomass on average 4.82% heavier than Aquatic Environments.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1102

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – No data received.
RT25 – No data received.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Acceptable'.
One taxonomic difference (*Ophelia rathkei*). Twenty-one individuals not picked from the residue, including three previously unpicked taxa. Count variance of two individuals. Bray-Curtis similarity index of 92.75%. Biomass on average 15.77% heavier than Unicomarine Ltd.

OS27 – NMBAQCS sample flag – 'Excellent'.
All individuals picked from the residue. Bray-Curtis similarity index of 100%. Biomass on average 12.15% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Acceptable'.
Fifty-three individuals not picked from the residue, including thirty-seven *Hydrobia ulvae*. Count variance of sixteen individuals. Bray-Curtis similarity index of 91.96%. Biomass on average 16.01% heavier than Unicomarine Ltd.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1103

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – Two generic and two specific differences. Number of AQC identifications in Mid group.
RT25 – All specimens correctly identified. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Acceptable'.
Two taxonomic differences (*Abra prismatica* and *Thysanocardia procera*). Three individuals not picked from the residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 94.74%. No biomass data supplied.
OS27 – NMBAQCS sample flag – 'Good'.
One taxonomic difference (*Pariambus typicus*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 95.89%. No biomass data supplied.
OS28 – NMBAQCS sample flag – 'Good'.
One individual not picked from the residue, this was a previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 96.43%. No biomass data supplied.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1104

Macrobenthos (Training Component)

MB12 – Estuarine sample. One taxonomic difference (*Tharyx* sp.A). Two individuals not picked from the residue, including one previously unpicked taxon. Count variance of two individuals. Bray-Curtis similarity index of 91.84%. Biomass on average 1.89% lighter than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT24 – One generic and two specific differences. Number of AQC identifications in Mid group.
RT25 – One generic and one specific difference. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – Three generic and three specific differences.

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

OS26 – NMBAQCS sample flag – 'Good'.
Six taxonomic differences (*Exogone naidina, Polydora quadrilobata, Heteromastus filiformis, Ampharete lindstroemi* and *Thracia villosiuscula*). Twenty-nine individuals not picked from the residue, including four previously unpicked taxa. Count variance of twenty individuals. Bray-Curtis similarity index of 98.82%. Biomass on average 4.32% heavier than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Acceptable'.
Twelve taxonomic differences (*Acanthocythereis dunelmensis, Chamelea striatula, Thracia* sp. juv., *Abyssoninoe hibernica, Jordaniella nivosa, Anaitides longipes, Pseudotanais forcipatus, Tanaopsis graciloides, Corbula gibba, Rhodine* sp. and *Dosinia* sp. juv.). Three individuals not picked from the residue, including one previously unpicked taxon. Count variance of nine individuals. Bray-Curtis similarity index of 91.48%. Biomass on average 2.65% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Acceptable'.
Six taxonomic differences (*Nucula nucleus, Aphaelochaeta marioni, Thracia* sp. juv., *Eulalia viridis,Cirriformia* sp. juv. and *Tapes* sp. juv.). Thirty-six individuals not picked from the residue, including two previously unpicked taxa. Count variance of two individuals. Bray-Curtis similarity index of 90.48%. Biomass on average 1.73% heavier than Unicomarine Ltd.

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

PS24 – NMBAQCS standard for median failed. All remaining NMBAQCS standards passed.
Data from centralised analysis; laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'sand' prior to analysis; described as 'sand' using the Folk triangle.
PS25 – NMBAQCS standard for IGS (SKi) failed. All remaining NMBAQCS standards passed.
Data from centralised analysis; laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed data for silt component above 8phi provided. The lack of data above 8phi would have caused the IGS(SKi) standard failure. Sediment described as 'mud' prior to analysis; described as 'sandy mud' using the Folk triangle.

Laboratory – LB1105

Macrobenthos (Training Component)

MB12 - Not participating in this component.

Ring Test (Training Component)

RT24 – One generic and two specific differences. Number of AQC identifications in Mid group.
RT25 – One generic and one specific difference. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 - Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Good'.
Fifty individuals not picked from the residue. Count variance of four individuals. Bray-Curtis similarity index of 98.48%. Biomass on average 51.12% heavier than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Good'.
Thirty-four individuals not picked from the residue, including two previously unpicked taxa. Count variance of thirty-seven individuals. Bray-Curtis similarity index of 96.15%. Biomass on average 26.67% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Count variance of sixty-one individuals. Bray-Curtis similarity index of 98.6%. Biomass on average 0.88% lighter than Aquatic Environments.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1106

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – No data received.
RT25 – No data received.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Good'.
Twelve individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 98.62%. Biomass on average 16.8% heavier than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Good'.
Five individuals not picked from residue. Count variance of two individuals. Bray-Curtis similarity index of 98.78%. Biomass on average 28% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Good'.
All individuals extracted from residue. Count variance of six individuals. Bray-Curtis similarity index of 98%. Biomass on average 32.58% heavier than Unicomarine Ltd.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1107

Macrobenthos (Training Component)

MB12 – Estuarine sample. One taxonomic difference (*Corophium volutator*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 59.83%. No biomass data supplied. Residue/fauna stained. Laboratory policy stated as not recording nematodes, bryozoans, hydroids and copepods.

Ring Test (Training Component)

RT24 – Two generic and three specific differences. Number of AQC identifications in Mid group.
RT25 – One generic and two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – Two generic and five specific differences.

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

OS26 – NMBAQCS sample flag – 'Good'.
Two taxonomic differences (*Caprella linearis* and *Thyasira flexuosa*). Four individuals not picked from residue. Count variance of four individuals. Bray-Curtis similarity index of 98.21%. No biomass data supplied.
OS27 – NMBAQCS sample flag – 'Good'.
One taxonomic difference (*Ophiura albida*). Three individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 96.45%. No biomass data supplied.
OS28 – NMBAQCS sample flag – 'Acceptable'.
Five taxonomic differences (*Golfingia vulgaris, Pholoe inornata, Euclymene* sp. and *Nucula nucleus*). Ten individuals not picked from residue. Count variance of two. Bray-Curtis similarity index of 90.77%. No biomass data supplied.

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

PS24 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. No sediment description data received.
PS25 – NMBAQCS standards for %silt/clay, median, mean and IGS (SKi) failed. NMBAQCS standard for sorting passed.
Laser diffraction analysis conducted. Size distribution curve clearly displaced to the left of the majority of curves from 3.5 to 7.5phi. This could be the result of incomplete disaggregation of silt clay material. No sediment description data received.

Laboratory – LB1108

Macrobenthos (Training Component)

MB12 - Estuarine sample. One taxonomic difference (*Tharyx* sp.A). Three individuals not picked from the residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 86.28%. No biomass data supplied. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups except aquatic insects.

Ring Test (Training Component)

RT24 – Four generic and five specific differences. Number of AQC identifications in High group.
RT25 – Four generic and six specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR09 – Two generic and five specific differences.

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

OS26 – Not participating in this component.
OS27 – Not participating in this component.
OS28 – Not participating in this component.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1109

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – One generic and four specific differences. Number of AQC identifications in High group.
RT25 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR09 – Three specific differences.

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

OS26 – NMBAQCS sample flag – 'Good'.
Fifty-nine individuals not picked from the residue. Count variance of forty individuals. Bray-Curtis similarity index of 98.49%. Biomass supplied to five decimal places instead of four. Biomass on average 24.83% lighter than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Good'.

One taxonomic difference (*Amphictene auricoma*). One individual not picked from the residue. Bray-Curtis similarity index of 97.73%. Biomass supplied to five decimal places instead of four. Biomass on average 5.1% lighter than Unicomarine Ltd.

OS28 – NMBAQCS sample flag – 'Good'.

All individuals extracted from residue. Count variance of one individual. Bray-Curtis similarity index of 99.44%. Biomass supplied to five decimal places instead of four. Biomass on average 12.18% lighter than Unicomarine Ltd.

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

PS24 – NMBAQCS standards for %silt/clay, sorting and IGS (SKi) failed. Median and mean NMBAQCS standards passed.

Laser diffraction analysis conducted. Size distribution curve displaced below the majority of curves from 4 to 8phi, indicating a larger silt/clay component. Sediment described as 'sand' prior to analysis; described as 'fine sand' using the Folk triangle.

PS25 – Not participating in this exercise.

Laboratory – LB1110

Macrobenthos (Training Component)

MB12 - Not participating in this component.

Ring Test (Training Component)

RT24 – Not participating in this component.

RT25 – Not participating in this component.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Fail'.

One taxonomic difference (*Manayunkia aestuarina*). Thirty-seven individuals not picked from the residue, including two new taxa. Count variance of twelve individuals. Bray-Curtis similarity index of 82.37%. Biomass on average 23.92% heavier than Unicomarine Ltd.

OS27 – NMBAQCS sample flag – 'Good'.

One taxonomic difference (*Aphrodita aculeate* juv.). All individuals extracted from residue. Count variance of six individuals. Bray-Curtis similarity index of 98.44%. Biomass on average 56.21% heavier than Unicomarine Ltd.

OS28 – NMBAQCS sample flag – 'Fail'.

One taxonomic difference (*Tubificoides* cf. *galiciensis*). No >1mm residue fraction supplied for re-analysis. Thirteen individuals not picked from the 0.5-1mm residue fraction, including one previously unpicked taxon. Count variance of four individuals. Bray-Curtis similarity index of 71.38%. Biomass on average 35.42% heavier than Unicomarine Ltd.

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

PS24 – Not participating in this component.

PS25 – Not participating in this component.

Laboratory – LB1111

Macrobenthos (Training Component)

MB12 - Estuarine sample. One taxonomic difference (*Capitella* sp.). One individual not picked from the residue. Count variance of three individuals. Bray-Curtis similarity index of 96.97%. No biomass data supplied. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups except copepods and aquatic insects.

Ring Test (Training Component)

RT24 – One specific difference. Number of AQC identifications in Low group.
RT25 – All specimens correctly identified. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR09 – One generic and six specific differences.

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

OS26 – NMBAQCS sample flag – 'Good'.
One individual not picked from the residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 98.04%. No biomass data supplied.
OS27 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS28 – NMBAQCS sample flag – 'Excellent'.
Some data altered prior to audit submission. All individuals extracted from residue. Bray-Curtis similarity index of 100%. No biomass data supplied.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1112

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – One specific difference. Number of AQC identifications in Low group.
RT25 – All specimens correctly identified. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LB09 – One specific difference.

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

OS26 – NMBAQCS sample flag – 'Good'.
Two individuals not picked from residue. Count variance of six individuals. Bray-Curtis similarity index of 99.45%. Biomass on average 5.11% lighter than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Good'.
One taxonomic difference (*Pseudocuma longicornis*). One individual not picked from residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 95.08%. Biomass on average 17.01% lighter than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 1.92% lighter than Unicomarine Ltd.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1113

Macrobenthos (Training Component)

MB12 – No data received.

Ring Test (Training Component)

RT24 – No data received.
RT25 – No data received.

Laboratory Reference (Training Component)

LR09 – No data received.

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

OS26 – NMBAQCS sample flag – 'Excellent'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 4.44% heavier than Aquatic Environments.
OS27 – NMBAQCS sample flag – 'Excellent'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 4.86% lighter than Aquatic Environments.
OS28 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Count variance of two individuals. Bray-Curtis similarity index of 96.3%. Biomass on average 20.61% lighter than Aquatic Environments.

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

PS24 – No data received. All NMBAQCS standards deemed failed.
PS25 – No data received. All NMBAQCS standards deemed failed.

Laboratory – LB1114

Macrobenthos (Training Component)

MB12 – Estuarine sample. One taxonomic difference (*Tharyx* sp.A). One individual not picked from the residue. Bray-Curtis similarity index of 84.34%. Biomass on average 2.32% lighter than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT24 – Exercise used for in-house training.
RT25 – Exercise used for in-house training.

Laboratory Reference (Training Component)

LR09 – Four specific differences.

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

OS26 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
One taxonomic difference (?*Minuspio cirrifera*). One individual not picked from the residue. Count variance of eleven individuals. Bray-Curtis similarity index of 99.5%. Biomass on average 4.38% heavier than Aquatic Environments.
OS27 – NMBAQCS sample flag – 'Excellent'. External audit conducted by Aquatic Environments.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 4.64% heavier than Aquatic Environments.
OS28 – NMBAQCS sample flag – 'Good'. External audit conducted by Aquatic Environments.
One taxonomic difference (*Tubificoides amplivasatus*). All individuals extracted from residue. Count variance of nine individuals. Bray-Curtis similarity index of 97.3%. Biomass on average 5.49% heavier than Aquatic Environments.

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

PS24 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'muddy sand' prior to analysis; described as 'sand' using the Folk triangle.

PS25 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'sandy mud' prior to analysis; described as 'sandy mud' using the Folk triangle.

Laboratory – LB1115

Macrobenthos (Training Component)

MB12 – Estuarine sample. Three taxonomic differences (*Nephtys hombergii* and *Tharyx* sp.A). One individual not picked from the residue, this was a previously unpicked taxon. Count variance of two individuals. Bray-Curtis similarity index of 68%. Biomass on average 7.31% heavier than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT24 – One generic and one specific difference. Number of AQC identifications in Low group.
RT25 – One generic and two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – Two generic and four specific differences.

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

OS26 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 3.87% lighter than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Good'.
One taxonomic difference (*Mysella bidentata*). Twenty-one individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 96.42%. Biomass on average 9.12% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Acceptable'.
Three individuals not picked from residue, including two previously unpicked taxa. Bray-Curtis similarity index of 94.55%. Biomass on average 0.82% heavier than Unicomarine Ltd.

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

PS24 – NMBAQCS standard for median failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'sand' prior to analysis; described as 'sand' using the Folk triangle.
PS25 – NMBAQCS standard for IGS(SKi) failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed data for silt component above 8phi provided. The lack of data above 8phi would have caused the IGS(SKi) standard failure. Sediment described as 'mud' prior to analysis; described as 'sandy mud' using the Folk triangle.

Laboratory – LB1116

Macrobenthos (Training Component)

MB12 – Estuarine sample. No taxonomic differences. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 12.99% heavier than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy statement (MB sample detail form) not received.

Ring Test (Training Component)

RT24 – One generic and one specific difference. Number of AQC identifications in Low group.
RT25 – One specific difference. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – No specimens received.

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

OS26 – Not participating in this exercise.
OS27 – Not participating in this exercise.
OS28 – Not participating in this exercise.

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

PS24 – NMBAQCS standard for sorting failed. All remaining NMBAQCS standards passed.
Sieve and pipette analysis conducted. No major differences in size distribution curve compared to the sieve and pipette *replicate* data curve. Sediment described as 'muddy sand' prior to analysis; no Folk triangle sediment description data received.
PS25 – No data received. All NMBAQCS standards deemed failed.

Laboratory – LB1117

Macrobenthos (Training Component)

MB12 - Estuarine sample. Three taxonomic differences (*Neanthes succinea, Polydora cornuta* and *Tharyx* sp.A). Three individuals not picked from the residue, including two previously unpicked taxa. Count variance of six individuals. Bray-Curtis similarity index of 48.8%. Biomass on average 5.27% lighter than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Component)

RT24 – Four generic and five specific differences. Number of AQC identifications in High group.
RT25 – One specific difference. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – Three generic and six specific differences.

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

OS26 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass supplied to five or six decimal places instead of four. Biomass on average 0.22% heavier than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Good'.
All individual extracted from residue. Count variance of one individual. Bray-Curtis similarity index of 98.9%. Biomass supplied to five or six decimal places instead of four. Biomass on average 38.49% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Good'.
Four taxonomic differences (*Cerianthus lloydii, Caulleriella zetlandica, Abludomelita obtusata* and *Ceratia proxima*). All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 98.52%. Biomass supplied to five decimal places instead of four. Biomass on average 6.88% lighter than Unicomarine Ltd.

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

PS24 – NMBAQCS standard for sorting failed. NMBAQCS standard for median not provided; deemed failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve displaced to the left of the majority of curves from 0.5 to 2phi, indicating a larger coarse sand fraction. Sediment described as 'light brown mixed sand' prior to analysis; described as 'light brown very slightly muddy mixed sand' using the Folk triangle.
PS25 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'dark brown fluid slightly sandy mud with organic fragments' prior to analysis; described as 'slightly gravely sandy mud' using the Folk triangle.

Laboratory – LB1118

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – One generic and one specific difference. Number of AQC identifications in Low group.
RT25 – One specific difference. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – One generic and one specific difference.

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

OS26 – No data matrix for sample selection received; not participating in this exercise?
OS27 – No data matrix for sample selection received; not participating in this exercise?
OS28 – No data matrix for sample selection received; not participating in this exercise?

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

PS24 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'medium sand (small clay fraction)' prior to analysis; described as 'medium sand' using the Folk triangle.
PS25 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'mud' prior to analysis; described as 'sandy mud' using the Folk triangle.

Laboratory – LB1119

Macrobenthos (Training Component)

MB12 - Not participating in this component.

Ring Test (Training Component)

RT24 – One generic and one specific difference. Number of AQC identifications in Low group.
RT25 – One generic and two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR09 – All specimens correctly identified.

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

OS26 – Not participating in this component.
OS27 – Not participating in this component.
OS28 – Not participating in this component.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1120

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – Not participating in this component.

RT25 – Not participating in this component.

Laboratory Reference (Training Component)

LR09 - Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Good'.
Fauna received unsplit, *i.e.* one faunal vial. Eleven individuals not picked from the residue. Count variance of ten individuals. Bray-Curtis similarity index of 95.58%. Biomass not comparable due to unsplit fauna.
OS27 – NMBAQCS sample flag – 'Acceptable'.
Fauna received unsplit, *i.e.* one faunal vial. Eleven individuals not picked from the residue, including two previously unpicked taxa. Count variance of three individuals. Bray-Curtis similarity index of 91.49%. Biomass not comparable due to unsplit fauna.
OS28 – NMBAQCS sample flag – 'Fail'.
Fauna received unsplit, *i.e.* one faunal vial. Some identification / enumeration *in situ*. Four individuals not picked from the residue. Count variance of one hundred and seventy-nine individuals, primarily due to the enumeration of dead / empty *Hydrobia ulvae*. Bray-Curtis similarity index of 70.95%. Biomass not comparable due to unsplit fauna.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1121

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – Not participating in this component.
RT25 – Not participating in this component.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Acceptable'.
Three taxonomic differences (*Retusa obtusa, Abra nitida* and *Cossura pygodactyla*). One individual not picked from the residue. Count variance of twenty individuals. Bray-Curtis similarity index of 90.22%. Biomass on average 13.28% heavier than Unicomarine Ltd.
OS27 – NMBAQCS sample flag – 'Acceptable'.
Two taxonomic differences (*Brachystomia scalaris* and *Lepidochitona cinerea*). Seven individuals not picked from the residue, including one previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 90%. Biomass on average 9.18% heavier than Unicomarine Ltd.
OS28 – NMBAQCS sample flag – 'Acceptable'.
Seven taxonomic differences (*Atylus guttatus, Sphaerosyllis hystrix, Chone* sp., *Pholoe inornata, Lumbrineris gracilis, Euclymene santandarensis?* and *Mtylius edulis* juv.). Two individuals not picked from the residue, including one previously unpicked taxon. Count variance of two individuals. Bray-Curtis similarity index of 93.85%. Biomass on average 9.41% heavier than Unicomarine Ltd.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1122

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – Not participating in this component.
RT25 – Not participating in this component.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – Not participating in this component.
OS27 – Not participating in this component.
OS28 – Not participating in this component.

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

PS24 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'coarse sand' prior to analysis; no Folk triangle sediment description data received.
PS25 – NMBAQCS standards for median and mean not provided; deemed failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve slightly displaced to the left of the majority of curves from 2.5 to 5.5phi, indicating a larger fine sand component. Sediment described as 'fine silt' prior to analysis; no Folk triangle sediment description data received.

Laboratory – LB1123

Macrobenthos (Training Component)

MB12 – Not participating in this component.

Ring Test (Training Component)

RT24 – Not participating in this component.
RT25 – Not participating in this component.

Laboratory Reference (Training Component)

LR09 – Not participating in this component.

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

OS26 – NMBAQCS sample flag – 'Good'.
Five individuals not picked from the residue. Count variance of seven individuals. Bray-Curtis similarity index of 99.02%. No biomass data supplied.
OS27 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS28 – NMBAQCS sample flag – 'Good'.
One individual not picked from the residue. Bray-Curtis similarity index of 99.4%. No biomass data supplied.

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

PS24 – Not participating in this component.
PS25 – Not participating in this component.

Laboratory – LB1124

Macrobenthos (Training Component)

MB12 – Estuarine sample. Two taxonomic differences (*Tubificoides pseudogaster* agg. and *Tharyx* sp.A). Thirteen individuals not picked from the residue, including two previously unpicked taxa. Bray-Curtis similarity index of 60.34%. No biomass data supplied. Residue/fauna not stained. Laboratory policy stated as not extracting nematodes, bryozoans, hydroids, copepods, tunicates, anthozoans and aquatic insects.

Ring Test (Training Component)

RT24 – Not participating in this component.
RT25 – Not participating in this component.

Laboratory Reference (Training Component)

LR09 – Three generic and four specific differences.

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

OS26 – Not participating in this component.
OS27 – Not participating in this component.
OS28 – Not participating in this component.

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

PS24 – Not participating in this component.
PS25 – 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. All Scheme participants now use e-mail as their primary means of communication. E-mail capabilities must be made a prerequisite for participation in the Scheme. All primary correspondence for Scheme year twelve 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 submitted data is to be perceived as far worse than a participatory "Fail" flag.
4. A minority of participating laboratories have received 'deemed fail' flags as a result of not informing Unicomarine Ltd. of their intentions to abstain from particular exercises. The RT exercises are directly influenced by the number of participants, *i.e.* fewer participants enable less abundantly encountered taxa to be circulated. Some laboratories receive RT material but do not return data; two laboratories have received ring tests and not submitted data or given details of their abstention for a number of years. Participating laboratories must only subscribe to components for which they intend to provide data; participating laboratories should ensure that any changes to the level of their participation in the Scheme is communicated to Unicomarine Ltd.
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. PS exercises have highlighted the need for a prescriptive method for laser analysis (including equipment specifications) for the analysis of UK NMMP samples. Replicate samples analysed using the same broad technique resulted in highly variable summary statistics. A particle size standard operating procedure 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 adopting future taxonomic developments.
8. Differences in the literature used for identification of invertebrates have been highlighted by the RT, MB and OS exercises. Unpublished keys from workshops, *etc.* could be posted on the Scheme's website. Funding has been made available, through the Scheme, for the development of a UK Standard Taxonomic Literature List in Scheme year 12 (based upon Unicomarine current literature database as a starting point). Funding must also be available for the maintenance and expansion of the literature database.
9. The Own Sample component has shown repeated taxonomic errors for some laboratories from the same UK NMMP sites over several years. Participating laboratories are encouraged to redress or resolve disagreements for taxonomic errors reported in their Own Samples even if their 'whole samples' achieve a 'pass' flag.
10. There are still some problems of individuals and taxa missed at the sorting stage of macrobenthic sample (MB) and Own Sample analysis. The figures for these sorting errors this year still remain a cause for concern, but they are generally improved upon last year's figures. In the MB12 exercise up to 2 taxa (25% of the actual total taxa in the sample) were not extracted. On average the number of taxa not extracted from the residue in MB12 was less than one taxon, however the average sample only contained nine taxa in total. Just two of the participating laboratories extracted all the countable individuals from their MB12 residues. In the worst instance 13.5% of total individuals in the sample were not extracted. The situation was slightly worse for the OS samples where a maximum of 4 taxa and up to 27% of the taxa were not extracted. In the worst instances 59 individuals were not picked from the residue and up to 22% of the total individuals remained in the residue. On average for the OS exercise 0.52 taxa were not extracted compared with 0.84, 1.73, 1.98, 2.04, 1.25, 1.48, 0.45 and 1.39 taxa from last eight years of data, respectively. Enumeration of sorted individuals is generally good. When taxa and individuals are missed during the extraction of fauna from the sediment, laboratories should determine why certain taxa have not been extracted. This could be due to the taxon not being recognised as countable or due to problems with the effect of stains upon the specimens. There may also be a problem within certain taxonomic groups (*e.g.* crustaceans floating within sample or molluscs settled within the coarser sediment fractions). Additional training may be required and a review of existing extraction techniques and internal quality control measures may be beneficial.
11. In Scheme year seven a NMBAQCS Sorting Methods Questionnaire was 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.

12. 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 detailing the correct identification of the taxa circulated. Participants are encouraged to review their exercise reports and provide feedback concerning content and format wherever appropriate.
13. 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.
14. 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.
15. 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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Tables

Table 1. Results from the analysis of Macrobenthic sample MB12 by the participating laboratories.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	Number of Taxa				Number of Individuals				Not extracted			Individuals	Similarity	Taxonomic
LabCode	PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	New Taxa	Ind	%ind	Count Error	index	errors
LB1104	8	8	0	0.0	280	284	-4	1.4	1	2	0.7	-2	91.84	1
LB1107	15	13	2	13.3	59	58	1	1.7	0	0	0.0	1	59.83	1
LB1108	9	11	-2	18.2	23	27	-4	14.8	2	3	11.1	-1	86.28	1
LB1111	9	9	0	0.0	130	134	-4	3.0	0	1	0.7	-3	96.97	1
LB1113	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1114	6	6	0	0.0	41	42	-1	2.4	0	1	2.4	0	84.34	1
LB1115	6	7	-1	14.3	73	76	-3	3.9	1	1	1.3	-2	68.00	3
LB1116	12	12	0	0.0	120	120	0	0.0	0	0	0.0	0	100.00	0
LB1117	8	10	-2	20.0	210	207	3	1.4	2	3	1.4	6	48.80	3
LB1124	6	8	-2	25.0	83	96	-13	13.5	2	13	13.5	0	60.34	2

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

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB12.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1104	UM count	-	276	-	-	1	-	7	-	284
	PL missed	-	1	-	-	1	-	0	-	2
	%missed	-	0.4	-	-	100.0	-	0.0	-	0.7
LB1107	UM count	1	24	4	-	28	-	1	-	58
	PL missed	0	0	0	-	0	-	0	-	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1108	UM count	-	9	-	-	12	-	6	-	27
	PL missed	-	0	-	-	2	-	1	-	3
	%missed	-	0.0	-	-	16.7	-	16.7	-	11.1
LB1111	UM count	-	123	1	-	3	-	7	-	134
	PL missed	-	0	0	-	0	-	1	-	1
	%missed	-	0.0	0.0	-	0.0	-	14.3	-	0.7
LB1113	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1114	UM count	-	34	1	-	-	-	7	-	42
	PL missed	-	0	0	-	-	-	1	-	1
	%missed	-	0.0	0.0	-	-	-	14.3	-	2.4
LB1115	UM count	-	69	4	-	-	-	3	-	76
	PL missed	-	1	0	-	-	-	0	-	1
	%missed	-	1.4	0.0	-	-	-	0.0	-	1.3
LB1116	UM count	-	100	11	-	1	-	8	-	120
	PL missed	-	0	0	-	0	-	0	-	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1117	UM count	-	194	7	-	-	-	6	-	207
	PL missed	-	1	1	-	-	-	1	-	3
	%missed	-	0.5	14.3	-	-	-	16.7	-	1.4
LB1124	UM count	-	79	11	-	-	-	6	-	96
	PL missed	-	8	1	-	-	-	4	-	13
	%missed	-	10.1	9.1	-	-	-	66.7	-	13.5

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 MB12. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1104	PL	-	0.07869	-	-	-	-	2.01127	-	2.08996
	UM	-	0.0828	-	-	-	-	2.0466	-	2.1294
	%diff.	-	-5.2	-	-	-	-	-1.8	-	-1.9
LB1107	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1108	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1111	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1113	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1114	PL	-	0.0387	0.0001	-	-	-	2.5059	-	2.5447
	UM	-	0.0426	0.0001	-	-	-	2.561	-	2.6037
	%diff.	-	-10.1	0.0	-	-	-	-2.2	-	-2.3
LB1115	PL	-	0.0317	0.0001	-	-	-	0.0914	-	0.1232
	UM	-	0.0229	0.0001	-	-	-	0.0912	-	0.1142
	%diff.	-	27.8	0.0	-	-	-	0.2	-	7.3
LB1116	PL	-	0.0487	0.0001	-	0.0001	-	0.9782	-	1.0271
	UM	-	0.0389	0.0001	-	0.0002	-	0.8545	-	0.8937
	%diff.	-	20.1	0.0	-	-100.0	-	12.6	-	13.0
LB1117	PL	-	0.08539	0.00014	-	-	-	0.69087	-	0.77640
	UM	-	0.1333	0.0001	-	-	-	0.6839	-	0.8173
	%diff.	-	-56.1	28.6	-	-	-	1.0	-	-5.3
LB1124	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-

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

Table 4. Variation in faunal content of samples distributed as MB12.

Taxa*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total taxa
LB1104	0	5	0	0	1	0	3	0	9
LB1107	1	6	2	0	3	0	1	0	13
LB1108	0	5	0	0	3	0	2	1	11
LB1111	0	5	1	0	2	0	2	0	10
LB1113	-	-	-	-	-	-	-	-	-
LB1114	0	3	1	0	0	0	2	0	6
LB1115	0	3	1	0	0	0	2	1	7
LB1116	0	4	1	0	1	0	3	3	12
LB1117	0	6	1	0	0	0	2	1	10
LB1124	0	4	1	0	0	0	3	0	8
Mean	0	5	1	0	1	0	2	1	10
Max	1	6	2	0	3	0	3	3	13
Min	0	3	0	0	0	0	1	0	6

*UM data used for all faunal groups (excludes colonial taxa).

Individuals*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total Ind.
LB1104	0	276	0	0	1	0	7	0	284
LB1107	1	24	4	0	28	0	1	0	58
LB1108	0	9	0	0	12	0	6	0	27
LB1111	0	123	1	0	4	0	7	0	135
LB1113	-	-	-	-	-	-	-	-	-
LB1114	0	34	1	0	0	0	7	0	42
LB1115	0	69	4	0	0	0	3	0	76
LB1116	0	100	11	0	1	0	8	0	120
LB1117	0	194	7	0	0	0	6	0	207
LB1124	0	79	11	0	0	0	6	0	96
Mean	0	101	4	0	5	0	6	0	116
Max	1	276	11	0	28	0	8	0	284
Min	0	9	0	0	0	0	1	0	27

*UM data used for all faunal groups (excludes colonial taxa).

Table 5. Results from the analysis of Own Samples (OS26 to OS28) 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
LB1101	OS26	69	69	0	0.0	2174	2178	-4	0.2	0	0	0.0	-4	99.70	0	External Audit
LB1101	OS27	13	13	0	0.0	160	160	0	0.0	0	0	0.0	0	100.00	0	External Audit
LB1101	OS28	70	71	-1	1.4	926	920	6	0.6	0	0	0.0	6	98.92	0	External Audit
LB1102	OS26	7	11	-4	36.4	161	184	-23	12.5	3	21	11.4	-2	92.75	1	-
LB1102	OS27	7	7	0	0.0	48	48	0	0.0	0	0	0.0	0	100.00	0	-
LB1102	OS28	11	11	0	0.0	224	261	-37	14.2	0	53	20.3	16	91.96	0	-
LB1103	OS26	34	36	-2	5.6	112	116	-4	3.4	1	3	2.6	-1	94.74	2	No biomass data
LB1103	OS27	8	8	0	0.0	36	37	-1	2.7	0	0	0.0	-1	95.89	1	No biomass data
LB1103	OS28	12	12	0	0.0	28	28	0	0.0	1	1	3.6	1	96.43	0	No biomass data
LB1104	OS26	66	71	-5	7.0	2323	2332	-9	0.4	4	29	1.2	20	98.82	6	-
LB1104	OS27	82	82	0	0.0	270	264	6	2.2	1	3	1.1	9	91.48	12	Biomass to 6dp
LB1104	OS28	47	50	-3	6.0	321	355	-34	9.6	2	36	10.1	2	90.48	6	Biomass to 6dp
LB1105	OS26	9	9	0	0.0	1626	1672	-46	2.8	0	50	3.0	4	98.48	0	Subsampled
LB1105	OS27	19	21	-2	9.5	887	958	-71	7.4	2	34	3.5	-37	96.15	0	Subsampled
LB1105	OS28	90	90	0	0.0	2299	2238	61	2.7	0	0	0.0	61	98.62	0	External Audit
LB1106	OS26	10	11	-1	9.1	464	476	-12	2.5	1	12	2.5	0	98.62	0	-
LB1106	OS27	13	13	0	0.0	118	121	-3	2.5	0	5	4.1	2	98.78	0	-
LB1106	OS28	8	8	0	0.0	146	152	-6	3.9	0	0	0.0	-6	98.00	0	-
LB1107	OS26	27	27	0	0.0	336	336	0	0.0	0	4	1.2	4	98.21	2	No biomass data
LB1107	OS27	25	26	-1	3.8	69	72	-3	4.2	1	3	4.2	0	96.45	1	No biomass data
LB1107	OS28	55	55	0	0.0	384	396	-12	3.0	0	10	2.5	-2	90.77	5	No biomass data
LB1109	OS26	15	15	0	0.0	685	704	-19	2.7	0	59	8.4	40	98.49	0	Biomass to 5dp
LB1109	OS27	26	26	0	0.0	198	199	-1	0.5	0	1	0.5	0	97.73	1	Biomass to 5dp
LB1109	OS28	25	25	0	0.0	89	88	1	1.1	0	0	0.0	1	99.44	0	Biomass to 5dp
LB1110	OS26	10	13	-3	23.1	279	328	-49	14.9	2	37	11.3	-12	82.37	1	-
LB1110	OS27	23	23	0	0.0	254	260	-6	2.3	0	0	0.0	-6	98.44	1	-
LB1110	OS28	19	19	0	0.0	430	447	-17	3.8	1	13	2.9	-4	71.38	1	>1mm residue not supplied for audit
LB1111	OS26	7	8	-1	12.5	25	26	-1	3.8	1	1	3.8	0	98.04	0	No biomass data.
LB1111	OS27	7	7	0	0.0	16	16	0	0.0	0	0	0.0	0	100.00	0	No biomass data.
LB1111	OS28	17	17	0	0.0	26	26	0	0.0	0	0	0.0	0	100.00	0	No biomass data; some data altered.
LB1112	OS26	38	38	0	0.0	733	729	4	0.5	0	2	0.3	6	99.45	0	-
LB1112	OS27	20	21	-1	4.8	30	31	-1	3.2	1	1	3.2	0	95.08	1	-
LB1112	OS28	14	14	0	0.0	56	56	0	0.0	0	0	0.0	0	100.00	0	-
LB1113	OS26	4	4	0	0.0	3	3	0	0.0	0	0	0.0	0	100.00	0	External Audit
LB1113	OS27	24	24	0	0.0	23	23	0	0.0	0	0	0.0	0	100.00	0	External Audit
LB1113	OS28	20	20	0	0.0	23	25	-2	8.0	0	0	0.0	-2	96.30	0	External Audit
LB1114	OS26	66	66	0	0.0	1479	1469	10	0.7	0	1	0.1	11	99.46	1	External Audit
LB1114	OS27	31	31	0	0.0	213	213	0	0.0	0	0	0.0	0	100.00	0	External Audit
LB1114	OS28	15	15	0	0.0	358	349	9	2.5	0	0	0.0	9	97.33	1	External Audit
LB1115	OS26	9	9	0	0.0	16	16	0	0.0	0	0	0.0	0	100.00	0	-
LB1115	OS27	29	29	0	0.0	323	345	-22	6.4	1	21	6.1	-1	96.42	1	-
LB1115	OS28	6	8	-2	25.0	26	29	-3	10.3	2	3	10.3	0	94.55	0	-
LB1116	OS26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating
LB1116	OS27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating
LB1116	OS28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating
LB1117	OS26	19	19	0	0.0	66	66	0	0.0	0	0	0.0	0	100.00	0	Biomass to 5/6 d.p.
LB1117	OS27	17	16	1	5.9	46	45	1	2.2	0	0	0.0	1	98.90	0	Biomass to 5/6 d.p.
LB1117	OS28	50	50	0	0.0	542	540	2	0.4	0	0	0.0	2	98.52	4	Biomass to 5/6 d.p.
LB1118	OS26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating?
LB1118	OS27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating?
LB1118	OS28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating?
LB1120	OS26	32	32	0	0.0	227	248	-21	8.5	0	11	4.4	-10	95.58	0	Biomass not comparable
LB1120	OS27	8	10	-2	20.0	43	51	-8	15.7	2	11	21.6	3	91.49	0	Biomass not comparable
LB1120	OS28	6	6	0	0.0	399	224	175	43.9	0	4	1.8	179	70.95	0	Biomass not comparable
LB1121	OS26	21	22	-1	4.5	260	241	19	7.3	0	1	0.4	20	90.22	3	-
LB1121	OS27	23	23	0	0.0	57	61	-4	6.6	1	7	11.5	3	90.00	2	-
LB1121	OS28	42	44	-2	4.5	260	260	0	0.0	1	2	0.8	2	93.85	7	-
LB1123	OS26	24	24	0	0.0	2143	2141	2	0.1	0	5	0.2	7	99.02	0	No biomass data.
LB1123	OS27	6	6	0	0.0	12	12	0	0.0	0	0	0.0	0	100.00	0	No biomass data.
LB1123	OS28	9	9	0	0.0	83	84	-1	1.2	0	1	1.2	0	99.40	0	No biomass data.

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See forthcoming annual report, 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 (OS26-28).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1101	AE count	2	1362	289	-	37	1	79	408	2178
OS26	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
LB1101	AE count	-	65	9	-	19	-	65	2	160
OS27	UM missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1101	AE count	11	755	18	-	36	5	77	18	920
OS28	UM missed	0	1	0	-	0	0	0	0	1
	%missed	0.0	0.1	0.0	-	0.0	0.0	0.0	0.0	0.1
LB1102	UM count	1	2	-	-	169	-	11	1	184
OS26	PL missed	1	0	-	-	14	-	5	1	21
	%missed	100.0	0.0	-	-	8.3	-	45.5	100.0	11.4
LB1102	UM count	-	46	2	-	-	-	-	-	48
OS27	PL missed	-	0	0	-	-	-	-	-	0
	%missed	-	0.0	0.0	-	-	-	-	-	0.0
LB1102	UM count	-	51	83	-	5	-	122	-	261
OS28	PL missed	-	2	10	-	3	-	38	-	53
	%missed	-	3.9	12.0	-	60.0	-	31.1	-	20.3
LB1103	UM count	2	39	-	-	3	35	35	2	116
OS26	PL missed	0	1	-	-	0	0	2	0	3
	%missed	0.0	2.6	-	-	0.0	0.0	5.7	0.0	2.6
LB1103	UM count	-	5	-	-	10	21	1	-	37
OS27	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1103	UM count	-	6	-	-	17	3	2	-	28
OS28	PL missed	-	0	-	-	0	0	1	-	1
	%missed	-	0.0	-	-	0.0	0.0	50.0	-	3.6
LB1104	UM count	1	629	1	-	33	31	1632	5	2332
OS26	PL missed	0	8	0	-	0	1	20	0	29
	%missed	0.0	1.3	0.0	-	0.0	3.2	1.2	0.0	1.2
LB1104	UM count	7	95	-	-	59	8	85	10	264
OS27	PL missed	0	1	-	-	0	0	1	1	3
	%missed	0.0	1.1	-	-	0.0	0.0	1.2	10.0	1.1
LB1104	UM count	1	220	49	-	-	1	41	43	355
OS28	PL missed	0	10	1	-	-	0	10	15	36
	%missed	0.0	4.5	2.0	-	-	0.0	24.4	34.9	10.1
LB1105	UM count	-	-	1657	-	1	-	-	14	1672
OS26	PL missed	-	-	45	-	0	-	-	5	50
	%missed	-	-	2.7	-	0.0	-	-	35.7	3.0
LB1105	UM count	-	735	197	1	3	-	10	12	958
OS27	PL missed	-	14	7	1	3	-	1	8	34
	%missed	-	1.9	3.6	100.0	100.0	-	10.0	66.7	3.5
LB1105	AE count	2	1734	51	2	48	2	180	219	2238
OS28	UM missed	0	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	0.0
LB1106	UM count	-	323	147	-	5	-	-	1	476
OS26	PL missed	-	9	3	-	0	-	-	0	12
	%missed	-	2.8	2.0	-	0.0	-	-	0.0	2.5
LB1106	UM count	-	91	23	-	-	-	4	3	121
OS27	PL missed	-	4	0	-	-	-	1	0	5
	%missed	-	4.4	0.0	-	-	-	25.0	0.0	4.1
LB1106	UM count	-	139	11	-	-	-	1	1	152
OS28	PL missed	-	0	0	-	-	-	0	0	0
	%missed	-	0.0	0.0	-	-	-	0.0	0.0	0.0

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS26-28).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1107	UM count	10	186	-	-	4	128	5	3	336
OS26	PL missed	0	0	-	-	0	4	0	0	4
	%missed	0.0	0.0	-	-	0.0	3.1	0.0	0.0	1.2
LB1107	UM count	-	24	-	-	14	10	17	7	72
OS27	PL missed	-	0	-	-	0	0	3	0	3
	%missed	-	0.0	-	-	0.0	0.0	17.6	0.0	4.2
LB1107	UM count	64	262	-	-	15	31	16	8	396
OS28	PL missed	1	9	-	-	0	0	0	0	10
	%missed	1.6	3.4	-	-	0.0	0.0	0.0	0.0	2.5
LB1109	UM count	2	58	6	-	12	-	616	10	704
OS26	PL missed	0	1	1	-	0	-	57	0	59
	%missed	0.0	1.7	16.7	-	0.0	-	9.3	0.0	8.4
LB1109	UM count	-	11	-	-	6	5	177	-	199
OS27	PL missed	-	0	-	-	0	0	1	-	1
	%missed	-	0.0	-	-	0.0	0.0	0.6	-	0.5
LB1109	UM count	-	17	-	-	6	18	46	1	88
OS28	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1110	UM count	2	96	147	-	1	-	68	14	328
OS26	PL missed	0	20	2	-	1	-	13	1	37
	%missed	0.0	20.8	1.4	-	100.0	-	19.1	7.1	11.3
LB1110	UM count	-	20	-	-	-	126	114	-	260
OS27	PL missed	-	0	-	-	-	0	0	-	0
	%missed	-	0.0	-	-	-	0.0	0.0	-	0.0
LB1110	UM count	1	294	127	-	1	-	23	1	447
OS28	PL missed	0	4	2	-	0	-	6	1	13
	%missed	0.0	1.4	1.6	-	0.0	-	26.1	100.0	2.9
LB1111	UM count	-	3	-	1	-	1	18	3	26
OS26	PL missed	-	0	-	1	-	0	0	0	1
	%missed	-	0.0	-	100.0	-	0.0	0.0	0.0	3.8
LB1111	UM count	-	12	-	-	-	-	4	-	16
OS27	PL missed	-	0	-	-	-	-	0	-	0
	%missed	-	0.0	-	-	-	-	0.0	-	0.0
LB1111	UM count	-	13	-	-	1	3	9	-	26
OS28	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1112	UM count	8	662	-	2	10	1	33	13	729
OS26	PL missed	0	1	-	0	0	0	1	0	2
	%missed	0.0	0.2	-	0.0	0.0	0.0	3.0	0.0	0.3
LB1112	UM count	1	17	-	-	8	2	3	-	31
OS27	PL missed	0	0	-	-	0	0	1	-	1
	%missed	0.0	0.0	-	-	0.0	0.0	33.3	-	3.2
LB1112	UM count	-	30	19	-	1	-	4	2	56
OS28	PL missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1113	AE count	-	1	-	-	1	-	-	1	3
OS26	UM missed	-	0	-	-	0	-	-	0	0
	%missed	-	0.0	-	-	0.0	-	-	0.0	0.0
LB1113	AE count	-	14	-	1	1	5	-	2	23
OS27	UM missed	-	0	-	0	0	0	-	0	0
	%missed	-	0.0	-	0.0	0.0	0.0	-	0.0	0.0
LB1113	AE count	2	16	1	-	1	-	5	-	25
OS28	UM missed	0	0	0	-	0	-	0	-	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	-	0.0

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS26-28).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1114	AE count	-	702	-	1	285	6	423	52	1469
OS26	UM missed	-	1	-	0	0	0	0	0	1
	%missed	-	0.1	-	0.0	0.0	0.0	0.0	0.0	0.1
LB1114	AE count	-	24	1	1	13	128	40	6	213
OS27	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
LB1114	AE count	-	42	260	-	42	-	5	-	349
OS28	UM missed	-	0	0	-	0	-	0	-	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	-	0.0
LB1115	UM count	1	7	-	-	1	1	6	-	16
OS26	PL missed	0	0	-	-	0	0	0	-	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1115	UM count	3	162	-	-	2	28	150	-	345
OS27	PL missed	0	2	-	-	0	0	19	-	21
	%missed	0.0	1.2	-	-	0.0	0.0	12.7	-	6.1
LB1115	UM count	-	22	1	-	-	-	6	-	29
OS28	PL missed	-	1	1	-	-	-	1	-	3
	%missed	-	4.5	100.0	-	-	-	16.7	-	10.3
LB1116	UM count	-	-	-	-	-	-	-	-	0
OS26	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1116	UM count	-	-	-	-	-	-	-	-	0
OS27	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1116	UM count	-	-	-	-	-	-	-	-	0
OS28	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1117	UM count	1	22	-	-	5	-	38	-	66
OS26	PL missed	0	0	-	-	0	-	0	-	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	-	0.0
LB1117	UM count	1	11	-	-	5	22	6	-	45
OS27	PL missed	0	0	-	-	0	0	0	-	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1117	UM count	3	248	-	-	7	5	269	8	540
OS28	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1118	UM count	-	-	-	-	-	-	-	-	0
OS26	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1118	UM count	-	-	-	-	-	-	-	-	0
OS27	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1118	UM count	-	-	-	-	-	-	-	-	0
OS28	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1120	UM count	-	197	11	-	16	3	21	-	248
OS26	PL missed	-	3	1	-	1	0	6	-	11
	%missed	-	1.5	9.1	-	6.3	0.0	28.6	-	4.4
LB1120	UM count	-	7	-	1	3	-	40	-	51
OS27	PL missed	-	0	-	1	2	-	8	-	11
	%missed	-	0.0	-	100.0	66.7	-	20.0	-	21.6
LB1120	UM count	-	57	-	-	1	-	166	-	224
OS28	PL missed	-	4	-	-	0	-	0	-	4
	%missed	-	7.0	-	-	0.0	-	0.0	-	1.8

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS26-28).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1121	UM count	-	47	31	-	79	2	82	-	241
OS26	PL missed	-	0	0	-	0	0	1	-	1
	%missed	-	0.0	0.0	-	0.0	0.0	1.2	-	0.4
LB1121	UM count	-	34	-	-	11	6	10	-	61
OS27	PL missed	-	0	-	-	0	1	6	-	7
	%missed	-	0.0	-	-	0.0	16.7	60.0	-	11.5
LB1121	UM count	-	98	-	-	150	6	6	-	260
OS28	PL missed	-	0	-	-	1	0	1	-	2
	%missed	-	0.0	-	-	0.7	0.0	16.7	-	0.8
LB1123	UM count	-	1698	426	-	4	-	13	-	2141
OS26	PL missed	-	2	3	-	0	-	0	-	5
	%missed	-	0.1	0.7	-	0.0	-	0.0	-	0.2
LB1123	UM count	-	7	3	-	2	-	-	-	12
OS27	PL missed	-	0	0	-	0	-	-	-	0
	%missed	-	0.0	0.0	-	0.0	-	-	-	0.0
LB1123	UM count	-	67	13	-	2	-	2	-	84
OS28	PL missed	-	0	1	-	0	-	0	-	1
	%missed	-	0.0	7.7	-	0.0	-	0.0	-	1.2

Key: PL - participating laboratory
UM - Unicomarine Ltd.
AE - Aquatic Environments (external auditor)
- - No data. See section 6 for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS26-OS28.

		Sample OS26								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1101	UM	0.0008	4.6840	0.0483	-	0.0364	0.0040	1.5561	0.2179	6.5475
	AE	0.0007	4.4100	0.0415	-	0.0287	0.0037	1.5331	0.1994	6.2171
	%diff.	12.5	5.8	14.1	-	21.2	7.5	1.5	8.5	5.0
LB1102	PL	-	0.0022	-	-	0.1413	-	19.0586	-	19.2021
	UM	-	0.0011	-	-	0.0865	-	16.0856	-	16.1732
	%diff.	-	50.0	-	-	38.8	-	15.6	-	15.8
LB1103	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1104	PL	0.0004	1.4043	0.0001	-	0.0355	0.1851	7.2473	0.0002	8.87290
	UM	0.0004	1.4339	0.0001	-	0.0370	0.1902	6.8277	0.0002	8.4895
	%diff.	0.0	-2.1	0.0	-	-4.2	-2.8	5.8	0.0	4.3
LB1105	PL	-	-	0.8062	-	0.0015	-	-	0.0002	0.80790
	UM	-	-	0.3942	-	0.0005	-	-	0.0002	0.3949
	%diff.	-	-	51.1	-	66.7	-	-	0.0	51.1
LB1106	PL	-	0.0533	0.0082	-	0.0003	-	-	0.0001	0.0619
	UM	-	0.0444	0.0068	-	0.0002	-	-	0.0001	0.0515
	%diff.	-	16.7	17.1	-	33.3	-	-	0.0	16.8
LB1107	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1109	PL	0.00344	0.19473	0.00040	-	0.00526	-	0.81857	0.00712	1.02952
	UM	0.0058	0.2928	0.0004	-	0.0095	-	0.9683	0.0084	1.2852
	%diff.	-68.6	-50.4	0.0	-	-80.6	-	-18.3	-18.0	-24.8
LB1110	PL	0.0101	0.0048	0.2356	-	-	-	0.0431	0.0003	0.2939
	UM	0.0076	0.0044	0.1705	-	-	-	0.0400	0.0011	0.2236
	%diff.	24.8	8.3	27.6	-	-	-	7.2	-266.7	23.9
LB1111	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1112	PL	0.0417	2.1699	-	0.0006	3.6008	0.0945	0.0680	2.1424	8.1179
	UM	0.0485	1.9926	-	0.0012	3.9852	0.1045	0.0721	2.3283	8.5324
	%diff.	-16.3	8.2	-	-100.0	-10.7	-10.6	-6.0	-8.7	-5.1
LB1113	UM	-	0.2823	-	-	0.4281	-	-	4.5815	5.292
	AE	-	0.2741	-	-	0.4207	-	-	4.3624	5.0572
	%diff.	-	2.9	-	-	1.7	-	-	4.8	4.4
LB1114	UM	-	13.1246	-	0.0001	0.3695	0.0022	4.3433	1.6308	19.4705
	AE	-	12.3558	-	0.0001	0.3493	0.0023	4.2659	1.6443	18.6177
	%diff.	-	5.9	-	0.0	5.5	-4.5	1.8	-0.8	4.4
LB1115	PL	0.0001	0.4545	-	-	0.4076	0.1143	0.9319	-	1.9084
	UM	0.0003	0.4475	-	-	0.4716	0.1247	0.9382	-	1.9823
	%diff.	-200.0	1.5	-	-	-15.7	-9.1	-0.7	-	-3.9
LB1116	PL	-	-	-	-	-	-	-	-	0.00000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1117	PL	0.00334	0.29341	-	-	9.32286	-	1.89057	-	11.51018
	UM	0.0028	0.0494	-	-	9.4935	-	1.9387	-	11.4844
	%diff.	16.2	83.2	-	-	-1.8	-	-2.5	-	0.2
LB1118	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1120	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1121	PL	-	0.1437	0.0035	-	0.0246	0.8986	0.1271	-	1.1975
	UM	-	0.1239	0.0023	-	0.0163	0.7876	0.1084	-	1.0385
	%diff.	-	13.8	34.3	-	33.7	12.4	14.7	-	13.3
LB1123	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
AE - Aquatic Environments (external auditor)
"-" - No data. See section 6 for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS26-OS28.

Sample OS27

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1101	UM	-	0.7118	0.0039	-	0.0134	-	0.0419	0.0001	0.77110
	AE	-	0.6407	0.0029	-	0.0121	-	0.0391	0.0001	0.6949
	%diff.	-	10.0	25.6	-	9.7	-	6.7	0.0	9.9
LB1102	PL	-	0.7805	0.0003	-	-	-	-	-	0.7808
	UM	-	0.6857	0.0002	-	-	-	-	-	0.6859
	%diff.	-	12.1	33.3	-	-	-	-	-	12.2
LB1103	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1104	PL	0.078920	0.512963	-	-	0.337107	0.077400	0.267375	0.091625	1.365390
	UM	0.0819	0.5130	-	-	0.2985	0.0759	0.2739	0.0860	1.3292
	%diff.	-3.8	0.0	-	-	11.5	1.9	-2.4	6.1	2.7
LB1105	PL	-	0.5955	0.0693	-	-	-	0.9044	0.0001	1.56926
	UM	-	0.3231	0.0604	-	-	-	0.7671	0.0001	1.1507
	%diff.	-	45.7	12.8	-	-	-	15.2	0.0	26.7
LB1106	PL	-	0.0273	0.0025	-	-	-	0.0001	0.0001	0.0300
	UM	-	0.0189	0.0022	-	-	-	0.0004	0.0001	0.0216
	%diff.	-	30.8	12.0	-	-	-	-300.0	0.0	28.0
LB1107	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1109	PL	-	0.01179	-	-	0.00569	0.04293	2.47875	-	2.53916
	UM	-	0.0209	-	-	0.0110	0.0602	2.5766	-	2.6687
	%diff.	-	-77.3	-	-	-93.3	-40.2	-3.9	-	-5.1
LB1110	PL	-	0.1310	-	-	-	1.6881	0.5510	-	2.3701
	UM	-	0.1090	-	-	-	0.4514	0.4775	-	1.0379
	%diff.	-	16.8	-	-	-	73.3	13.3	-	56.2
LB1111	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1112	PL	0.0089	0.0491	-	-	0.0070	0.0490	0.0036	-	0.1176
	UM	0.0108	0.0636	-	-	0.0107	0.0503	0.0022	-	0.1376
	%diff.	-21.3	-29.5	-	-	-52.9	-2.7	38.9	-	-17.0
LB1113	UM	-	0.1838	-	0.0001	0.0015	0.3189	-	0.4771	0.981
	AE	-	0.2113	-	0.0001	0.0013	0.3298	-	0.4866	1.0291
	%diff.	-	-15.0	-	0.0	13.3	-3.4	-	-2.0	-4.9
LB1114	UM	-	0.1532	0.0001	0.0001	0.0039	0.3466	0.1397	0.0004	0.6440
	AE	-	0.1420	0.0001	0.0001	0.0028	0.3310	0.1378	0.0003	0.6141
	%diff.	-	7.3	0.0	0.0	28.2	4.5	1.4	25.0	4.6
LB1115	PL	0.3535	2.0912	-	-	0.0029	0.9335	8.4243	-	11.8054
	UM	0.3414	1.8604	-	-	0.0017	0.8548	7.6703	-	10.7286
	%diff.	3.4	11.0	-	-	41.4	8.4	9.0	-	9.1
LB1116	PL	-	-	-	-	-	-	-	-	0.00000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1117	PL	0.074630	0.167537	-	-	0.003010	13.275670	0.018970	-	13.539817
	UM	0.0720	0.1374	-	-	0.0030	8.0967	0.0187	-	8.3278
	%diff.	3.5	18.0	-	-	0.3	39.0	1.4	-	38.5
LB1118	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1120	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1121	PL	-	0.1104	-	-	0.0035	0.0038	1.5446	-	1.6623
	UM	-	0.0611	-	-	0.0025	0.0026	1.4435	-	1.5097
	%diff.	-	44.7	-	-	28.6	31.6	6.5	-	9.2
LB1123	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
AE - Aquatic Environments (external auditor)
"-" - No data. See section 6 for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS26-OS28.

		Sample OS28								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1101	UM	0.2618	4.9141	0.0013	-	0.0415	0.1571	7.8164	0.0149	13.2071
	AE	0.2441	4.4096	0.0012	-	0.0383	0.1662	7.6973	0.0136	12.5703
	%diff.	6.8	10.3	7.7	-	7.7	-5.8	1.5	8.7	4.8
LB1102	PL	-	1.1711	0.0277	-	0.0100	-	8.0481	-	9.2569
	UM	-	0.8014	0.0140	-	0.0107	-	6.9485	-	7.7746
	%diff.	-	31.6	49.5	-	-7.0	-	13.7	-	16.0
LB1103	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1104	PL	0.002240	1.195022	0.002909	-	-	0.001640	0.082975	0.002335	1.28712
	UM	0.0023	1.1725	0.0031	-	-	0.0017	0.0800	0.0052	1.2648
	%diff.	-2.7	1.9	-6.6	-	-	-3.7	3.6	-122.7	1.7
LB1105	UM	0.0008	5.1697	0.0050	0.0002	9.6123	0.0002	202.6594	3.7668	221.21440
	AE	0.0008	5.0403	0.0047	0.0001	9.4809	0.0002	204.9314	3.6982	223.1566
	%diff.	0.0	2.5	6.0	50.0	1.4	0.0	-1.1	1.8	-0.9
LB1106	PL	-	0.0434	0.0006	-	-	-	0.0001	0.0001	0.0442
	UM	-	0.0290	0.0005	-	-	-	0.0002	0.0001	0.0298
	%diff.	-	33.2	16.7	-	-	-	-100.0	0.0	32.6
LB1107	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1109	PL	-	0.02547	-	-	0.01362	0.12578	0.49615	0.00069	0.66171
	UM	-	0.0385	-	-	0.0225	0.1557	0.5254	0.0002	0.7423
	%diff.	-	-51.2	-	-	-65.2	-23.8	-5.9	71.0	-12.2
LB1110	PL	0.0008	0.9160	0.0609	-	0.0009	-	0.0162	-	0.9948
	UM	0.0007	0.6011	0.0293	-	0.0008	-	0.0105	-	0.6424
	%diff.	12.5	34.4	51.9	-	11.1	-	35.2	-	35.4
LB1111	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1112	PL	-	0.0567	0.0097	-	-	-	0.0050	0.0119	0.0833
	UM	-	0.0616	0.0088	-	-	-	0.0039	0.0106	0.0849
	%diff.	-	-8.6	9.3	-	-	-	22.0	10.9	-1.9
LB1113	UM	0.0087	0.2591	0.0003	-	0.0009	0.0001	0.0383	0.0138	0.321
	AE	0.0080	0.3305	0.0002	-	0.0006	0.0001	0.0359	0.0121	0.3874
	%diff.	8.0	-27.6	33.3	-	33.3	0.0	6.3	12.3	-20.6
LB1114	UM	-	0.1922	0.0370	-	0.0149	-	0.0034	-	0.2475
	AE	-	0.1853	0.0321	-	0.0132	-	0.0033	-	0.2339
	%diff.	-	3.6	13.2	-	11.4	-	2.9	-	5.5
LB1115	PL	-	0.0942	-	-	-	-	2.0768	-	2.1710
	UM	-	0.0693	-	-	-	-	2.0838	-	2.1531
	%diff.	-	26.4	-	-	-	-	-0.3	-	0.8
LB1116	PL	-	-	-	-	-	-	-	-	0.00000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1117	PL	0.00576	1.42366	-	-	0.14864	23.73401	16.84336	3.18680	45.34223
	UM	0.0056	1.1716	-	-	0.1095	27.7480	16.5355	2.8894	48.4596
	%diff.	2.8	17.7	-	-	26.3	-16.9	1.8	9.3	-6.9
LB1118	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1120	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1121	PL	-	0.1452	-	-	0.1078	0.0072	1.5561	-	1.8163
	UM	-	0.1023	-	-	0.0630	0.0055	1.4745	-	1.6453
	%diff.	-	29.5	-	-	41.6	23.6	5.2	-	9.4
LB1123	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
AE - Aquatic Environments (external auditor)
"-" - No data. See section 6 for details.

Table 8. Summary of the results of particle size analysis of the *replicate* samples from sediment circulation PS24.

PS24	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS24 - 42 - laser	1.13	1.65	1.67	0.65	0.070
PS24 - 43 - laser	1.32	1.66	1.68	0.66	0.080
PS24 - 44 - laser	1.42	1.62	1.66	0.66	0.110
PS24 - 45 - laser	0.99	1.65	1.67	0.64	0.070
PS24 - 46 - laser	1.14	1.63	1.65	0.65	0.070
PS24 - 47 - laser	1.07	1.64	1.66	0.66	0.070
PS24 - 48 - laser	1.25	1.64	1.67	0.66	0.080
PS24 - 35 - sieve	3.41	2.16	2.24	0.72	0.10
PS24 - 36 - sieve	3.60	2.11	2.21	0.73	0.13
PS24 - 37 - sieve	3.31	2.13	2.21	0.72	0.10
PS24 - 38 - sieve	3.23	2.09	2.19	0.71	0.14
PS24 - 39 - sieve	3.43	2.12	2.21	0.72	0.12
PS24 - 40 - sieve	3.25	2.12	2.20	0.73	0.11
PS24 - 41 - sieve	3.17	2.11	2.19	0.72	0.11

Table 9. Summary of the results of particle size analysis of the *replicate* samples from sediment circulation PS25.

PS25	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS25 - 42 - laser	79.89	6.25	6.14	2.25	-0.020
PS25 - 43 - laser	80.41	6.28	6.16	2.21	-0.030
PS25 - 44 - laser	80.33	6.27	6.14	2.22	-0.040
PS25 - 45 - laser	79.81	6.23	6.12	2.22	-0.010
PS25 - 46 - laser	80.44	6.23	6.13	2.19	-0.020
PS25 - 47 - laser	80.59	6.26	6.15	2.21	-0.020
PS25 - 48 - laser	79.91	6.22	6.12	2.22	-0.010
PS25 - 35 - sieve	81.22	6.70	-	-	-
PS25 - 36 - sieve	79.61	6.68	-	-	-
PS25 - 37 - sieve	83.15	6.86	-	-	-
PS25 - 38 - sieve	82.27	6.91	-	-	-
PS25 - 39 - sieve	81.81	6.89	-	-	-
PS25 - 40 - sieve	77.85	7.27	-	-	-
PS25 - 41 - sieve	78.61	6.74	-	-	-

Table 10. Summary of the particle size information received from participating laboratories for the twenty-fourth particle size distribution PS24.

LabCode	Method	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
LB1104* - PS24	L	1.16	1.50	1.53	0.75	0.070
LB1107 - PS24	L	2.45	1.92	1.94	0.66	0.110
LB1109 - PS24	L	6.32	1.86	1.87	1.03	0.428
LB1114 - PS24	L	2.89	1.73	1.76	0.70	-0.110
LB1115 - PS24	L	1.16	1.50	1.53	0.75	0.070
LB1116 - PS24	DS	2.55	2.10	2.15	-0.71	-0.150
LB1117 - PS24	L	4.57	-	1.59	1.26	0.250
LB1118 - PS24	L	4.28	1.88	1.94	0.89	-0.19
LB1122 - PS24	L	1.98	1.80	1.65	0.77	-0.07

Key to methods:
L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette
L* - replicated data - not included in z-score calculations
"-" - No data. See Section 6 for details.
Shaded cells - maximum and minimum values for each derived statistic.

Table 11. Summary of the particle size information received from participating laboratories for the twenty-fifth particle size distribution PS25.

LabCode	Method	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
LB1104* - PS25	L	78.75	5.57	5.42	1.90	-0.100
LB1107 - PS25	L	66.40	3.83	4.33	1.66	0.420
LB1114 - PS25	L	78.86	5.79	5.70	1.92	0.030
LB1115 - PS25	L	78.75	5.57	5.42	1.90	-0.100
LB1117 - PS25	L	76.46	5.53	5.50	1.97	0.020
LB1118 - PS25	L	81.56	5.93	5.78	1.80	0.080
LB1122 - PS25	L	72.25	-	-	2.02	-0.030

Key to methods:
L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette
L* - replicated data - not included in z-score calculations
- - No data. See Section 6 for details.
Shaded cells - maximum and minimum values for each derived statistic.

Table 12. The identifications of the fauna made by participating laboratories for RT24. Names are given only where different from the AQC identification.

RT24	Taxon	LB1101	LB1103	LB1105	LB1107	LB1109	LB1112	LB1114	LB1116
RT2401	Amphictene auricoma	- -	[Pectinaria] -	[Pectinaria] -	- -	- -	- -	0 0	- -
RT2402	Abra alba	- -	- -	- -	- -	- -	- -	0 0	- -
RT2403	Corophium lacustre	- -	- -	- -	- -	- acutum	- -	0 0	- -
RT2404	Ampelisca typica	- -	- -	- -	- -	- -	- -	0 0	- -
RT2405	Tragula fenestrata	Chrysallida suturalis	Chrysallida obtusata	- -	Turbonilla rufescens	- [fenestata]	- -	0 0	- -
RT2406	Magelona alleni	- -	- -	- -	- -	- -	- -	0 0	- -
RT2407	Perioculodes longimanus	Ampelisca sp.	- -	- -	- -	- -	- -	0 0	- -
RT2408	Acanthodoris pilosa	Adalaria proxima	- -	- -	- -	- -	- -	0 0	- -
RT2409	Ampelisca brevicornis	- -	- -	- -	- -	- -	- -	0 0	- -
RT2410	Assiminea grayana	- -	- -	- -	- -	- -	- -	0 0	- -
RT2411	Peresiella clymenoides	- [chymencides]	Mediomastus fragilis	- -	- -	- -	- -	0 0	- -
RT2412	Nuculoma tenuis	Nucula sp.	- -	Nucula nitidosa	- -	- -	- -	0 0	Nucula nucleus
RT2413	Ovatella myosotis	- -	- -	- -	Auriculinella bidentata	- -	- -	0 0	- -
RT2414	Urothoe marina	- -	- -	- brevicornis	- -	- -	- -	0 0	- -
RT2415	Magelona johnstoni	- mirabilis	- -	- -	- -	- -	- -	0 0	- -
RT2416	Crangon crangon	- -	- -	- -	- allmani	- trispinosus	- allmanni	0 0	- -
RT2417	Tritaeta gibbosa	Dexamine spinosa	- -	- -	- -	- -	- -	0 0	- -
RT2418	Branchiomma bombyx	Pseudopotamilla reniformis	- -	[Branchioma] -	- -	Bispira volutacornis	- -	0 0	- -
RT2419	Corbula gibba	- -	- -	- -	- -	- -	- -	0 0	- -
RT2420	Modiolarca tumida	[Musculus] [marmoratus]	- -	- -	- -	- -	- -	0 0	- -
RT2421	Pseudocuma longicornis	Campylaspis legendrei	- -	- -	- -	- -	- -	0 0	- -
RT2422	Cyathura carinata	- -	- -	- -	- -	- -	- -	0 0	- -
RT2423	Aricidea minuta	- catherinae	- -	- -	- -	- suecica	- -	0 0	- -
RT2424	Amphiura filiformis	Ophiactis balli	- -	- -	- -	- -	- -	0 0	- -
RT2425	Eusyllis blomstrandi	- -	- -	- -	- -	- -	- -	0 0	- -

RT24	Taxon	LB1102	LB1104	LB1106	LB1108	LB1111	LB1113	LB1115	LB1117
RT2401	Amphictene auricoma	0 0	- -	0 0	[Pectinaria] -	- -	0 0	- -	- -
RT2402	Abra alba	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2403	Corophium lacustre	0 0	- -	0 0	- acutum	- -	0 0	- -	- -
RT2404	Ampelisca typica	0 0	- armoricana	0 0	- -	- -	0 0	- -	- -
RT2405	Tragula fenestrata	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2406	Magelona alleni	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2407	Perioculodes longimanus	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2408	Acanthodoris pilosa	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2409	Ampelisca brevicornis	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2410	Assiminea grayana	0 0	- -	0 0	Pusillina inconspicua	- -	0 0	- -	- -
RT2411	Peresiella clymenoides	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2412	Nuculoma tenuis	0 0	- -	0 0	[Nucula] -	- -	0 0	- -	Tellimya ferrugino
RT2413	Ovatella myosotis	0 0	Auriculinella bidentata	0 0	Acteon tornatilis	- -	0 0	Leucophyta bidentata	Odostomia unident
RT2414	Urothoe marina	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2415	Magelona johnstoni	0 0	- -	0 0	- -	- -	0 0	- -	- [mirabilis Form A
RT2416	Crangon crangon	0 0	- -	0 0	Philoceras trispinosus	- -	0 0	- -	- -
RT2417	Tritaeta gibbosa	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2418	Branchiomma bombyx	0 0	[Brachioma] -	0 0	- -	- -	0 0	- -	Pseudopotamilla renif
RT2419	Corbula gibba	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2420	Modiolarca tumida	0 0	- -	0 0	[Musculus] [marmoratus]	- -	0 0	- -	Musculus discors
RT2421	Pseudocuma longicornis	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2422	Cyathura carinata	0 0	- -	0 0	Anthura gracilis	- -	0 0	- -	- -
RT2423	Aricidea minuta	0 0	- -	0 0	- [??minuta]	- suecica	0 0	- -	- roberti
RT2424	Amphiura filiformis	0 0	- -	0 0	- -	- -	0 0	- -	- -
RT2425	Eusyllis blomstrandi	0 0	- [blomstrandii]	0 0	- -	- -	0 0	- -	- -

Table 13. The identifications of the fauna made by participating laboratories for RT25. Names are given only where different from the AQC identification.

RT25	Taxon	LB1101	LB1103	LB1105	LB1107	LB1109	LB1112	LB1
RT2501	Pagurus bernhardus	- -	- -	- -	- -	0 0	- -	0
RT2502	Pisidia longicornis	- -	- -	- -	- -	0 0	- -	0
RT2503	Palaemon macrodactylus	Palaemonidae ?	- -	- -	- longirostris	0 0	- -	0
RT2504	Pandalus borealis	- -	- -	- -	- -	0 0	- -	0
RT2505	Crangon allmanni	- -	- -	- -	- [allmani]	0 0	- -	0
RT2506	Pasiphaea multidentata	- -	- -	- -	- -	0 0	- -	0
RT2507	Galathea intermedia	- -	- -	- -	- -	0 0	- -	0
RT2508	Crangon crangon	- -	- -	- -	- -	0 0	- -	0
RT2509	Palaemonetes varians	- -	- -	Palaemon adspersus	- -	0 0	- -	0
RT2510	Carcinus maenas	- -	- -	- -	- -	0 0	- -	0
RT2511	Palaemon elegans	- -	- -	- -	- -	0 0	- -	0
RT2512	Pilumnus hirtellus	Porcellana platycheles	[Pilumus] -	- -	Pachgrapsus marmoratus	0 0	- -	0
RT2513	Palaemon longirostris	- [longicornis]	- -	- -	- -	0 0	- -	0
RT2514	Macropodia rostrata	Inachus phalangium	- -	- -	- -	0 0	- -	0
RT2515	Liocarcinus holsatus	- -	- -	[Polybius] -	- -	0 0	- -	0
RT2516	Thoralus cranchii	Eualus occultus	[Thoralas] -	- -	- -	0 0	- -	0
RT2517	Gastrosaccus spinifer	Nyctiphanes couchi	- -	- -	- -	0 0	- -	0
RT2518	Palaemon serratus	- -	- -	- -	- -	0 0	- -	0
RT2519	Pontophilus norvegicus	- -	- -	- -	- -	0 0	- -	0
RT2520	Pisidia longicornis	- -	- -	- -	- -	0 0	- -	0
RT2521	Palaemonetes varians	Palaemon adspersus	- -	- -	- -	0 0	- -	0
RT2522	Pandalus montagui	- -	- -	- -	- -	0 0	- -	0
RT2523	Philocheras trispinosus	- -	- -	- -	[Crangon] -	0 0	[Crangon] -	0
RT2524	Hippolyte varians	- -	- -	- -	- -	0 0	- -	0
RT2525	Pandalina brevirostris	- -	- -	- -	- -	0 0	- -	0

RT25	Taxon	LB1102	LB1104	LB1106	LB1108	LB1111	LB1113	LB1
RT2501	Pagurus bernhardus	0 0	- -	0 0	- -	- -	0 0	-
RT2502	Pisidia longicornis	0 0	- -	0 0	- -	- -	0 0	-
RT2503	Palaemon macrodactylus	0 0	- -	0 0	- elegans	- -	0 0	-
RT2504	Pandalus borealis	0 0	- -	0 0	- -	- -	0 0	-
RT2505	Crangon allmanni	0 0	- [allmani]	0 0	- -	- -	0 0	-
RT2506	Pasiphaea multidentata	0 0	- -	0 0	- -	- -	0 0	-
RT2507	Galathea intermedia	0 0	- -	0 0	- -	- -	0 0	-
RT2508	Crangon crangon	0 0	- -	0 0	- -	- -	0 0	- allm
RT2509	Palaemonetes varians	0 0	- -	0 0	- -	- -	0 0	-
RT2510	Carcinus maenas	0 0	- -	0 0	- -	- -	0 0	-
RT2511	Palaemon elegans	0 0	- -	0 0	- -	- -	0 0	-
RT2512	Pilumnus hirtellus	0 0	Liocarcinus arcuatus	0 0	Liocarcinus puber	- -	0 0	-
RT2513	Palaemon longirostris	0 0	- -	0 0	- -	- -	0 0	-
RT2514	Macropodia rostrata	0 0	- -	0 0	- -	- -	0 0	-
RT2515	Liocarcinus holsatus	0 0	- -	0 0	- -	- -	0 0	-
RT2516	Thoralus cranchii	0 0	- -	0 0	Eualus occultus	- -	0 0	Eulalas c
RT2517	Gastrosaccus spinifer	0 0	- -	0 0	Nyctiphanes couchi	- -	0 0	-
RT2518	Palaemon serratus	0 0	- -	0 0	- longirostris	- -	0 0	-
RT2519	Pontophilus norvegicus	0 0	- -	0 0	- -	- -	0 0	-
RT2520	Pisidia longicornis	0 0	- -	0 0	Liocarcinus spp.	- -	0 0	-
RT2521	Palaemonetes varians	0 0	- -	0 0	- -	- -	0 0	-
RT2522	Pandalus montagui	0 0	- -	0 0	- -	- -	0 0	-
RT2523	Philocheras trispinosus	0 0	- -	0 0	[Crangon] -	[Crangon] -	0 0	-
RT2524	Hippolyte varians	0 0	- -	0 0	- -	- -	0 0	-
RT2525	Pandalina brevirostris	0 0	- -	0 0	- -	- -	0 0	-

Table 14. Summary of the results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR09.

	Differences	
LabCode	Generic	Specific
LB1104	3	3
LB1107	2	5
LB1108	2	5
LB1109	0	3
LB1111	1	6
LB1112	0	1
LB1113	-	-
LB1114	0	4
LB1115	2	4
LB1116	-	-
LB1117	3	6
LB1118	1	1
LB1119	0	0
LB1124	3	4

Key: "-" - No data.

See Section 6 for details.

Table 15. Results from the Own Samples (OS26-28) 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	
LB1101	OS26	69	62.1 - 75.9	PASS	0	0.0	-	0	0.0	-	2174	1960.2 - 2395.8	PASS	0	0.0	-	6.5475	4.9737 - 7.4605	*PASS*	90.0	99.70	PASS	Good
LB1101	OS27	13	11.0 - 15.0	PASS	0	0.0	-	0	0.0	-	160	144.0 - 176.0	PASS	0	0.0	-	0.7711	0.5559 - 0.8339	*PASS*	90.0	100.00	PASS	Excellent
LB1101	OS28	70	63.9 - 78.1	PASS	0	0.0	-	0	0.0	-	926	828.0 - 1012.0	PASS	0	0.0	-	13.2071	10.0562 - 15.0844	*PASS*	90.0	98.92	PASS	Good
LB1102	OS26	7	9.0 - 13.0	Fail	3	27.3	-	1	12.5	-	161	165.6 - 202.4	Fail	21	11.4	-	19.2021	12.9386 - 19.4078	*PASS*	90.0	92.75	PASS	Acceptable
LB1102	OS27	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	48	43.2 - 52.8	PASS	0	0.0	-	0.7808	0.5487 - 0.8231	*PASS*	90.0	100.00	PASS	Excellent
LB1102	OS28	11	9.0 - 13.0	PASS	0	0.0	-	0	0.0	-	224	234.9 - 287.1	Fail	53	20.3	-	9.2569	6.2197 - 9.3295	*PASS*	90.0	91.96	PASS	Acceptable
LB1103	OS26	34	32.4 - 39.6	PASS	1	2.8	-	2	5.7	-	112	104.4 - 127.6	PASS	3	2.6	-	-	-	-	90.0	94.74	PASS	Acceptable
LB1103	OS27	8	6.0 - 10.0	PASS	0	0.0	-	1	12.5	-	36	33.3 - 40.7	PASS	0	0.0	-	-	-	-	90.0	95.89	PASS	Good
LB1103	OS28	12	10.0 - 14.0	PASS	1	8.3	-	0	0.0	-	28	25.2 - 30.8	PASS	1	3.6	-	-	-	-	90.0	96.43	PASS	Good
LB1104	OS26	66	63.9 - 78.1	PASS	4	5.6	-	6	9.0	-	2323	2098.8 - 2565.2	PASS	29	1.2	-	8.8729	6.7916 - 10.1874	*PASS*	90.0	98.82	PASS	Good
LB1104	OS27	82	73.8 - 90.2	PASS	1	1.2	-	12	14.8	-	270	237.6 - 290.4	PASS	3	1.1	-	1.3654	1.0634 - 1.5950	*PASS*	90.0	91.48	PASS	Acceptable
LB1104	OS28	47	45.0 - 55.0	PASS	2	4.0	-	6	12.5	-	321	319.5 - 390.5	PASS	36	10.1	-	1.2871	1.0118 - 1.5178	*PASS*	90.0	90.48	PASS	Acceptable
LB1105	OS26	9	7.0 - 11.0	PASS	0	0.0	-	0	0.0	-	1626	1504.8 - 1839.2	PASS	50	3.0	-	0.8079	0.3159 - 0.4739	*Fail*	90.0	98.48	PASS	Good
LB1105	OS27	19	18.9 - 23.1	PASS	2	9.5	-	0	0.0	-	887	862.2 - 1053.8	PASS	34	3.5	-	1.5693	0.9206 - 1.3808	*Fail*	90.0	96.15	PASS	Good
LB1105	OS28	90	81.0 - 99.0	PASS	0	0.0	-	0	0.0	-	2299	2014.2 - 2461.8	PASS	0	0.0	-	221.2144	178.5253 - 267.7879	*PASS*	90.0	98.62	PASS	Good
LB1106	OS26	10	9.0 - 13.0	PASS	1	9.1	-	0	0.0	-	464	428.4 - 523.6	PASS	12	2.5	-	0.0619	0.0412 - 0.0618	*Fail*	90.0	98.62	PASS	Good
LB1106	OS27	13	11.0 - 15.0	PASS	0	0.0	-	0	0.0	-	118	108.9 - 133.1	PASS	5	4.1	-	0.0300	0.0173 - 0.0259	*Fail*	90.0	98.78	PASS	Good
LB1106	OS28	8	6.0 - 10.0	PASS	0	0.0	-	0	0.0	-	146	136.8 - 167.2	PASS	0	0.0	-	0.0442	0.0238 - 0.0358	*Fail*	90.0	98.00	PASS	Good
LB1107	OS26	27	24.3 - 29.7	PASS	0	0.0	-	2	7.4	-	336	302.4 - 369.6	PASS	4	1.2	-	-	-	-	90.0	98.21	PASS	Good
LB1107	OS27	25	23.4 - 28.6	PASS	1	3.8	-	1	4.0	-	69	64.8 - 79.2	PASS	3	4.2	-	-	-	-	90.0	96.45	PASS	Good
LB1107	OS28	55	49.5 - 60.5	PASS	0	0.0	-	5	9.1	-	384	356.4 - 435.6	PASS	10	2.5	-	-	-	-	90.0	90.77	PASS	Acceptable
LB1109	OS26	15	13.0 - 17.0	PASS	0	0.0	-	0	0.0	-	685	633.6 - 774.4	PASS	59	8.4	-	1.0295	1.0282 - 1.5422	*PASS*	90.0	98.49	PASS	Good
LB1109	OS27	26	23.4 - 28.6	PASS	0	0.0	-	1	3.8	-	198	179.1 - 218.9	PASS	1	0.5	-	2.5392	2.1350 - 3.2024	*PASS*	90.0	97.73	PASS	Good
LB1109	OS28	25	22.5 - 27.5	PASS	0	0.0	-	0	0.0	-	89	79.2 - 96.8	PASS	0	0.0	-	0.6617	0.5938 - 0.8908	*PASS*	90.0	99.44	PASS	Good
LB1110	OS26	10	11.0 - 15.0	Fail	2	15.4	Review	1	9.1	Review	279	295.2 - 360.8	Fail	37	11.3	Reproeess	0.2939	0.1789 - 0.2683	*Fail*	90.0	82.37	Fail	Fail
LB1110	OS27	23	20.7 - 25.3	PASS	0	0.0	-	1	4.3	-	254	234.0 - 286.0	PASS	0	0.0	-	2.3701	0.8303 - 1.2455	*Fail*	90.0	98.44	PASS	Good
LB1110	OS28	19	17.0 - 21.0	PASS	1	5.3	Review	1	5.6	Review	430	402.3 - 491.7	PASS	13	2.9	-	0.9948	0.5139 - 0.7709	*Fail*	90.0	71.38	Fail	Fail
LB1111	OS26	7	6.0 - 10.0	PASS	1	12.5	-	0	0.0	-	25	23.4 - 28.6	PASS	1	3.8	-	-	-	-	90.0	98.04	PASS	Good
LB1111	OS27	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	16	14.0 - 18.0	PASS	0	0.0	-	-	-	-	90.0	100.00	PASS	Excellent
LB1111	OS28	17	15.0 - 19.0	PASS	0	0.0	-	0	0.0	-	26	23.4 - 28.6	PASS	0	0.0	-	-	-	-	90.0	100.00	PASS	Excellent
LB1112	OS26	38	34.2 - 41.8	PASS	0	0.0	-	0	0.0	-	733	656.1 - 801.9	PASS	2	0.3	-	8.1179	6.8259 - 10.2389	*PASS*	90.0	99.45	PASS	Good
LB1112	OS27	20	18.9 - 23.1	PASS	1	4.8	-	1	5.0	-	30	27.9 - 34.1	PASS	1	3.2	-	0.1176	0.1101 - 0.1651	*PASS*	90.0	95.08	PASS	Good
LB1112	OS28	14	12.0 - 16.0	PASS	0	0.0	-	0	0.0	-	56	50.4 - 61.6	PASS	0	0.0	-	0.0833	0.0679 - 0.1019	*PASS*	90.0	100.00	PASS	Excellent
LB1113	OS26	4	2.0 - 6.0	PASS	0	0.0	-	0	0.0	-	3	1.0 - 5.0	PASS	0	0.0	-	5.2919	4.0458 - 6.0686	*PASS*	90.0	100.00	PASS	Excellent
LB1113	OS27	24	21.6 - 26.4	PASS	0	0.0	-	0	0.0	-	23	20.7 - 25.3	PASS	0	0.0	-	0.9814	0.8233 - 1.2349	*PASS*	90.0	100.00	PASS	Excellent
LB1113	OS28	20	18.0 - 22.0	PASS	0	0.0	-	0	0.0	-	23	22.5 - 27.5	PASS	0	0.0	-	0.3212	0.3099 - 0.4649	*PASS*	90.0	96.30	PASS	Good
LB1114	OS26	66	59.4 - 72.6	PASS	0	0.0	-	1	1.5	-	1479	1322.1 - 1615.9	PASS	1	0.1	-	19.4705	14.8942 - 22.3412	*PASS*	90.0	99.46	PASS	Good
LB1114	OS27	31	27.9 - 34.1	PASS	0	0.0	-	0	0.0	-	213	191.7 - 234.3	PASS	0	0.0	-	0.6440	0.4913 - 0.7369	*PASS*	90.0	100.00	PASS	Excellent
LB1114	OS28	15	13.0 - 17.0	PASS	0	0.0	-	1	6.7	-	358	314.1 - 383.9	PASS	0	0.0	-	0.2475	0.1871 - 0.2807	*PASS*	90.0	97.33	PASS	Good
LB1115	OS26	9	7.0 - 11.0	PASS	0	0.0	-	0	0.0	-	16	14.0 - 18.0	PASS	0	0.0	-	1.9084	1.5858 - 2.3788	*PASS*	90.0	100.00	PASS	Excellent
LB1115	OS27	29	26.1 - 31.9	PASS	1	3.4	-	1	3.6	-	323	310.5 - 379.5	PASS	21	6.1	-	11.8054	8.5829 - 12.8743	*PASS*	90.0	96.42	PASS	Good
LB1115	OS28	6	6.0 - 10.0	PASS	2	25.0	-	0	0.0	-	26	26.1 - 31.9	Fail	3	10.3	-	2.1710	1.7225 - 2.5837	*PASS*	90.0	94.55	PASS	Acceptable
LB1116	OS26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-
LB1116	OS27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-
LB1116	OS28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-
LB1117	OS26	19	17.0 - 21.0	PASS	0	0.0	-	0	0.0	-	66	59.4 - 72.6	PASS	0	0.0	-	11.5102	9.1875 - 13.7813	*PASS*	90.0	100.00	PASS	Excellent
LB1117	OS27	17	14.0 - 18.0	PASS	0	0.0	-	0	0.0	-	46	40.5 - 49.5	PASS	0	0.0	-	13.5398	6.6622 - 9.9934	*Fail*	90.0	98.90	PASS	Good
LB1117	OS28	50	45.0 - 55.0	PASS	0	0.0	-	4	8.0	-	542	486.0 - 594.0	PASS	0	0.0	-	45.3422	38.7677 - 58.1515	*PASS*	90.0	98.52	PASS	Good
LB1118	OS26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-
LB1118	OS27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-
LB1118	OS28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-
LB1120	OS26	32	28.8 - 35.2	PASS	0	0.0	-	0	0.0	-	227	223.2 - 272.8	PASS	11	4.4	-	-	-	-	90.0	95.58	PASS	Good
LB1120	OS27	8	8.0 - 12.0	PASS	2	20.0	-	0	0.0	-	43	45.9 - 56.1	Fail	11	21.6	-	-	-	-	90.0	91.49	PASS	Acceptable
LB1120	OS28	6	4.0 - 8.0	PASS	0	0.0	-	0	0.0	-	399	201.6 - 246.4	Fail	4	1.8	-	-	-	-	90.0	70.95	Fail	Fail
LB1121	OS26	21	19.8 - 24.2	PASS	0	0.0	-	3	13.6	-	260	216.9 - 265.1	PASS	1	0.4	-	1.1975	0.8308 - 1.2462	*PASS*	90.0	90.22	PASS	Acceptable
LB1121	OS27	23	20.7 - 25.3	PASS	1	4.3	-	2	9.1	-	57	54.9 - 67.1	PASS	7	11.5	-	1.6623	1.2078 - 1.8116	*PASS*	90.0	90.00	PASS	Acceptable
LB1121	OS28	42	39.6 - 48.4	PASS	1	2.3	-	7	16.3	-	260	234.0 - 286.0	PASS	2	0.8	-	1.8163	1.3162 - 1.9744	*PASS*	90.0	93.85	PASS	Acceptable
LB1123	OS26	24	21.6 - 26.4	PASS	0	0.0	-	0	0.0	-	2143	1926.9 - 2355.1	PASS	5	0.2	-	-	-	-	90.0	99.02	PASS	Good
LB1123	OS27	6	4.0 - 8.0	PASS	0	0.0	-	0	0.0	-	12	10.0 - 14.0	PASS	0	0.0	-	-	-	-	90.0	100.00	PASS	Excellent
LB1123	OS28	9	7.0 - 11.0	PASS	0	0.0	-	0	0.0	-	83	75.6 - 92.4	PASS	1	1.2	-	-	-	-	90.0	99.40	PASS	Good

Table 16. Z-score results for the derived statistics supplied by participating laboratories for the particle size (PS) exercises - PS24 and PS25 - NMBAQC / UK NMMP standards applied.

PS24																	
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	1.19	-1.44	PASS	1.64	-1.37	PASS	1.67	-0.80	PASS	0.65	-0.92	PASS	0.079	0.31	PASS	-
SieveRepAv	3.34	0.30	PASS	2.12	1.77	PASS	2.21	1.86	PASS	0.72	-0.39	PASS	0.116	0.58	PASS	-
LB1104*	1.16	-1.47	PASS	1.5	-2.30	Fail	1.53	-1.46	PASS	0.75	-0.17	PASS	0.070	0.25	PASS	Sand/Sand
LB1107	2.5	-0.42	PASS	1.92	0.46	PASS	1.94	0.55	PASS	0.66	-0.87	PASS	0.110	0.54	PASS	-/-
LB1109	6.32	2.70	Fail	1.86	0.06	PASS	1.87	0.21	PASS	1.03	2.01	Fail	0.428	2.90	Fail	Sand / Fine Sand
LB1113	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1114	2.89	-0.07	PASS	1.73	-0.79	PASS	1.76	-0.33	PASS	0.70	-0.56	PASS	-0.110	-1.09	PASS	Muddy Sand/Sand
LB1115	1.16	-1.47	PASS	1.5	-2.30	Fail	1.53	-1.46	PASS	0.75	-0.17	PASS	0.070	0.25	PASS	Sand/Sand
LB1116	2.55	-0.34	PASS	2.1	1.64	PASS	2.15	1.58	PASS	-0.71	-11.56	Fail	-0.150	-1.38	PASS	Muddy Sand/-
LB1117	4.57	1.29	PASS	-	-	Deemed Fail	1.59	-1.17	PASS	1.26	3.81	Fail	0.250	1.58	PASS	light brown mixed sand/light brown v.slightly muddy mixed sand
LB1118	4.82	1.49	PASS	1.88	0.20	PASS	1.94	0.55	PASS	0.89	0.92	PASS	-0.19	-1.68	PASS	Medium sand (small clay fraction)/as pre
LB1122	1.98	-0.80	PASS	1.80	-0.33	PASS	1.65	-0.87	PASS	0.77	-0.02	PASS	-0.070	-0.79	PASS	Coarse sand/-

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

PS25																
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	80.20	0.75	PASS	6.25	0.44	PASS	6.14	1.40	PASS	2.22	1.64	PASS	-0.021	-0.84	PASS	Mud/Sandy mud
SieveRepAv	80.65	0.89	PASS	6.86	1.54	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1104*	78.75	0.29	PASS	5.57	-0.77	PASS	5.42	-0.84	PASS	1.90	-0.39	PASS	-0.100	-2.62	Fail	-
LB1107	66.4	-3.68	Fail	3.83	-3.87	Fail	4.33	-4.24	Fail	1.66	-1.94	PASS	0.42	9.14	Fail	-/-
LB1113	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1114	78.86	0.32	PASS	5.79	-0.38	PASS	5.70	0.03	PASS	1.92	-0.27	PASS	0.030	0.32	PASS	sM/sM
LB1115	78.75	0.29	PASS	5.57	-0.77	PASS	5.42	-0.84	PASS	1.90	-0.39	PASS	-0.1	-2.62	Fail	Mud/Sandy mud
LB1116	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1117	76.46	-0.45	PASS	5.53	-0.84	PASS	5.50	-0.59	PASS	1.97	0.06	PASS	0.020	0.10	PASS	Dk bwn,fluid,sl.sandy mud + org frag/sl.grav,sandy,mud
LB1118	81.56	1.19	PASS	5.93	-0.13	PASS	5.78	0.28	PASS	1.80	-1.04	PASS	0.080	1.45	PASS	Mud/Sandy mud
LB1122	72.25	-1.80	PASS	-	-	Deemed Fail	-	-	Deemed Fail	2.02	0.38	PASS	-0.030	-1.03	PASS	Fine silt/-

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

Table 17. Comparison of the overall performance of laboratories in the Own Sample exercises from 1995/96 to 2004/05 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
11 (2004/05)*	26, 27, 28	51	3	94

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

Table 18. Comparison of each laboratory's performance in the Own Sample exercises from Scheme year 02 (1995/96) to Scheme year 11 (2004/05).

	Scheme Year 2	Scheme Year 3			Scheme Year 4			Scheme Year 5			Scheme Year 6			Scheme Year 7			Scheme Year 8			Scheme Year 9			Scheme Year 10			Scheme Year 11		
LabCode	**OS01**	**OS02**	**OS03**	**OS04**	**OS05**	**OS06**	**OS07**	**OS08**	**OS09**	**OS10**	**OS11**	**OS12**	**OS13**	**OS14**	**OS15**	**OS16**	**OS17**	**OS18**	**OS19**	**OS20**	**OS21**	**OS22**	**OS23**	**OS24**	**OS25**	**OS26**	**OS27**	**OS28**
LB1101	99.44	98.39	100	100	100	99.31	99.75	98.59	98.59	100	98.14	66.26	88.78	96.95	99.09	98.95	98.99	84.62	91.09	99.37	99.24	98.67	96.48	97.92	99.37	99.7	100	98.92
LB1102	98.1	98.48	100	88.89	100	100	98.67	96.39	89.13	100	99.16	97.92	95.87	98.98	85.19	72.15	95.65	57.98	91.2	98.06	94.44	-	89.55	83.33	73.75	92.75	100	91.96
LB1103	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	88.89	43.32	83.72	99	94.6	85.11	94.74	95.89	96.43
LB1104	100	100	100	100	98.88	100	100	97.46	100	83.33	89.29	95.65	94.48	76.92	92.82	95.43	92.68	96.68	97.43	96.91	93.74	91.23	93.29	97.35	94.12	98.82	91.48	90.48
LB1105		73.15	68.7	96.12	-	-	-	93.33	90.46	93.1	87.15	98.56	98.24	95.9	92.57	91.22	-	-	-	86.15	98.43	96.78	95.23	96.92	95.97	98.48	96.15	98.62
LB1106	98.54	-	-	-	99.68	99.87	90.2	91.73	43.85	35.71	97.27	98.7	97.56	94.12	97.4	98.08	96.94	95.4	98.84	-	-	-	98.26	96.21	98.72	98.62	98.78	98.00
LB1107	-	-	-	-	95.75	92.56	96.37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	98.21	96.45	90.77
LB1108	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	-	-	-	-	-	-
LB1109	92.83	94.19	99.04	97.96	99.45	99.03	95.72	100	99.66	99.79	100	70	75.56	83.58	77.62	99.71	98.39	95.87	100	100	100	95.24	96.85	90.26	96.55	98.49	97.73	99.44
LB1110	97.17	98.93	96.58	98.4	100	98.8	98.04	91.32	98.8	98.35	99.23	90.38	98.13	99.21	91.1	96.22	99.55	93.98	95.24	99.07	96.69	98.14	96.68	92.27	77.38	82.37	98.44	71.38
LB1111	-	-	-	-	-	-	-	-	-	-	-	-	-	92.09	96.52	82.22	91.5	99.34	97.22	84.94	76.92	80.46	89.16	99.83	96.18	98.04	100	100
LB1112	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.68	91.36	93.63	98.66	96.44	92.46	100	98.46	98	99.45	95.08	100
LB1113	-	-	-	-	60	62.5	83.82	87.5	93.5	94.12	74.21	76.6	70.98	74.02	81.74	78.47	78.95	90.36	100	70.25	94.68	78.57	98.11	100	100	100	100	96.3
LB1114	97.94	-	92.08	-	74.34	94.64	96.43	71.03	96.48	99.17	98.32	97.65	96.3	96.67	98.21	96.96	92.41	96.74	89.86	98.54	98.2	99.54	99.6	97.85	98.86	99.46	100	97.33
LB1115	97.91	96.3	85.8	89.82	75.29	95.44	74.89	73.3	97.33	93.01	73.02	99.5	90.5	93.13	94.57	90.32	96.67	94.12	90.39	94.27	96.43	96.77	83.74	90.72	96.77	100	96.42	94.55
LB1116	-	-	-	-	-	-	-	-	-	-	97.92	84.85	97.29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1117	-	-	-	-	89.9	-	-	-	-	-	95.8	49.56	67.28	72.73	89.52	70.87	55.86	71.28	90.77	72.58	98.56	99.61	95.89	95.82	97.62	100	98.9	98.52
LB1118	-	-	-	-	-	-	-	95.08	53.66	60.42	-	-	-	-	-	-	84.32	100	80.31	-	-	-	93.7	83.94	91.23	-	-	-
LB1119	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	96.89	72.07	56.22	-	-	-	-	-	-	-	-	-
LB1120	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.5	92.07	100	95.58	91.49	70.95
LB1121	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.22	90.00	93.85
LB1122	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1123	98.18	100	83.33	95.77	100	100	94.74	-	-	-	98.21	97.79	100	-	-	-	-	-	-	97.52	99.43	92.86	98.76	92.31	99.5	99.02	100	99.40
LB1124	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Key: Shaded cells = 'Fail' flag irrespective of subsequent remedial action.
- = no data / not participating; See Section 6 for details.

Figures

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS24. Seven samples analysed by sieve and seven samples analysed by Laser.

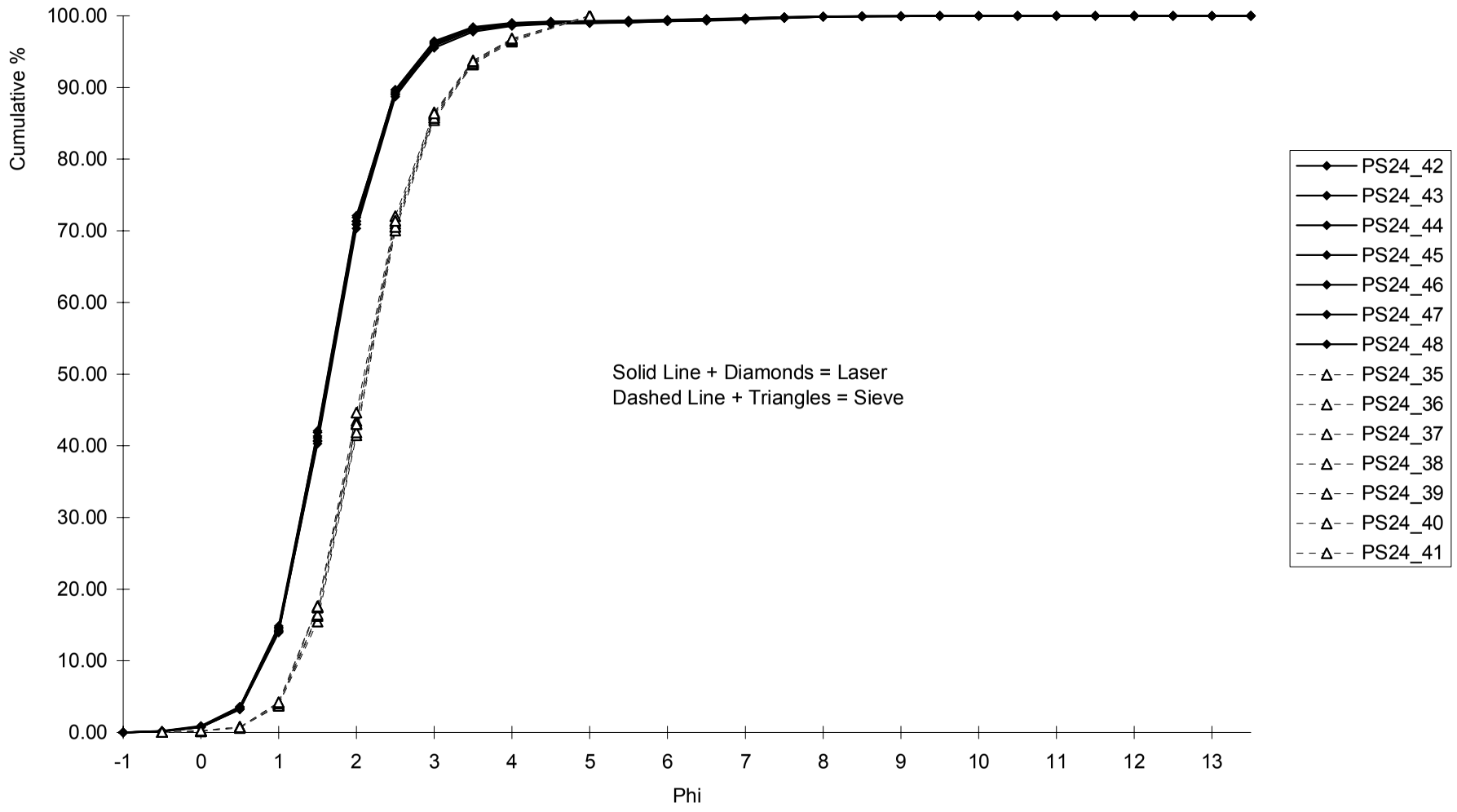


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS25. Seven samples analysed by sieve and seven samples analysed by Laser.

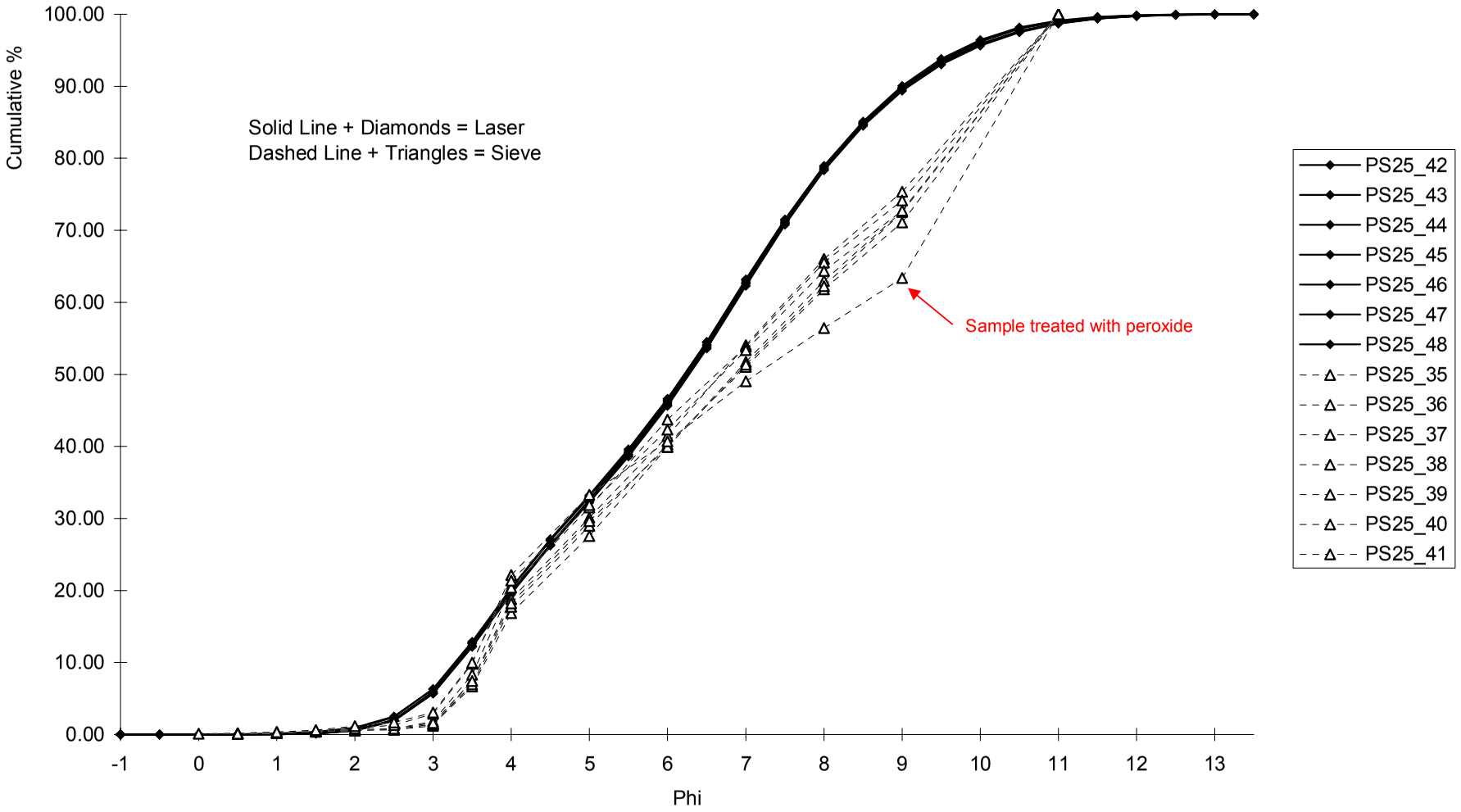


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS24.

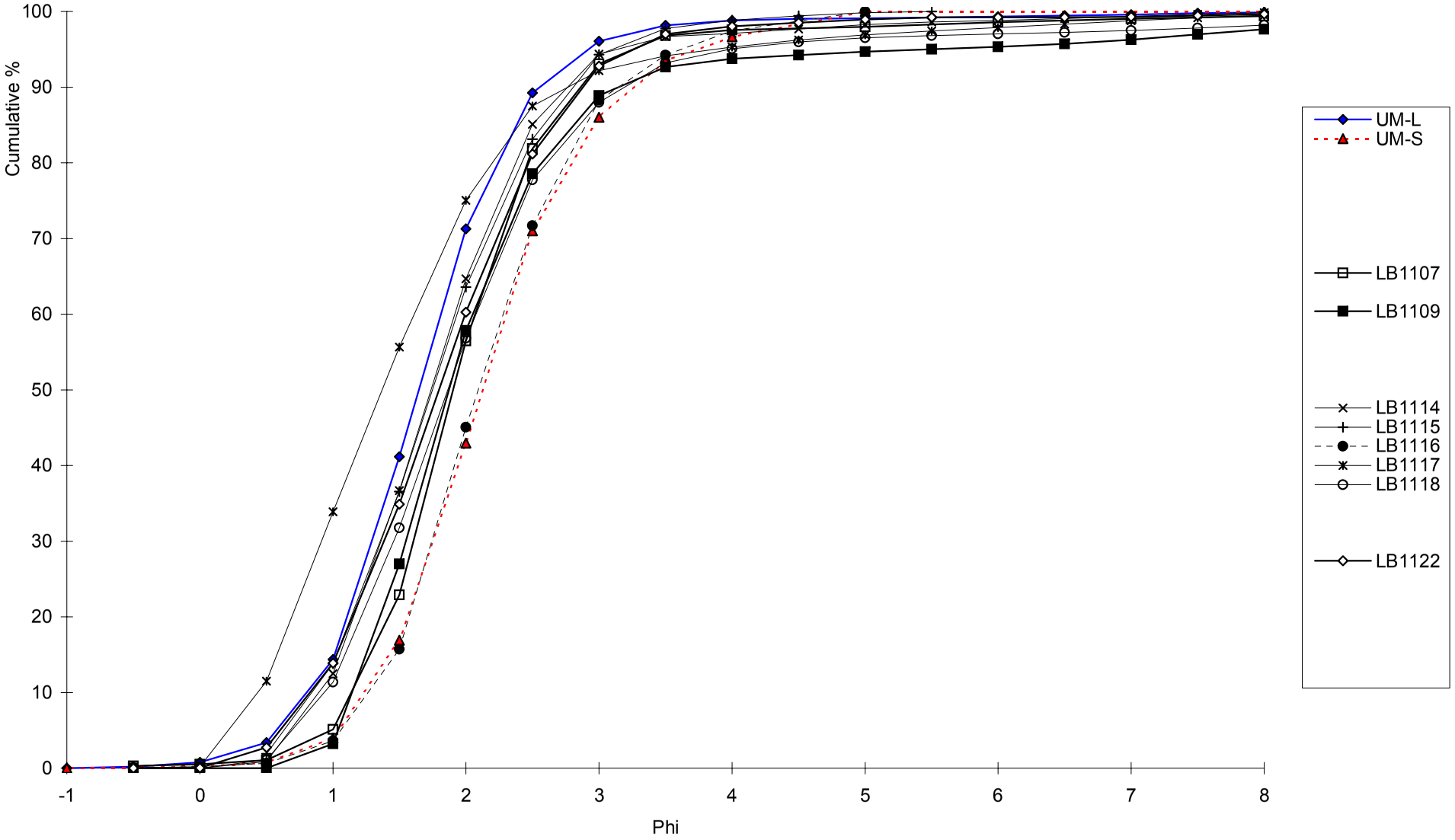


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS25.

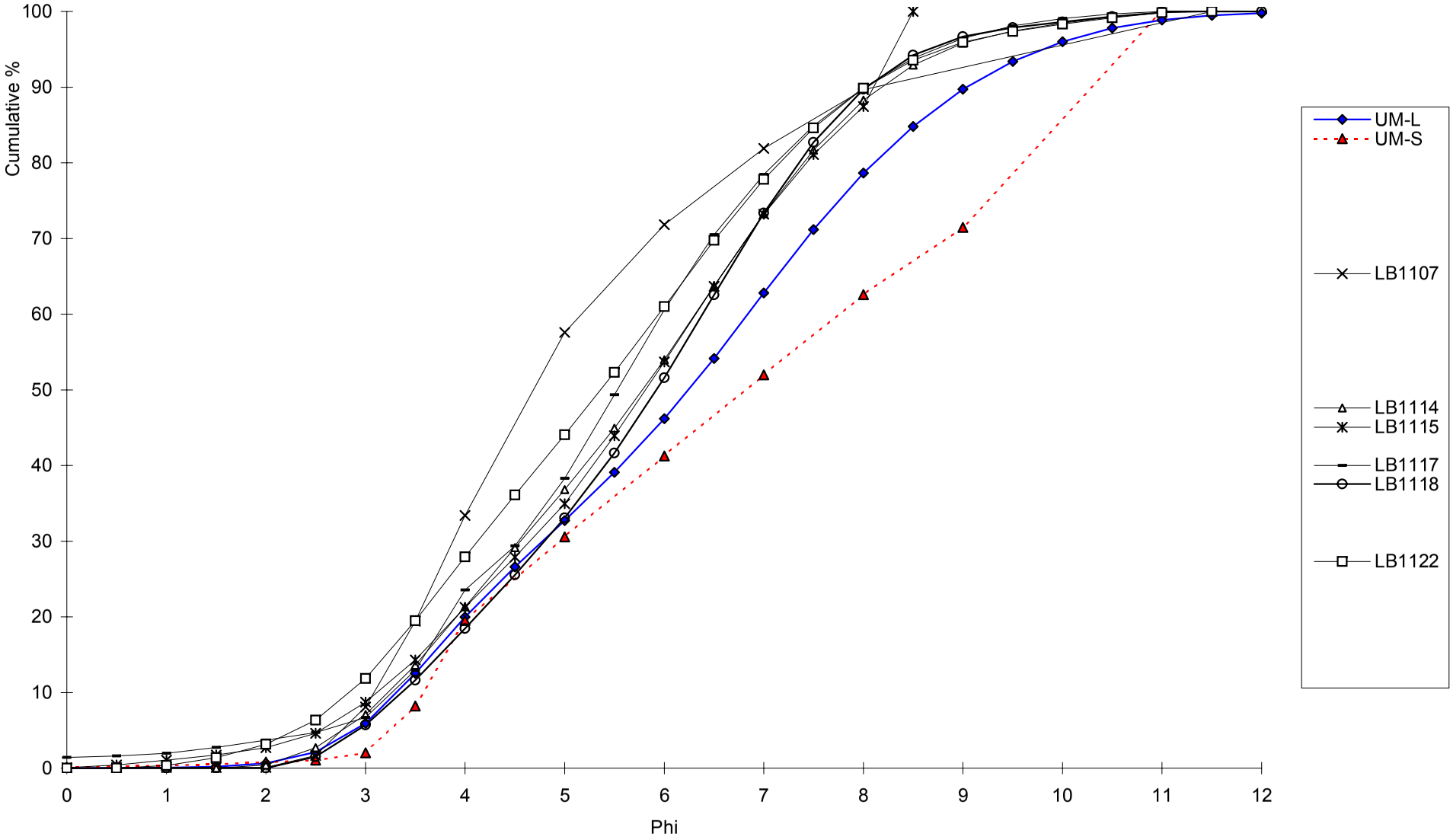


Figure 5. Z-scores for PS24 derived statistics (replicated data not displayed).

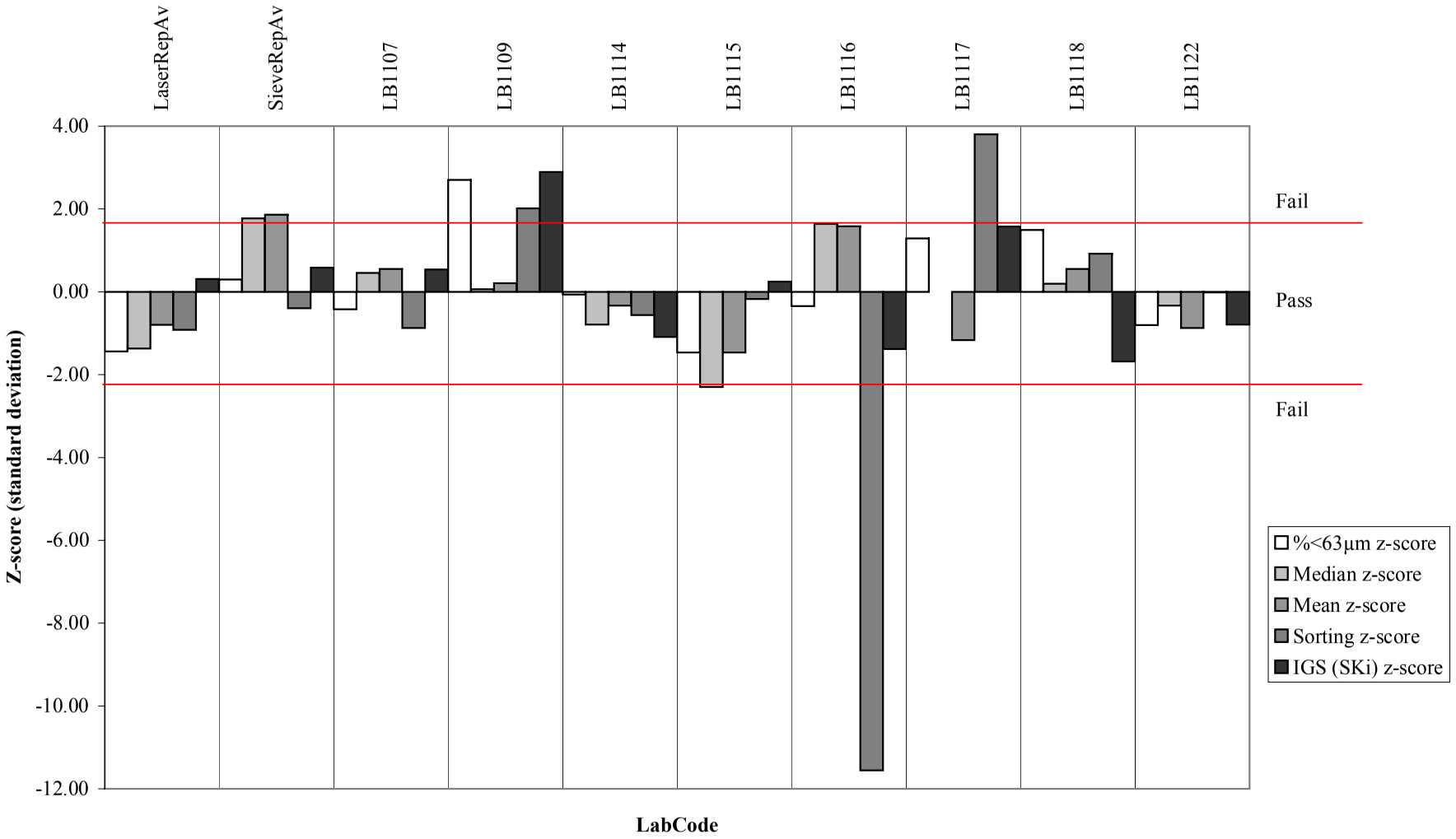


Figure 6. Z-scores for PS25 derived statistics (replicated data not displayed).

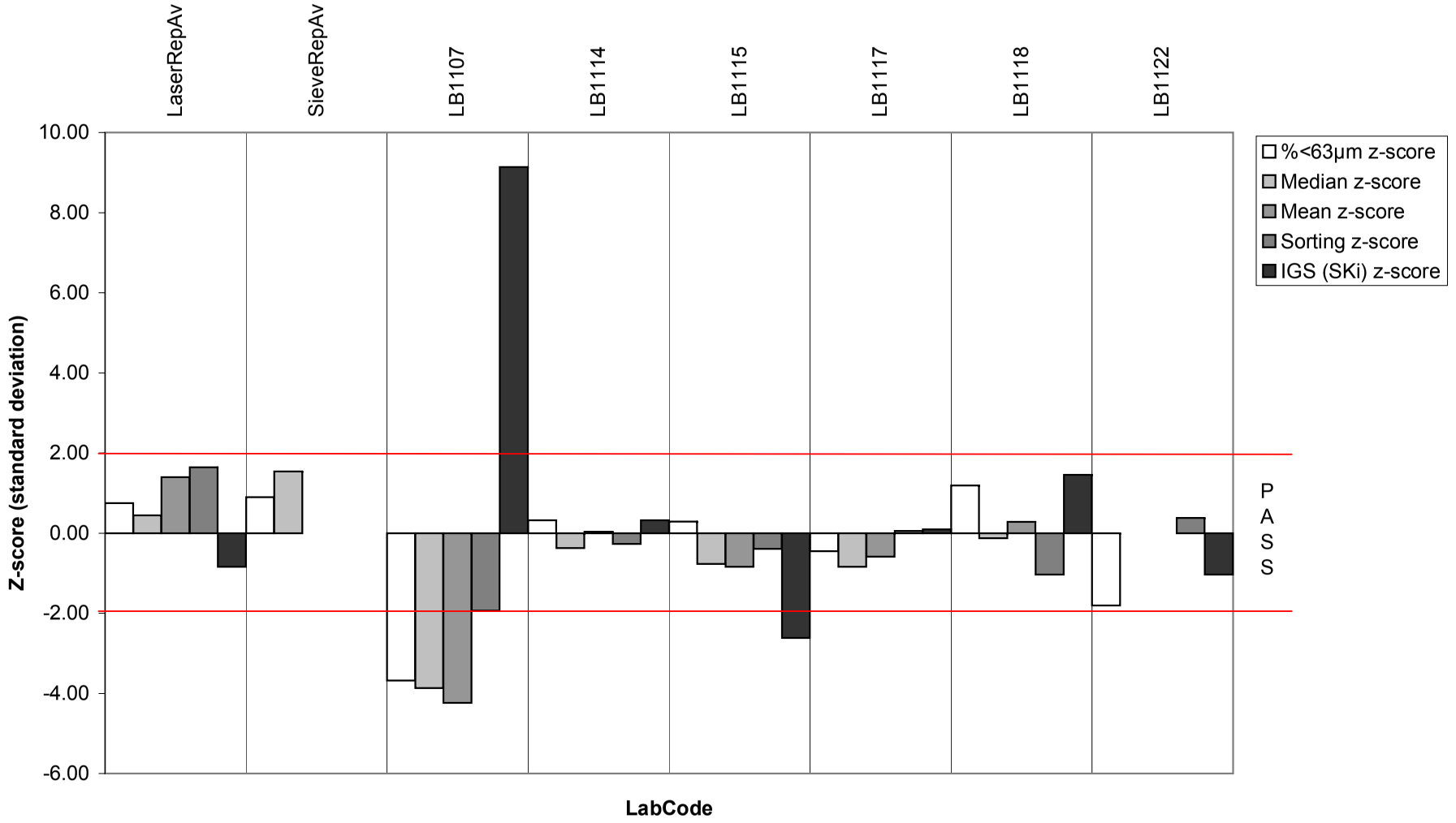


Figure 7. The number of differences from the AQC identification of specimens distributed in RT24 for each of the participating laboratories. Arranged in order of increasing number of differences.

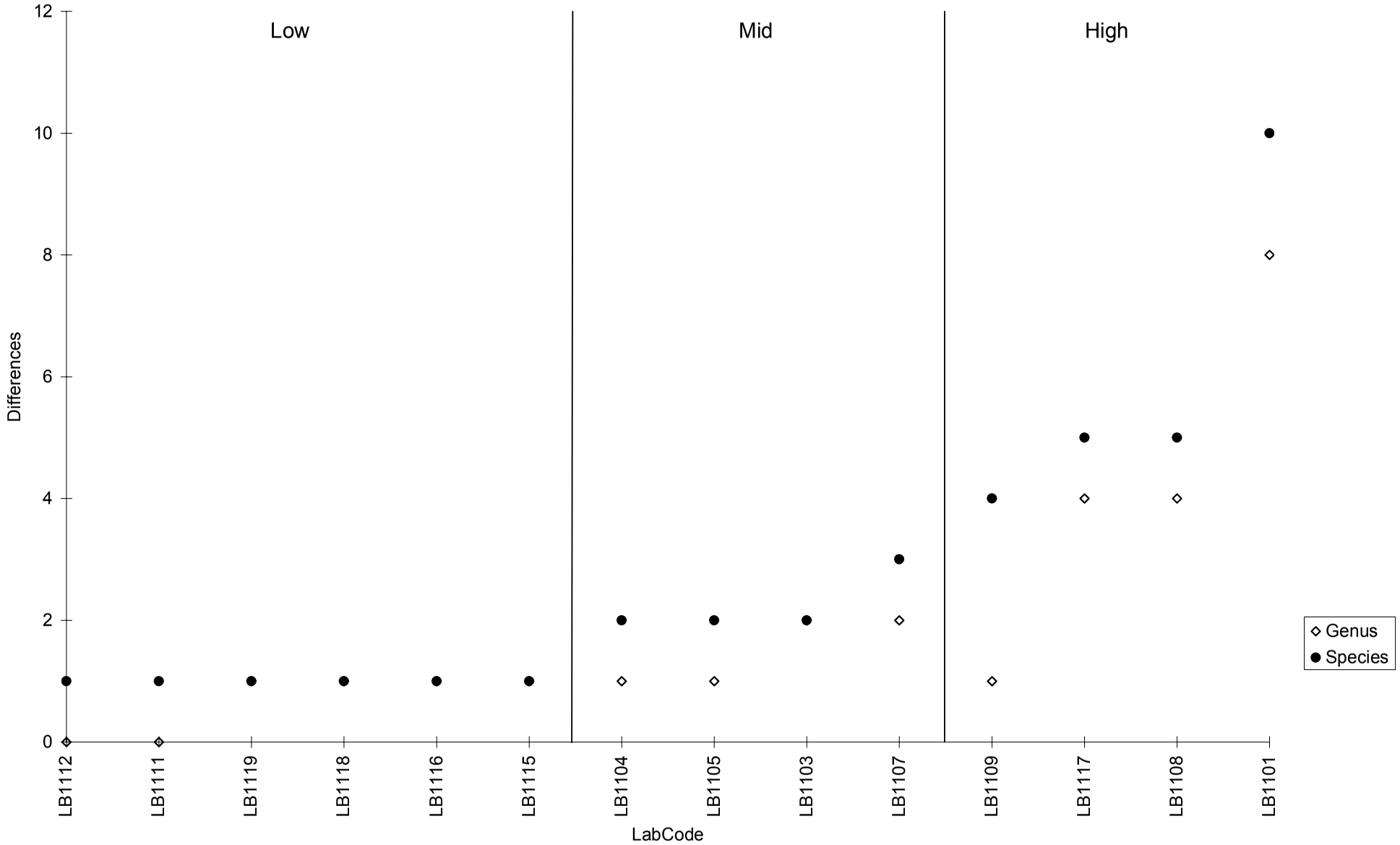
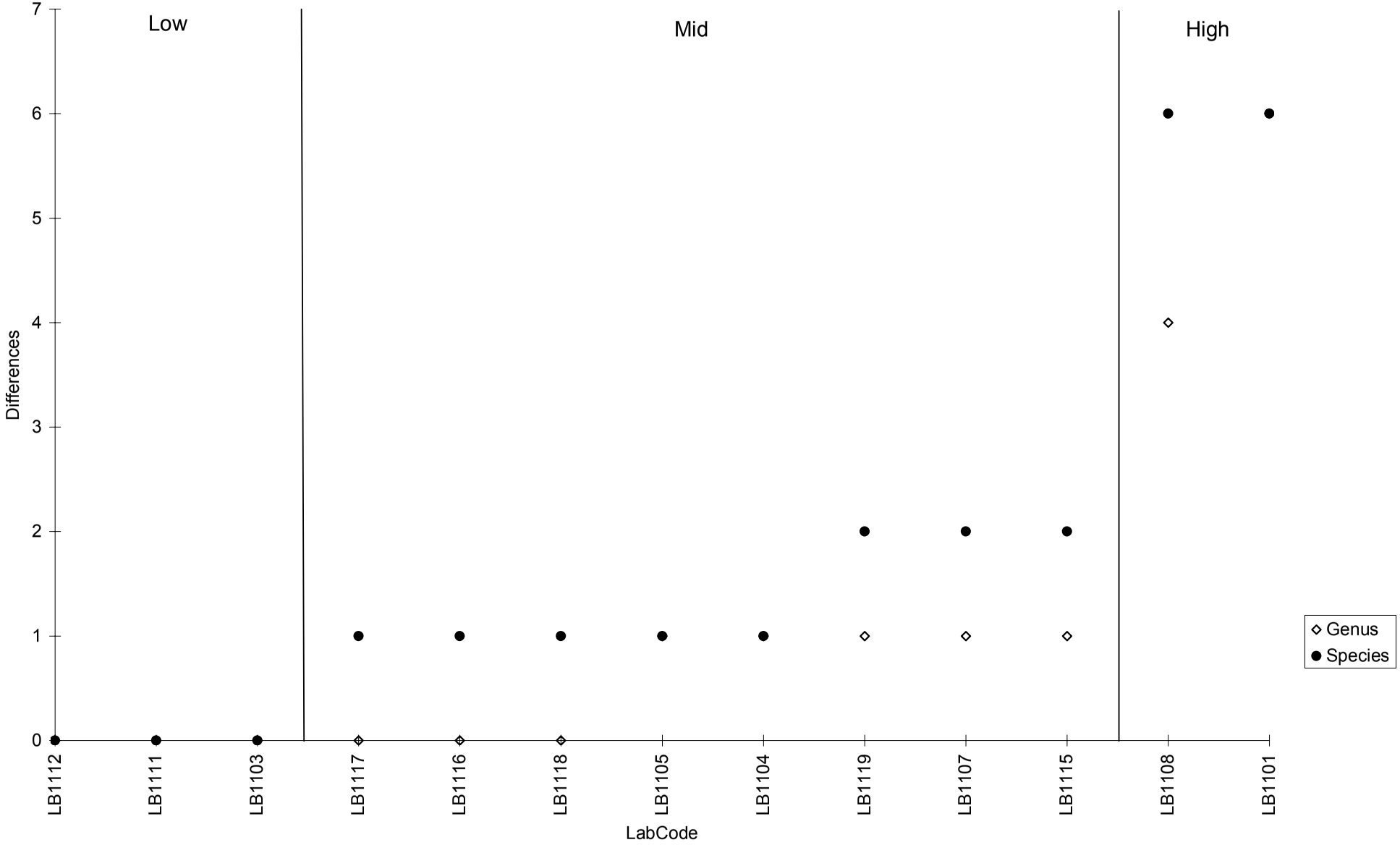


Figure 8. The number of differences from the AQC identification of specimens distributed in RT25 for each of the participating laboratories. Arranged in order of increasing number of differences.



Appendices

Appendix 1.

Participant Laboratory Reference Collection exercise (LR)

Objectives:

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

Protocol:

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

Preparation:

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

Timescale:

Please send specimens to Unicomarine Ltd. by 5th November 2004. Results and specimens will be returned as soon after receipt as practicable.

Appendix 2.

1. Description of Scheme Standards

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

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

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

1.1 Own Sample Standards

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

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

1.1.1 Primary Performance Targets

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

1.1.1.1 Extraction/Sorting efficiency - Total taxa target

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

1.1.1.2 Extraction/Sorting/Enumeration efficiency - Total individuals target

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

1.1.1.3 Biomass estimation accuracy - Total biomass target

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

1.1.1.4 Bray-Curtis comparison target

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

1.1.2 Secondary Performance Targets

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

1.1.2.1 Extraction efficiency - Taxa in residue target

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

1.1.2.2 Identification accuracy – Taxonomic errors target

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

1.1.2.3 Extraction efficiency - Individuals in residue target

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

1.1.2.4 Enumeration efficiency – Enumeration of extracted individuals target

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

1.1.3 Overall Sample Flag

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

100% BCSI	**Excellent**
95 - <100	**Good**
90 - <95	**Acceptable**
85 - <90	**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

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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.