BEQUALM - NMBAQC

Biological Effects Quality Assurance in Monitoring

National Marine Biological Analytical Quality Control

Annual Report

Year 12 - 2005/2006

National Marine Biological AQC Coordinating Committee – August 2007

BEQUALM

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report - Year 12 - 2005/2006

Section A – Report from the NMBAQC Co-ordinating Committee

Section B – Supplementary Report on Invertebrate, Particle Size, & Fish Components from the Scheme Contractor: Unicomarine Ltd.

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Section C – Supplementary Report on the Phytoplankton Component from the Marine Institute of Ireland, (PHY-ICN-05-MI3).

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SECTION A – Report from the NMBAQC Co-ordinating Committee

1. SCHEME REVIEW AND FUTURE ROLE.

The BEQUALM / NMBAQC scheme completed Year 12 in 2005/06. The scope of the scheme has changed significantly with the forthcoming implementation of 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 all data assessments and submissions. Hence, in addition to its role for the UK NMMP benthic programme, the NMBAQC group now has a remit to lead on quality assurance for all the WFD marine biological quality elements: invertebrates, transitional water fish, phytoplankton, macroalgae, and angiosperms. These new components are being phased into the scheme and the composition of the NMBAQC Coordinating Committee now reflects this (See Appendix 6.1). A workshop on fish and epibiota sampling took place in Year 11, followed by the first fish Ring Test circulation in Year 12 (February 2006). The phytoplankton component also commenced in Year 12 with the first phytoplankton identification and enumeration Ring Test organised by the Marine Institute, Galway, Ireland in September 2005. Plans were put in place to launch a macroalgal Ring Test in Year 13.

The UK NMMP programme came under review in 2005 with consequent changes both in its organisational infrastructure under DEFRA (Department of the Environment, Food, and Rural Affairs), its sampling strategies, and in data archiving. In 2006 the programme was re-titled the Clean Seas Environmental Monitoring Programme (CSEMP) and a new national data archiving facility was launched: the Marine Environment Monitoring and Assessment National database (MERMAN). The MERMAN database will store all former NMMP data, and new CSEMP data, including benthic invertebrate data, particle size data, along with data on trace metals, organic contaminants, nutrients and bioeffects. This data will subsequently be available to ICES/OSPAR (International Council for Exploration of the Sea/ Oslo-Paris Commission).

2. SCOPE OF THE SCHEME - YEAR 12 – 2005/06

The twelfth year of the NMBAQC Scheme continued assessment of the Invertebrate/Particle Size component and saw the introduction of new components on Fish and Phytoplankton.
Module exercises and workshops for Year 12:

Invertebrate / Particle Size Components:

a) Macrobenthic (MB) Module - 1 exercise - 1 contractor supplied macrobenthic sample.

b) Own Sample (OS) Module - 3 exercises - 3 participant supplied macrobenthic samples.

c) Particle Size (PS) Module – 2 exercises - 2 contractor supplied sediment samples.

d) Ring Test (RT) Module (Invertebrates) – 2 exercises
1 contractor supplied ring test of 25 "problematic" invertebrate species.
1 contractor supplied ring test of 25 diverse invertebrate species.

e) Lab Reference (LR) Module – 1 exercise – 1 set of 25 different invertebrate reference specimens.

f) Invertebrate Taxonomic Workshop for Beginners – Unicomarine Ltd. Letchworth, Oct, 2005.
The workshop programme is shown in Appendix 6.2.

Fish Component:

a) Ring Test (RT) Module (Fish) – 1 exercise
1 contractor supplied ring test of 25 marine fish species

Phytoplankton Component:

a) Cell Enumeration Ring Test – 2 contractor supplied samples of cultured phytoplankton cells with high and low cell concentrations.

b) Identification Ring Test – 1 contractor supplied set of 14 micrograph images of a diverse range of phytoplankton species.

c) Phytoplankton Ring Test Workshop – Marine Institute, Galway, March 2006.

The Invertebrate, Particle Size, and Fish samples were sent out to participants by Unicomarine Ltd at staggered intervals during the year with set time scales for sample or data returns. The Phytoplankton Cell Enumeration and Identification Ring Tests were circulated in September 2005 by the Marine Institute, Galway, Republic of Ireland. This was the first phytoplankton ring test operated under the BEQUALM /NMBAQC banner but the Marine Institute has organised a number of previous phytoplankton ring tests. These are summarised in below.

Marine Institute (MI) Phytoplankton (PHY) Intercomparison (ICN) exercises.

PHY-ICN-04-MI1	September 2004	External Proficiency Test. Ring Test Round 1. (6 labs participated)
PHY-ICN-04-MI2	October 2004	Internal Intercomparison Galway- Bantry
PHY-ICN-05-MI1	June 2005	Internal Intercomparison Galway- Bantry
PHY-ICN-05-MI2	September 2005	Internal Intercomparison Galway- Bantry
PHY-ICN-05-MI3	November 2005	External Proficiency Test. Ring Test Round 2. (First under NMBAQC/BEQUALM)

3. ISSUES ARISING

A detailed breakdown of the operation of the scheme components for Year 12 is contained in the supplementary reports in Sections B and C, and includes conclusions and recommendations. Only the main issues arising from scheme circulations are re-iterated below along with other issues raised in committee discussions.

3.1 Standard Protocols: Results to date show that the scheme requires the development of a standard protocol outlining precise processing requirements for benthic invertebrate samples. This should include details on extraction, enumerations, and identification processes and a review of the biomass procedure. The biomass procedural revision needs to consider how the biomass data will ultimately be utilised. The original concept for collecting biomass data was to facilitate construction of Species-Abundance-Biomass curves. However, to date no such analyses have been produced for NMMP reports. A standard operating procedure for particle size analysis is also needed as the particle size exercises have demonstrated variations of analytical results due to different methodologies.

3.2 Standard Literature: The scheme has produced a draft guide to taxonomic literature for marine invertebrates and fish. Participants should utilise this guide and feedback any information on amendments to the list. The scheme would benefit from standard literature lists for phytoplankton and macroalgae.

3.3 Participation: The number of participating labs for Year 12 in the Invertebrate/PSA component was 28, an increase from 24 in Year 11. Details of individual labs and their participation levels is

shown in Appendix 6.3. The Particle Size exercises were undertaken by 8 labs. The first Fish Ring Test was offered free of charge, and was taken up by 13 labs. The first Phytoplankton Ring Test attracted 10 labs, with 21 participating analysts.

There are a number of small consultancies and single-person operatives within the UK who undertake analysis of benthic invertebrate samples. Many of these do not join the scheme because of the costs. The committee aims to encourage these operatives to participate in some scheme modules by allowing them to band together to help offset the individual costs. However the logistics of this proposal have yet to be determined.

All participating labs in Year 12 were from the United Kingdom or Ireland. There has been little interest, to date, from neighbouring European countries. It is hoped that the incoming Water Framework Directive, with its imperative to utilise quality controlled data might encourage more participation from European countries within the WFD North East Geographical Implementation Group (NEAGIG) area. The development of the MarBEF (Marine Biodiversity and Ecosystem Functioning) EU Network of Excellence has helped raise the profile of quality assurance for marine ecological data (see website: **www.marbef.org**). However some quality control groups, similar to NMBAQC, are already operating in some EU states e.g. the Quality Assurance Panel of the German Marine Monitoring Programme (See Appendix 6.4).

3.4 NMMP Redesign: In 2005 a sub-group of the NMMP Working Group was tasked with redesigning the UK NMMP. For simplicity, the sub-group first considered the Scottish component of the NMMP. The next stage would be to roll out the programme across the rest of the UK.

The main focus of the NMMP has so far been on investigating temporal trends in contaminants at selected sites around the UK, and any associated trends in benthic communities. The power (performance) of the NMMP contaminant data to detect change was often poor, due to 'snap-shot' sampling (i.e. all samples taken at the same time and place) which fails to control local temporal and spatial variation in contaminant concentrations. There was a clear need to redesign the NMMP to improve the power (performance) of the contaminant monitoring programme.

New de-clustered NMMP sites were set up within the Scottish region for contaminant monitoring in 2005. It was agreed that the benthic fauna monitoring sites would remain unaltered in 2005 in order to complete a 4 year monitoring run (2002-05) since the last NMMP report. The new Scottish de-clustered sites for benthic macrofauna were adopted in 2006, with the expectation that de-clustered sites would subsequently be introduced across the UK NMMP programme. For further details of the rationale behind the re-design of the NMMP, see Appendix 6.5.

3.5 New Infrastructure: In 2005 DEFRA proposed a new structure for delivering the UK Marine Assessment and Monitoring Strategy with the creation of the Marine Assessment Policy Committee (MAPC). Under this, the Marine Assessment and Reporting Group (MARG) was established absorbing the role of the Marine Environment Monitoring Group (MEMG), with the aim of assessing all marine monitoring data, including that from the National Marine Monitoring Programme (NMMP). In the proposed new structure the AQC groups report to a Protocols Group, which then reports to MARG. The Protocols Group will define the methods/standards and AQC required across all programmes. Integrated assessments will be the focus of MARG and the operational groups will implement and report on their own programmes.

The original NMBAQC was set up to service the NMMP soft bottom sediment monitoring. The group has now been asked to expand its remit through BEQUALM to cover all WFD marine biological communities. The first meeting of MARG took place in Feb.2006 and recommended the concept of having three thematic groups (in addition to the Protocols Group). These were Clean and Safe Seas, Healthy and Biodiverse Seas, and Productive Seas. The NMMP sits under the Clean and Safe theme and later in 2006, the National Marine Monitoring Programme (NMMP) was renamed the Clean and

Safe Environment Monitoring Programme (CSEMP). A minute of the first MARG Meeting including summaries of the work areas assigned to the thematic groups is shown in Appendix 6.6.

3.6 WFD Fish Monitoring: Steve Coates from the Environment Agency was co-opted onto the committee to lead on fish. There has been little quality assurance to date on fish sampling or analysis. With the forthcoming commencement of WFD monitoring of transitional (estuarine) fish communities, a number of new fish teams are being created within UK competent monitoring authorities, and it is important to standardise methodologies. The EA are developing a Mini-Otter Trawl standard operating procedure to compliment the existing Beam Trawl method in the NMMP Green Book. Investigations are underway with a view to producing an updated version of the Wheeler's 1978 Key to Fishes of Northern Europe which is now out of print. The new guide could be in either ring-bound A4 format and/or an electronic CD-ROM and would have updated nomenclature, new line drawings of additional species as well as a selection of colour images.

3.7 WFD Phytoplankton Monitoring: Joe Silke from the Marine Institute (MI), Galway, Ireland was co-opted onto the committee to lead on phytoplankton. The MI operates a Marine Environment & Food Safety Service to provide essential scientific advice and a range of marine environmental monitoring services to help ensure Irish seafood products meet approved standards. This includes a national Harmful Algal Bloom **(**HABS) monitoring service that warns producers and consumers of concentrations of toxic plankton in Irish coastal waters that could contaminate shellfish or cause fish mortalities.

HABS accreditation requires intercomparison/proficiency tests with two circulations per annum testing cell counts of dominant species. These exercises are also appropriate for WFD phytoplankton monitoring. The MI has organised five phytoplankton intercomparison exercises up until the end of 2005 (see under Scope of Scheme)). The first of these to come under the banner of BEQUALM/NMBAQC was PHY-ICN-05-MI3 in November 2005 with a follow-up workshop held in Galway on 13th March 2006. The full report of PHY-ICN-05-MI3 is included in Section C. Additional exercises are planned. There is a need to liaise with other European organisations involved in phytoplankton QA such as the Helcom/ICES Phytoplankton Expert Group who held a Workshop and Training Course on Phytoplankton, at Helsingor, Sweden in September 2005.

4. SUBMISSION AND FLAGGING OF NMMP SAMPLE DATA.

a) Invertebrate data

Over the last 12 years of the NMBAQC scheme invertebrate data has been submitted by NMMP labs to the UK NMMP database operated by the Environment Agency. In Scheme Year 2 (1995/96) pass/fail criteria were introduced for Own Samples. Flags were initially attached to all samples, indicating sample data had not been validated. Following completion of the AQC process and achievement of pass levels the data flags were then removed for the relevant laboratories.

The committee decided to alter the application of the pass/fail criteria for the Own Sample exercise from scheme Year 8. Data flags are 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	Fail - Poor – Remedial action suggested
<85% BCSI	Fail - Bad – Remedial action required

The nomenclature for grades 85-90% and <84% has been modified in Year 12 from "Poor" and "Fail" to "Fail – Poor" and "Fail – Bad" to emphasize that any samples <90% are regarded as failures.

Where samples do not achieve the required standards (*i.e*. Acceptable or above) then remedial action is proposed for the failing sample along with its associated site replicates from the same NMMP sampling year. All other NMMP samples from the relevant laboratory (for the same sampling year) remain flagged until completion of requested remedial action.

The NMBAQC Committee has produced guidelines for remedial action (see Appendix 6.7). Specific details of appropriate remedial action for individual laboratories may be determined by the committee if necessary. Those labs submitting data to the NMMP database set MUST complete the remedial action and re-submit samples for audit, if required. **Data flags will only be removed from all the site replicates once a PASS has been achieved for all audited samples.** Non-NMMP laboratories will have remedial action recommended, although completion of such is optional.

A guidance note was produced in Year 11 concerning procedural details for 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 (see Appendix 6.8)**.**

In Year 12, nineteen labs participated in the OS exercise, submitting fifty-seven samples for audit. The grading of the samples for Years 8 – 12 is shown below. The percentage of samples achieving Pass level in Years 02-12 is shown in Section B (Table 17).

Status	**Year 8**	**Year 9**	**Year 10**	**Year 11**	**Year 12**
Excellent	3	2	4	10	10
Good	17	23	28	29	34
Acceptable	15	8	11	11	7
Fail - Poor	1	2	3	0	4
Fail - Bad	9	9	5	3	2
Total	**45**	**44**	**51**	**54**	**57**

Review of flagged samples and sites – Years 11 and 12.

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. Where one or more samples submitted by a lab fail then all samples from that laboratory for that year remain flagged until remedial action is completed. This policy was re-iterated in minutes of the committee meeting of 8th Sept. 2005.

For Year 11, flagging of specific samples and sites, mostly for NMMP sampling year 2003, was shown in Appendix 6.5 of the Year 11 Annual Report. In that report flagging was applied on a sample/site basis and non-audited samples were deemed valid by default. Of the 2003 samples, only 2, analysed by "Lab C", failed to achieve acceptable grades. Remedial action has still not been completed on these samples. Under the criteria in the paragraph above, all of the 2003 sites analysed by "Lab C" should have remained flagged, rather than non-audited samples being "deemed validated" as shown in the Year 11 report. (However, it could be argued that samples from site 270 Off Seaham should be excepted and validated, as the replicate selected from this site for OS27 achieved a Good grade.) It is evident that **the failure of a lab to carry out remedial action has significant consequences. In Year 11, the 2 failed samples from Lab C result in 14 sites (= 70 samples) remaining flagged. Thus nearly one quarter of the 56 NMMP 2003 sites for which data was presented for audit, remain flagged**. Some of the merits and demerits of a applying a "one out –all out" approach to sample flagging were discussed in the Year 11 report. It is clear that if all NMMP

labs completed remedial action as they are required to do then these disproportionate effects would not occur.

For Year 12 the NMMP data matrices submitted for Own Sample audits are shown in Appendix 6.9. Most of the data is derived from the previous sampling year, 2004, but also includes some data from 2002, 2003, and 2005, depending on whether labs are behind or ahead with their analysis schedules. Data was presented for 61 NMMP sites, although the NMMP Green Book (v.9, Dec.2005) cites 76 benthos sites. However, 7 additional sites are shown for Lab J for which no data was supplied.

In Year 12, 4 of the audited NMMP samples failed to achieve acceptable grades. Of these, 3 have since passed following completion of remedial action and all the associated 2004 sites and samples from labs A, B, and L have now been validated and the flags removed. Remedial action remains outstanding for one NMMP site from Lab C1 and all the 2004 samples from this lab remain flagged.

Lab B2 supplied 2004 data for selection of samples for audit but failed to supply the actual samples. Hence all 2004 samples from this lab remain flagged. Lab J supplied neither a 2004 data set nor any samples and all their 2004 samples must remain flagged. Lab C supplied data and samples but failed to provide the associated sample residues. It appears the 2004 NMMP sample residues from this lab have been inadvertently discarded. Thus the sample audits are incomplete and all their samples remain flagged for the meantime. In addition to this, samples from another 2 sites (Labs G & I) were compromised and data from these sites cannot be validated.

Although performance in the sample audits is generally satisfactory, **it is of considerable concern that so many NMMP samples remain flagged. For year 12, 28 sites (= 140 samples) currently remain flagged. This is unacceptably high, considering the huge expense involved in collection and analysis of samples.**

Laboratories responsible for NMMP samples must make more effort to fulfil their duties all the way from the field to the database. They are obligated to:

a. **Ensure samples are not compromised**

b. **Provide requested NMMP data sets**

c. **Supply requested samples and residues for audit**

d. **Complete all required remedial action**

e. **Complete post-audit data amendments**

f. **Ensure the data is submitted to the Merman database**

b) Particle Size data

Two PS exercises (PS26 & PS27) were distributed in Year 12. Twelve laboratories participated but only eight returned 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.** There has been no AQC flagging mechanism operating for sediment data on the NMMP database nor cross-referencing of sediment data and benthos data held on the database system.

Submission of PSA data to the NMMP database has been inconsistent between laboratories and has often been limited to median particle size and percentage silt & clay (along with %organic carbon). With the introduction of the new MERMAN database in 2006, the PSA submission format has been revised and now comprises five derived parameters (median particle size, mean particle size, sorting coefficient, inclusive graphic skewness, and kurtosis) as well as the raw data as percentage volumes within full phi size classes. The derived parameters can be calculated using spreadsheet programmes, such as GRADISTAT on Excel. However as a variety of calculating spreadsheets have been employed by different labs, there is a **need to clarify the precise formulae to be utilised for the PSA parameters** and for labs to check that these match what they are using.

5. FINANCIAL SUMMARY – Year 12 - 2005/2006

NMBAQC funds Year 11 carried forward	*£20,346.31*
Year 12 Scheme Exercise Costs	£53,670.04
Year 12 additional participant costs MBx2 and OSx4	£4,531.24
Total Year 12 Scheme Exercise Costs	**£58,201.24**
Total Year 12 Scheme income	**£59,751.25**
(Government Agencies	£33,422.50)
(External laboratories	£26,328.75)

Additional Scheme Development Costs Year 12

NMBAQC Beginners Taxonomic workshop	£3,850.00
(Workshop Income	£2,450.00)
NMBAQC subsidy for workshop (above)	£1,400.00
First Fish Ring Test (fully subsidised)	£2,750.00
Taxonomic Literature Database	£2,700.00
NMMP data QA	£1,607.40
NMBAQC funds Year 12 carried forward	***£17,866.77***

Additional Scheme Development Costs agreed to be carried to Year 13

NMBAQC Web site revamp	£2,500.00
Addition of images to Ring Test circulations	£2,900.00

6. APPENDICES

Appendix 6.1 – NMBAQC Coordinating Committee – Year 12 – 2005/06.

Matt Service (Chair)	DARD(NI) - (Department of Agriculture & Rural Development (Northern Ireland), Agriculture, Food and Environmental Science Division.
Myles O'Reilly (Contract Manager)	SEPA South East (Scottish Environment Protection Agency)
Tim Mackie (Secretary)	EHS, DOENI (Environment & Heritage Service, Department of Environment, Northern Ireland)
Alison Miles (Finance Manager)	Environment Agency (National Marine Service, Peterborough)
Will Musk* (Replaced Nigel Proctor Sep.05)	IECS (Institute of Estuarine & Coastal Studies. University of Hull)
Clare Greathead	FRS / SEERAD (Fisheries Research Services, Scottish Executive Environment & Rural Affairs Department)
Keith Cooper	CEFAS (Centre for Environment, Fisheries and Aquaculture Science)
Jenny Hill** (Replaced by Jane Hawkridge May 05)	JNCC (Joint Nature Conservation Committee, Peterborough)
Paolo Pizzolla** (Replaced Jenny Hill March 06)	JNCC (Joint Nature Conservation Committee, Peterborough)
Carol Milner	SEPA North Area, Dingwall
Francis O'Beirn	Marine Institute of Ireland, Galway
Joe Silke (Phytoplankton Lead) (Co-opted May 05)	Marine Institute of Ireland, Galway
Steve Coates (Fish Lead) (Co-opted May 05)	Environment Agency

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

Appendix 6.2 – Programme for Invertebrate Taxonomic Workshop for Beginners.

Day		Discussion / Demonstration / Practical	Aims	Session Leader
Monday 10th Oct. 2005	1:00pm	Arrival. Laboratory set-up.	Prepare laboratory equipment for practical sessions.	David Hall
	1:30pm	Introduction. General information. Lab. rules (H&S issues). Q&A session.	Welcome participants. Outline timetable / daily structure. Give history of Unicomarine and facilities. Present pub & food guide.	Martin Dyer & David Hall
	2:00pm	Demonstration - Sample Processing.	Requirements, SOP's and best practice for sample analysis.	David Hall
	2:20pm	Practical - Phyla recognition (1).	Review starting position of knowledge.	David Hall
	3:00pm	Demonstration - Porifera, Cnidaria, Platyhelminthes, Nematoda, Nemertea, Priapulida, Sipuncula & Echiura.	Introduce the major features / terminology used for these Phyla. Show major literature required for identification.	David Hall
	4:45pm	Practical – Examination of reference material.	Obtain familiarity with the major identification features. Gain experience of identification.	David Hall
Tuesday 11th Oct. 2005	9:00am	Demonstration - Annelida.	Introduce the major features / terminology used for these Phyla. Show major literature required for identification.	David Hall
	pm	Practical – Examination of reference material.	Obtain familiarity with the major identification features. Gain experience of identification.	David Hall
	4:30pm	Practical – test specimens.	Allow identification of unnamed material.	David Hall
Wednesday 12th Oct. 2005	9:00am	Demonstration - Mollusca.	Introduce the major features / terminology used for these Phyla. Show major literature required for identification.	Tim Worsfold
	pm	Practical – Examination of reference material.	Obtain familiarity with the major identification features. Gain experience of identification.	Tim Worsfold
	4:30pm	Practical – test specimens.	Allow identification of unnamed material.	Tim Worsfold
Thursday 13th Oct. 2005	9:00am	Demonstration - Crustacea.	Introduce the major features / terminology used for these Phyla. Show major literature required for identification.	Chris Ashelby
	pm	Practical – Examination of reference material.	Obtain familiarity with the major identification features. Gain experience of identification.	Chris Ashelby
	4:30pm	Practical – test specimens.	Allow identification of unnamed material.	Chris Ashelby
	7:30pm	Workshop Dinner – location, menu and prices TBA	-	-
Friday 14th Oct. 2005	9:00am	Demonstration – Bryozoa, Phoronida, Echinodermata & Tunicata.	Introduce the major features / terminology used for these Phyla. Show major literature required for identification.	David Hall
	am	Practical – Examination of reference material.	Allow identification of unnamed material.	David Hall
	pm	Practical - Phyla recognition (2).	Review of knowledge.	David Hall
	pm	Discussion - Summary of week. Q&A session. Departure.	Distribute/collect workshop feedback forms.	David Hall

Appendix 6.3 - NMBAQC Scheme - Participating Organisations – Year 12

a) Invertebrate/ PSA Component

AstraZeneca Ltd., (Brixham Environmental Laboratory)

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

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

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

Ecological Consultancy Services (Ecoserve) Ltd., Dublin

Ecomaris Ltd. (Huntingdon, Cambridgeshire)

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

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

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

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

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

Fish Vet Group, Inverness

FRS, Aberdeen (Fisheries Research Services, Scottish Executive Environment & Rural Affairs Department)

Fugro Survey Ltd. (Environmental Division, Great Yarmouth)

Hebog Environmental Ltd. (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)

Appendix 6.3 Contd. - NMBAQC Participants - Scheme Year 12

b) Laboratory Participation Levels*

Year 12 (2005/06) Labs.	MB	OS	PS	RT (Invert)	RT (Fish)	LR
AstraZeneca Ltd.		✓		✓	✓	✓
CEFAS	✓	✓	✓	✓	✓	✓
CMACS		✓				✓
DARDNI	✓	✓	✓	✓	✓	✓
Ecoserve Ltd		✓		✓		
Ecomaris Ltd.		✓				
EHS (Environment & Heritage Service).	✓	✓	✓	✓	✓	✓
Emu Ltd.		✓	✓	✓	✓	✓
EA NE – Newcastle	✓	✓	✓	✓		✓
EA NW – Warrington		✓				
EA Anglian – Lincoln		✓				
EA SE Thames – Camberley		✓		✓	✓	
EA Southern - West Malling		✓		✓	✓	✓
EA SW – Blandford		✓		✓	✓	✓
EA Wales – Cardiff		✓		✓	✓	✓
EA EMAP-Marine - Peterborough	✓	✓	✓	✓	✓	✓
Environmental Services (Inst. of Aquaculture)				✓		✓
ERT (Scotland) Ltd.	✓	✓	✓	✓	✓	✓
Fish Vet Group				✓		
Fisheries Research Services		✓	✓			
Fugro Survey Ltd.		✓				
Hebog Environmental Ltd.	✓			✓	✓	
IECS - University of Hull	✓	✓	✓	✓	✓	✓
Marine Ecological Surveys Ltd.		✓				
SAMS Research Services Ltd.	✓		✓	✓		✓
SEPA North Area	✓	✓		✓	✓	✓
SEPA South-east Area	✓	✓	✓	✓	✓	✓
SEPA South-west Area	✓	✓	✓	✓	✓	✓
TOTALS:	**12**	**24**	**12**	**21**	**16**	**18**

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

* Table shows participation sign-up. Some labs did not complete some of their exercises.

c) Other Contributing Organisations

Other organisations contribute funding to the NMBAQC 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)

Appendix 6.4 - German Marine Monitoring Programme

Umwelt Bundes Amt
für Mensch und Umwelt

Quality Assurance Panel of the German Marine Monitoring Programme of the North and Baltic Sea at the Federal Environmental Agency of Germany

Petra Schilling
Laboratory of Water Analysis, Federal Environmental Agency, P.O. Box 330022, D-14191 Berlin, Tel. +49 30 8903 2647,
Fax +49 30 8903 2285, http://www.umweltbundesamt.de/wasser/themen/q-blmp.htm

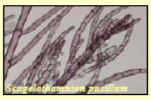
Working Group Biology

In the framework of the German Marine Monitoring Programme of the North and Baltic Sea (GMMP) there is a national working group on quality assurance which is supported by the Quality Assurance Panel at the Federal Environmental Agency. This group is divided in a chemical and a biological subgroup. The main task of the Quality Assurance Panel (QA panel) of the GMMP is to set up and further develop a quality management system on the basis of EN ISO/IEC 17025 for all laboratories which are involved in the GMMP. Therefore the biological Working Group of the QA panel regularly organises interlaboratory comparisons for biological parameters like phytoplankton, chlorophyll *a* and macrozoobenthos. Participation in these comparisons is mandatory for all laboratories involved in the GMMP. If there are enough capacities, additional laboratories can take part upon request. The aim of these activities is to check and improve the quality of the marine monitoring data as well as to optimise statistical methods for data assessment.

Monitoring pro-gramme	North Sea	Baltic Sea
Monitoring of eutrophication	Phytoplankton Zooplankton Macrophytobenthos Macrozoobenthos	Phytoplankton Zooplankton Macrophytobenthos Macrozoobenthos
Population monitoring	Phytoplankton and Zooplankton time series at permanent stations Macrozoobenthos (Transects) Macrophytobenthos	Phytoplankton and Zooplankton time series at permanent stations Macrozoobenthos (Transects) Fishes Breeding birds Migrating birds
Monitoring of contaminats in biota	Mussels, Fishes, *Fucus*, Sea bird eggs (organic pollutants, heavy metals)	Mussels, Fishes, Sea bird eggs (organic pollutants, heavy metals)
Monitoring of biological effects of contaminants	Fish and fish embryos (fish diseases, liver histopathology, nodules in the liver, malformations)	

Biological parameters of the GMMP	North Sea	Baltic Sea
Phytoplankton	Variety of species, Abundance, Biomass, Key species	Variety of species, Abundance, Biomass, Dominant species, Toxic species, Key species
	Chlorophyll a	Chlorophyll a, Phaeophytin
Macroalgae	Area covered	Variety of species, Abundance, Biomass
Angiosperms/ eel gras	Area covered	Variety of species, Abundance, Biomass
Zooplankton	Variety of species, Abundance	Variety of species, Abundance, Biomass
Benthic invertebrate fauna	Variety of species, Abundance, Biomass	Variety of species, Abundance, Biomass
Fishes		Stock monitoring of perch (Perca fluviatilis) Quantity of hauls, Abundance, Biomass

Phytoplankton, Macrophytobenthos

Phytoplankton interlaboratory comparisons:

- ***Determination and counting of 4 selected species from cultured algae***
  Supply of the ring test material: West Coast Centre for research and technology (FTZ), Büsum
  number of participants: 10
- ***Determination of 20 selected species of the North Sea and Baltic Sea via Photographs***
  Supply of the ring test material: Institute of fresh water und waste water biology (IFA.), Hamburg
  number of participants : 10
- ***Determination of species and their abundance in a natural phytoplankton sample of the North Sea***
  Supply of the ring test material: West Coast Centre for research and technology (FTZ), Büsum
  number of participants : 12
- ***Comparison of Chlorophyll-a determinations***
  Supply of the ring test material: University of Rostock, Institute of Biological Sciences, Marine Biology
  number of participants : 11

Phytoplankton workshops:

1st workshop: 30.03. – 02.04.1998, Institute of Oceanography (IFM) Kiel
Small naked flagellates

2nd workshop: 16.11. – 18.11.1998, West Coast Centre for research and technology (FTZ) Büsum
Species that are difficult to determine

3rd workshop: 18.09. – 22.09.2000, Biological Station Hiddensee
Taxonomy of blue-green algae and coccal green algae of the Baltic Sea

4th workshop: 13.01. – 17.01.2003, Wadden Sea Station Sylt (AWI)
Determination and taxonomy of marine dinoflagellates

Macrophytobenthos workshops:

1st workshop: 28.05. – 01.06.2001, Field Station Maasholm (IFM Kiel),
Taxonomy of marine macrophytes and their importance for the monitoring in the framework of the international marine conventions

2 nd workshop:11.04. – 15.04.2005, Biological Anstalt Helgoland (AWI-BAH)
Methods of macrophytobenthos monitoring in the context of the GMMP and the EU-WFD including exercises of identification of marine macrophytes, part 1: hard bottom monitoring

3rd workshop: 20.06. – 24.06.2005, Biological Station Hiddensee (University Greifswald)
Methods of macrophytobenthos monitoring in the context of the GMMP and the EU-WFD including exercises of identification of marine macrophytes, part 2: soft bottom monitoring

Macrozoobenthos

Makrozoobenthos interlaboratory comparisons:

- ***Determination of 25 selected macrozoobenthos species***
  Supply of the ring test material: Aqua-fact International Services, Ltd. Irland
  number of participants: 11
- ***Determination of selected macrozoobenthos species of the North Sea and Baltic Sea***
  Supply of the ring test material: University of Rostock, Institute of Biological Sciences, Marine Biology
  number of participants: 13
- ***Determination of selected macrozoobenthos species in a natural like sample of the western part of the Baltic Sea***
  Supply of the ring test material: University of Rostock, Institute of Biological Sciences, Marine Biology
  number of participants: 16


Macrozoobenthos workshops:

1st workshop: 23.03.-26.03.1998 Institute of Applied Ökology Neubroderstorf (IfAÖ)
Polychaeta

2nd workshop: 28.09.-01.10.1998 Institute of Applied Ökology Neubroderstorf (IfAÖ)
Amphipoda

3rd workshop: 22.03. – 26.03.2004 MARILIM, Kiel
Mollusca, Polychaeta, Oligochaeta

Documentation of methods: 1999 – pilot video on the sampling of macrozoobenthos

Appendix 6.5 - Rationale for NMMP Redesign

Rob Fryer, Ian Davies, Alistair McIntosh, Colin Moffat, Lynda Webster (FRS Lab. Aberdeen) & Judy Dobson, Brian Miller (SEPA).

Background

The main focus of the NMMP has so far been on investigating temporal trends in contaminants at selected sites around the UK. The power (performance) of the NMMP is acceptable for metals in sediment and shellfish, but is poor for metals in fish and for PAHs and PCBs in fish, sediment and shellfish. The poor power is partially due to 'snap-shot' sampling – all samples taken at the same time and place – which fails to control local temporal and spatial variation in contaminant concentrations. There is a clear need to redesign the NMMP to improve the power (performance) of the contaminant monitoring programme.

Other reasons for redesigning the NMMP include

- integrating the contaminant, biological effects and benthic components of the NMMP
- informing management of the status of UK coastal waters (the NMMP currently only informs on specific sites, not water bodies)
- responding more flexibly to local circumstances, e.g. adding contaminants of local interest, prioritising contaminants of local concern, and adjusting sampling protocols to suit local needs
- accommodating the changing elements to be reported in the future, e.g. with the WFD focusing on ecological status and using elements such as phytoplankton, macroalgae and angiosperms

A sub-group of the NMMP WG was tasked with redesigning the NMMP. For simplicity, the sub-group has first considered the Scottish component of the NMMP. The next stage is to roll out the programme across the rest of the UK.

This document presents proposals for monitoring sediment and fish in Scottish coastal waters. Proposals for shellfish monitoring are still under development and will be presented later. MEMG are asked to consider these proposals and approve them (with any modifications) for implementation in January 2005.

Guiding principals behind the redesign

Move towards sampling regions or water bodies, rather than specific sites, to generate more useful management information and to improve power (by controlling local spatial variation).

Each determinand / matrix combination will have one of the following priorities:

- full coverage – done everywhere
- partial coverage – not necessary to do everywhere, but mandatory where there is a known pressure, and sufficiently covered at a meta-region level (e.g. Scotland) to satisfy OSPAR JAMP/CEMP and other regulatory / management requirements
- voluntary – up to the monitoring organisation

Use sediments to inform on status (i.e. typical concentrations) and trends (in the medium-term of 10-20 years) in each region.

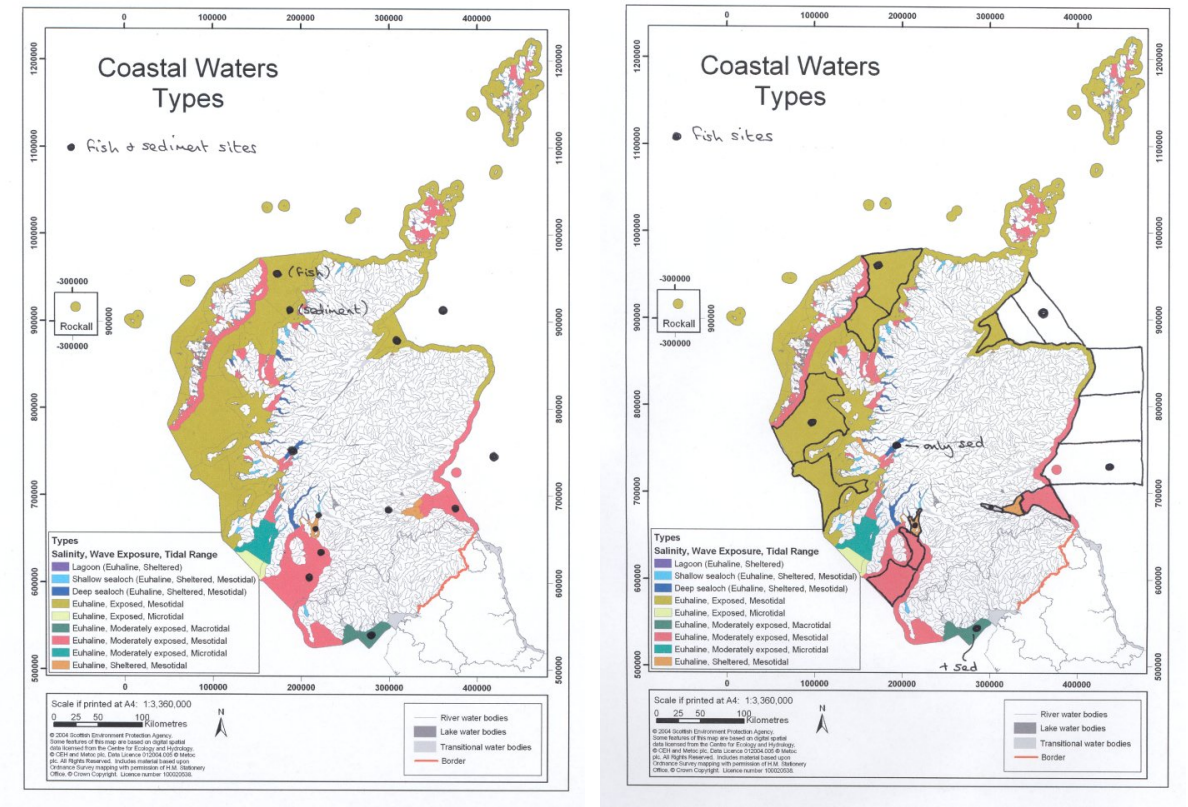
Contaminant monitoring in fish, on its own, is only likely to be of use informing on the status of Scottish coastal waters, where metal concentrations are typically close to background and PCB concentrations are high, variable and going nowhere. An important reason for measuring contaminants in fish is to provide supporting information for biological effects monitoring. It is also necessary to satisfy OSPAR requirements. (Trends in biota can be addressed using shellfish.)

Appendix 6.5 Contd. - Rationale for NMMP Redesign

PCB monitoring is expensive and has particularly poor power. PCBs are no longer being discharged into the environment. PCB monitoring should be reduced and viewed as long-term (> 20 years).

Sampling redesign

The left-hand map shows the current NMMP monitoring sites. The right-hand map shows how the revised NMMP might look (some fine detail is still to be resolved.)



Scottish coastal waters will be divided into regions. At present, these will be the Forth, East Coast, Moray Firth, North Minch, South Minch, and the Clyde (Figure 2). Other regions (e.g. Orkney, Shetland, and Fladen Ground) can be added later as required / resources allow.

Regions will be divided into strata, some based on WFD water bodies, some on hydrographically defined regions, others for geographical convenience to ensure good coverage (Figure 2). Sediment samples will be taken from each region using either a stratified random design or a fixed station design (with a random initial choice of stations). Sampling across a region will control local spatial variation. Both types of design will inform on trends and status by strata and by region. Stratified random designs are typically less powerful than fixed station designs, but are more robust. The number of samples per stratum will be flexible, but a minimum of five samples per stratum should give reasonable power (for metals and PAHs).

Typically, one fish monitoring area will be chosen in each region. Each fish monitoring area will be contained within one stratum, but will be larger than the current fish monitoring areas. This should make it easier to get fish and to control local spatial variation.

Appendix 6.5 Contd. - Rationale for NMMP Redesign

The number of samples will be flexible, but should be sufficient to provide enough tissue and to give adequate precision. At present, there is no strong basis for changing from current practice: e.g. five pools of five.

Alkylated PAHs in sediment, flame retardants in sediment and fish liver and a broader range of metals in fish liver will be added to the NMMP suite in line with the changing demands of e.g. OSPAR.

The following table gives the priority for each determinand / matrix combination

	Sediment (mandatory)	Fish (desirable)
metals	full coverage	partial coverage
parent PAHs	full coverage	n/a
alkylated PAHs	voluntary[2]	n/a
CBs	partial coverage[1]	partial coverage[1]
flame retardants	voluntary[2]	voluntary
benthic data	partial coverage	n/a
biological effects	n/a	partial coverage

[1]Only 2 sediment samples per stratum and only 2 pools of fish liver per area will be analysed for CBs – this provides long-term surveillance monitoring at relatively low cost.

[2]May be upgraded to partial coverage in the near future to accommodate demands of e.g. OSPAR

To ensure sufficient coverage of Scottish waters it is currently intended that, of the partial coverage and voluntary groups:

- CBs in sediment will continue to be measured in all regions
- biological effects will be measured in all fish samples
- benthic data will be collected in the Forth and Clyde (by SEPA)
- metals in fish muscle will be measured everywhere
- metals and CBs in fish liver, alkylated PAHs in sediment, and flame retardants in sediment and fish liver will be measured in all areas except the Forth and Clyde (by FRS)

Other issues

The new design will run in parallel with the old NMMP design for three years, at least in the regions monitored by FRS. This will allow calibration between the old and new time series. In one stratum of the Forth, the revised sediment sampling programme actually reinstates monitoring done before 1999, so calibration is less necessary.

Extra fields will need to be added to the NMMP database to record the new sampling information / design correctly.

Sediment samples from Loch Linnhe and sediment and fish samples from the Solway will continue to be collected as before, and will be reviewed later.

Data collected from the new design require more complicated methods of analysis. Fortunately, OSPAR assessment techniques exist for analysing length stratified fish data, which can be adapted to analysing geographically stratified sediment data. OSPAR MON colleagues should push the full implementation of the OSPAR assessment techniques within the OSPAR assessment framework.

Appendix 6.6 - Minute of 1st MARG Meeting

1. The first meeting of MARG (Marine Assessment and Reporting Group) was held at Institute of Marine Engineering Science and Technology, Mooregate, London on 2 February 2006.

2. The meeting was chaired by Beth Greenaway (BG) from Defra

3. The meeting was attended by Bill Turrell, Peter Holmes, Jim McKie and Colin Moffat from Scotland together with representatives from CEFAS, Defra, DTI, JNCC, EA, IACMST/GOOSAG, Met Office, Welsh Assembly and MDIP.

4. The meeting was addressed by a representative of IMarEST who gave a summary of the organisation, its history and details of the World Maritime Technology Conference (www.wmtc2006.com) to be held in London 6 – 10 March 2006.

5. Updated details of MAPC (the senior policy committee) and MARG were distributed.

6. BG provided a brief resume of the 1st meeting of the Marine Assessment Policy Committee (MAPC) which had taken place in December 2005 (SEERAD was represented at this meeting by Liam Kelly and Colin Moffat). There is a clear desire to ensure that the meeting is attended by senior policy leads from across the UK.

7. BG summarised the outcome of the MARG Workshop on the UK Marine Monitoring Strategy Tier 3 Development held on 1 February 2006. Scottish representatives at this Workshop were Bill Turrell, Peter Holmes, Jim McKie and Colin Moffat. At the Workshop a proposal for a restructuring of marine assessment and monitoring was proposed by Bill Turrell. This was followed by a presentation on integration by Colin Moffat. Overall, Scottish representatives played a significant role in developing the concepts during the workshop both through general participation and through chairing the breakout groups.

   - *Protocols Group* - a need to have a protocols group was confirmed. This will incorporate the current AQC groups.

   - *Data management* – it was concluded that there is not a need for a new group, but that data management will be achieved through MDIP and MEDAG.

   - *Integrated Assessment* – it was concluded that there was no need for a separate 'Integrated Assessment Group' but that this process would be done by the new thematic groups which would deliver this to MARG who would undertake the overall integrated assessment. This means that there is a need to review and amend accordingly the ToR of MARG.

   - The Workshop recommended the adoption of the concept of having three thematic groups which tie in directly with the UK and Scottish Visions of

     a. Clean and Safe
     b. Healthy and Biologically Diverse
     c. Productive

     seas and oceans (see Annex 1).

Appendix 6.6 Contd. - Minute of 1st MARG Meeting

- Bill Turrell provided a summary of the output from the Integrated Monitoring and Data Collection breakout sessions. There was a clear need to develop a simple score card system. The example used was the Millennium Ecosystem Assessment and it was concluded that this represented a good basis on which to proceed. Each theme group will be presented with the generic score card so that all theme groups are starting from the same basis. The theme group will populate their scorecard and also define a pragmatic, high-level explanation of what is e.g. a clean sea. This will be returned to MARG who ensure consistency between the themes. The theme groups will then start to put data into the skeleton scorecard. This is where gaps will be identified and where we will perhaps come up against difficulties.

- The current drivers were assigned to the various Theme Groups as summarised in Table 1.

Table 1: Summary of areas of work assigned to the three themes.

Clean and Safe	Healthy and Biologically Diverse	Productive
WFD (Chemical status)	WFD (Ecological Status)	Offshore Activities
OSPAR Eutrophication	OSPAR Eutrophication	Shellfish Hygiene
Hazardous Substances	OSPAR Biodiveristy	FEPA/COPA
Radioactivity	Birds and Habitats Directives	Flood Prevention
Shellfish Waters/ Hygiene Directives	Conservation of Seals Act	SEA/EIA
Climate change	Common Fisheries Policy (CFP)	CFP (Fishery Assessment)
Litter	GOOS	Renewables
Bathing Waters Directive	Ocean Climate	Spatial Planning
Oil spills and discharges	Climate Change (Impacts)	Climate Change (Impacts)

- Current groups were brigaded under the Theme Groups as summarised in Table 2.

Table 2: Assignment of current groups to themes.

Clean and Safe	Healthy and Biologically Diverse	Productive
NMMP WG	New Biodiversity Group	GCSDM
EST	GOOSAG	SEA
	MECN	New Seabed Mapping Grp
	MTT	New Fishery Group (ie FRS/CEFAS/DARD)
	NERC	
	New Seabed Mapping Grp	
	New Fishery Group (i.e. FRS/CEFAS/DARD)	

Appendix 6.6 - Contd. - Minute of 1st MARG Meeting

- A need was highlighted to provide generic ToR for each Thematic Group as well as arriving at a high-level description for the Themes based on using UK Ministerial Strategies and the European Directives.
- The Theme Groups, using the generic scorecard, should draft a list of themed drivers, based on the expert knowledge of existing monitoring regimes, and identify gaps with the objective of ultimately producing the scorecard

8. The Terms of Reference for MARG were reviewed and amended in light of earlier discussions. Further it was concluded that the overarching strategy should be renamed UK Marine Assessment and Monitoring Strategy.

9. There was some discussion about Devolved Administration 'buy-in'. Scotland was well represented at both the Workshop and MARG from the perspective of scientific input. Indeed, Scotland drove, through BT and CM, a lot of the ideas and concepts which have resulted in the proposal as it now exists. However, there was a desire from Defra to have senior policy input, in part to assist with the likes of the secretariat. I would anticipate that a letter will arrive at the SE from John Roberts.

10. In the light of the Workshop and subsequent discussions at MARG the UKMMS (to be renamed UKMAMS) will be amended by Defra and circulated for comment.

11. In essence there are to be four groups (three Theme Groups and a Protocols Group) and there is a need to identify a chair for each of these groups and the associated secretariat. Note – this process should result in a reduced number of groups as, for example, the current UKNMMP WG will cease to exist in its current form. The closure of MEMG was also confirmed.

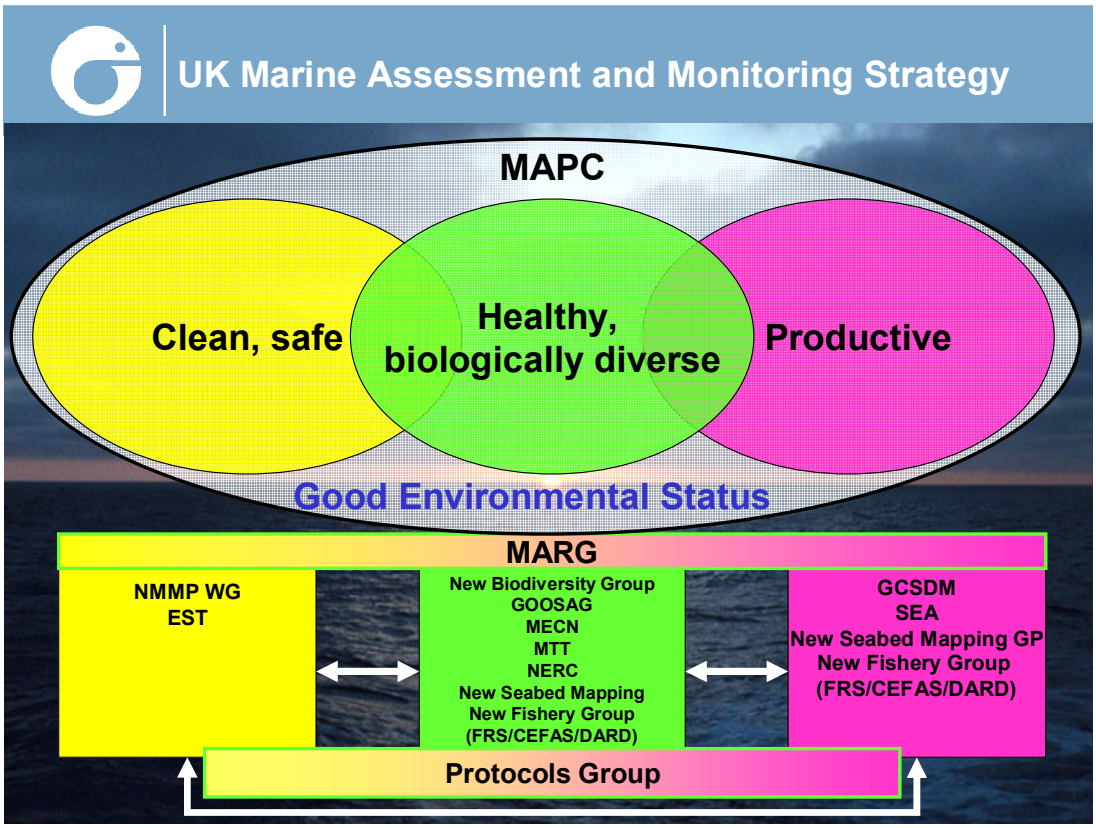
12. There has been no conclusion drawn with respect to the spending review. However, there would appear to be a need for business cases to be on the back burner – there is an issue in terms of any Defra led initiatives for funding and how this may feed into the Devolved Administrations.

13. In conclusion, progress is being made, there has been some streamlining and the focus is clearly on the vision of clean, healthy, safe, biodiverse and productive seas and oceans.

Colin Moffat
6 February 2006

Appendix 6.6 - Contd. - Minute of 1st MARG Meeting

Annex 1 – Schematic of the proposed structure for delivering the UK Marine Assessment and Monitoring Strategy



Appendix 6.7 Remedial Action Guidelines

If an Own Sample achieves either a 'Fail-Poor' or a Fail Bad ' flag (i.e. <90% BCSI) then 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 re-audited 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 6.7 (Cont.)

NMBAQC Scheme Remedial 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 6.8 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 – (i.e. 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 6.9 NMMP Sample Flagging

Lab No.	Data Matrices Submitted	Own Samples Selected	Grade	Flag Status
A	2004_NMMP45 CMT5	RepB (OS29)	Good	Validated
	2004_NMMP55 CMT7	RepB (OS30)	Fail -Poor	*Validated
	2004_NMMP70 STN H Irvine Bay	RepB (OS31)	Acceptable	Validated
	2004_NMMP76 L.Linnhe	-	-	Validated
B	2004_NMMP175 Kingston Hudds	RepC (OS31)	Fail -Poor	*Validated
	2004_NMMP208 Kincardine	RepC (OS30)	Good	Validated
	2004_NMMP176? Cromarty Firth	RepC (OS29)	Good	Validated
B1	2002_NMMP25 Offshore Solway	Macro1 (OS29)	Good	Validated
	2002_NMMP35 Firth of Clyde	Macro1 (OS30)	Good	Validated
B2	2003_NMMP25 Offshore Solway	-	-	**Flagged**
	2003_NMMP35 Firth of Clyde	-	-	**Flagged**
	2003_NMMP85 Minches	RepD1 (OS29)	(not supplied)	**Flagged**
	2003_NMMP95 Moray Firth (intermediate)	RepA1 (OS30)	(not supplied)	**Flagged**
	2003_NMMP105 Moray Firth (offshore)	RepD1 (OS31)	(not supplied)	**Flagged**
	2003_NMMP165 Forth/Tay Offshore	-	-	**Flagged**
C	2004_NMMP210 Yarrow Slake	-	-	**Flagged**
	2004_NMMP220 Budle Bay	-	-	**Flagged**
	2004_NMMP225 Hebburn	-	-	**Flagged**
	2004_NMMP235 Ferry Crossing	RepD (OS29)	Acceptable (incomplete)	n/a
	2004_NMMP265 Alex. Bridge	-	-	**Flagged**
	2004_NMMP270 Off Seaham	-	-	**Flagged**
	2004_NMMP275 Sandy Point	-	-	**Flagged**
	2004_NMMP305 Bamlett's Bight	RepA (OS30)	Acceptable (incomplete)	n/a
	2004_NMMP315 No23 Buoy	-	-	**Flagged**
	2004_NMMP325 Phillips Buoy	RepE (OS31)	Fail -Poor (incomplete)	Flagged
C1	2004_NMMP755 Seacombe Ferry, Mersey	RepE (OS29)	Acceptable	**Flagged**
	2004_NMMP765 Ch. C1 Buoy	-	-	**Flagged**
	2004_NMMP766 u/s 11 mile post, Ribble	RepB (OS30)	Excellent	**Flagged**
	2004_NMMP767 North Bay, Morecambe Bay	RepD (OS31)	Fail -Poor	Remedial Action outstanding
	2004_NMMP768 St. Bees	-	-	**Flagged**
D	2004_NMMP356 Inside Spurn	RepB (OS29)	Good	Validated
	2004_NMMP357 Grimsby Roads	RepB (OS30)	Good	Validated
	2004_NMMP358 Sunk Island	-	-	Validated
	2004_NMMP388 WW19 off Boston	RepB (OS31)	Good	Validated
E	2004_NMMP390 Blackwater	Rep1 (A&B) (OS29)	Good	Validated
	2005_NMMP576 Jennycliffe	RepB & D (OS30) (OS31)	Good	Validated
F	2004_NMMP435 Woolwich	RepA & B (OS29) (OS30)	Good	Validated
	2004_NMMP455 Mucking	RepB (OS31)	Good	Validated
G	2004_NMMP505 Dock Head	RepB (OS29)	Acceptable	Validated
	2004_NMMP505 Dock Head	RepD (OS30)	Good	Validated
	2004_NMMP526 Burham	RepD (OS31)	Good	Validated
	(2004_NMMP527 Sun Pier - samples compromised)	-	-	n/a

* Validated - following completion of remedial action.

Appendix 6.9 - Contd. NMMP Sample Flagging

Lab No.	Data Matrices Submitted	Own Samples Selected	Grade	Flag Status
H	2004_NMMP245 NSTF14	-	-	Validated
	2004_NMMP345 NSTF53	RepC (OS29)	Excellent	Validated
	2004_NMMP536 Lyme Bay	RepD (OS30)	Good	Validated
	2004_NMMP605 Celtic Deep	RepE (OS31)	Good	Validated
I	2004_NMMP555 Warren Point	RepC (OS29)	Good	Validated
	2004_NMMP565 Hamoaze	RepE (OS30)	Good	Validated
	2004_NMMP566 Upper South Deep	RepB (OS31)	Good	Validated
	(2004_NMMP567 Wytch - samples compromised)	-	-	n/a
	2004_NMMP576 Jennycliffe	-	-	Validated
J	(2004_625 Purton)	No Data supplied		**Flagged**
	(2004_635 Bedwin)	No Data supplied		**Flagged**
	(2004_645 Peterstone)	No Data supplied		**Flagged**
	(2004_646 Cosheston Point	No Data supplied		**Flagged**
	(2004_647 Ynys-hir)	No Data supplied		**Flagged**
	(2004_648 Bontddu)	No Data supplied		**Flagged**
	(2004_690 Mostyn Bank)	No Data supplied		**Flagged**
K	2005_NMMP845 BL5	-	-	Validated
	2005_NMMP? BL7	RepA (OS31)	Good	Validated
	2005_NMMP820 BR3	RepC (OS29)	Good	Validated
	2005_NMMP880 Kilderry	RepA (OS30)	Good	Validated
	2005_NMMP825 IS1	-	-	Validated
L	2004_NMMP806 NMP4	RepD (OS30)	Fail -Bad	*Validated
	2004_NMMP807 NMP5	RepC (OS31)	Excellent	Validated
	2004_NMMP808 Buoy(NMP6)	-	-	Validated
	2004_NMMP815 Buoy(NMP3)	RepE (OS29)	Excellent	Validated
	2004_NMMP865 NC2(NMP2)			Validated
	2004_NMMP875 NC1(NMP1)			Validated

* Validated - following completion of remedial action.

Section B – Supplementary Report on Invertebrate, Particle Size, & Fish Components.

From Scheme Contractor: Unicomarine Ltd.

SCHEME OPERATION – YEAR 12 – 2005/06

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 twelfth year of operation of the Invertebrate, Particle Size, and Fish components of the National Marine Biological Analytical Quality Control (NMBAQC) Scheme.

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

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

This Scheme year included an additional ring test exercise, the first ring test targeting small or juvenile fish taxa. The analytical procedures of the various modules were the same as for the eleventh year of the Scheme. The results for each of the Scheme exercises are presented and discussed. Comments are provided on the performance for each of the participating laboratories in each of the exercises.

Analysis of the **Macrobenthic sample (MB)** by the participating laboratories and subsequent re-analysis by Unicomarine Ltd. provided information on the efficiency of extraction of the fauna; accuracy of enumeration and identification and the reproducibility of biomass estimations. Agreement between the laboratories and Unicomarine Ltd. was generally good with results markedly higher than those achieved in previous MB exercises. The samples posed very few problems associated with faunal extraction or identification of the taxa. Extraction efficiency, irrespective of sorting, was on average 98.5%; all laboratories extracted greater than 95% of the individuals from the residue; five laboratories extracted all fauna from the residue. Comparison of the results from the laboratories with those from analysis by Unicomarine Ltd. was made using the Bray-Curtis similarity index (untransformed). The value of the index varied between approximately 93.9% and 100% and was better than 95% in 63% of comparisons; three laboratories achieved 100% Bray-Curtis similarity.

The Scheme year ten 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 2004) 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 similar 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 91% of comparisons and better than 95% in 83% of all comparisons. The Bray-Curtis similarity index ranged from 49% to 100% with an average figure of 96%. The Bray-Curtis similarity index was greater than 95% in 81% of comparisons and in most cases (91%) the value of the index was greater than 90%, these samples all achieved 'pass' flags. Ten samples achieved 'excellent' pass flags with Bray-Curtis similarity scores of 100%.

The **Particle Size exercises (PS)** were conducted as in the previous Scheme year. 'Pass/fail' criteria were applied based upon z-scores from the major derived statistics with an acceptable range of ±2 standard deviations (See Appendix 2: Description of the Scheme standards 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 relatively good agreement between laboratories. The first particle size exercise

of the Scheme year (PS26) received nine data returns (including replicated data) that resulted in seven 'fail' and thirty-eight 'pass' flags. The second particle size exercise of the Scheme year (PS27) received nine data returns (including replicated data) that resulted in six 'fail' and thirty-nine 'pass' flags.

Three **Ring Tests (RT)** of twenty-five animal specimens were distributed. One set consisted of twenty-five of the most misidentified invertebrate taxa from all the previous ring tests (RT26), another set contained general invertebrate fauna (RT27) and a third ring test was circulated that comprised fish taxa (RT28). The 'targeted' ring test (RT26) was sent covertly under the guise of a general ring test to prevent laboratories reviewing previous results. The 'targeted' ring test (RT26 – 'previous RT problem taxa'), as expected, posed several problems for species identification. On average each participating laboratory recorded 4.3 generic errors and 11.1 specific errors. Several of the specimens were responsible for high numbers of errors; five specimens were incorrectly identified by over ten of the fourteen participating laboratories. For the general set of fauna (RT27) there was fairly good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd. On average each participating laboratory recorded 2.9 generic errors and 5.4 specific errors. The majority of the generic errors can be attributed to two polychaete and two crustacean taxa. The fish ring test (RT28) produced good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd. On average each participating laboratory recorded 1.7 generic errors and 3.1 specific errors. Five specimens were responsible for 14% of all generic and 60% of specific errors recorded.

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

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

1. Introduction

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

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

The twelfth year of the Scheme (2005/06) followed the format of the eleventh year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. Twenty-eight laboratories participated in the Scheme. Fifteen laboratories were government laboratories; thirteen were private consultancies. Half of the participants (14) were responsible for UK NMMP sample analysis (excluding subcontracted samples).

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

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

2. Description of the Scheme Modules

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

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

2.1 General

2.1.1 Logistics

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

2.1.2 Data returns

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

2.1.3 Confidentiality

To preserve the confidentiality of participating laboratories, each are identified by a four-digit Laboratory Code. Each Scheme year twelve participant was given a confidential LabCode in August 2005, 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 twelve will be recorded as LB1204.

In the present report all references to Laboratory Codes are the post-July 2005 codes (Scheme year twelve).

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

2.2 Macrobenthic Samples (MB)

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

2.2.1 Preparation of the Samples

Sample MB13 was collected from the coast of Harwich (off Stone Pier); in an area of sandy 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 1.0 mm sieve mesh; participating laboratories were instructed to employ their normal methods. The participating laboratories were required to complete a Macrobenthic Sample Details Form, which specified their processing methodology (for example, stating whether nematodes are extracted). The extracted fauna were to be separated, identified and stored in individually labelled vials. Labels were provided and cross-referenced to the recording sheets.

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

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.* 2004 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 submitted data matrix.

2.3.1 *Analysis required*

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

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

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

Six 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 2005/06. One of the samples was derived from aggregate material and the second was from natural marine sediments, both were 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 two analysis techniques.

2.4.1 *Preparation of the Samples*

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

The numbering of the replicate samples was random. All of the odd-numbered 'B' components (a total of 14) were sent for particle size analysis to assess the degree of inter-sample variation. Half the replicates were analysed using 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) – (Invertebrates and Fish)

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

Three sets of twenty-five specimens were distributed in 2005/06. The first of the year's RT circulations (RT26) comprised 'targeted' misidentified invertebrate specimens from previous ring test circulations. Participating laboratories were unaware of theme of this ring test. The second circulation (RT27) was a general invertebrate ring test. The specimens included representatives of the major phyla and approximately 40% of the taxa were annelids, 32% were crustaceans, 16% were molluscs, 8% were other minor phyla and 4% were echinoderms. The third circulation (RT28) 'targeted' specimens of fish and was circulated to fewer laboratories that routinely identify fish. Details of substratum, salinity, depth and geographical location were provided for all ring test specimens to assist identification.

2.5.1 Preparation of the Samples

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

For the standard RT (RT27) and the 'targeted' RTs (RT26 & RT28), all specimens were taken from replicate trawls, grabs or cores within a single survey and in most cases they were replicates from a single sampling station.

2.5.2 Analysis required

The participating laboratories were required to identify each of the RT specimens to species and provide the Species Directory code (Howson & Picton, 1997) for the specimen (where available). If a laboratory would not routinely have identified the specimen to the level of species then this should be detailed in the 'confidence level' field. Laboratories can also add brief notes and information on the keys or other literature used to determine their identifications. Specimens from RT26 and RT27 were to be returned to Unicomarine Ltd. for verification and resolution of any disputed identifications. This was the same procedure as for earlier circulations. Specimens from RT28 (fish) were retained by the participant laboratories for incorporation into their in-house reference collections or training material. 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. In Year 11 up to five unidentified problem taxa could be included. **For Year 12, each laboratory was invited, if they wished, to include any number of unidentified or problematic taxa**. Specimens wherever possible were to be representatives from UK NMMP reference collections.

2.6.2 Analysis

A prepared results sheet was distributed with the exercise's instructions with attached labels for the laboratories to identify each of the specimens. Participating laboratories were permitted **twelve 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 2005/06 were undertaken, in varying numbers, by twenty-eight laboratories. Differences in the number of exercises in which laboratories participated meant that some exercises had more data returned than others. There were, as in previous years, large differences between laboratories in their ability to meet the target deadlines. Sub-contracting by participating laboratories of certain sample analyses also contributed to delays.

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

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

3.1 Macrobenthic Samples (MB)

3.1.1 General comments

The distributed macrobenthic sample (MB13) was from a coastal location off Harwich (Stone Pier). The distributed samples comprised approximately half a litre of medium to fine sand taken from a depth of approximately five metres. The samples contained on average twelve species and twenty-four individuals, covering a variety of phyla. The composite list from all samples was twenty-seven species. Two out of the eight samples returned had been stained with Rose Bengal during sample processing. None of the laboratories subsampled their residues. Eight of the nine laboratories participating in this exercise returned samples and data. Detailed results have been reported to the participating laboratories (Hall, 2006a), additional comments are added below.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB13, 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 variation between laboratories in the percentage of taxa identified in the samples. At most one taxon (and 9.1% of the total taxa in the sample) were either not extracted or not recognised within the picked material. In half of the samples returned Unicomarine Ltd. recorded the same number of taxa as 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. Five laboratories (63%) extracted representatives of all the species present in their samples. On average laboratories missed less than one taxon in their residues, and in the worst instances one new taxon was 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 one additional individual from all samples except LB1201, LB1204, LB1208, LB1221 and LB1224. 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 all of the samples was less than 5% of the true total number in the sample. In the worst instances one individual, 4.0% 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 one. A breakdown of the missed individuals by taxonomic group is presented in Table 2.

3.1.2.3 Uniformity of identification

Most of the species in the distributed sample were identified correctly by the participating laboratories. Five of the participating laboratories had no taxonomic differences (Table 1, column 15). In the worst instances two taxonomic differences were recorded. On average half a taxonomic difference was encountered per sample. A taxon commonly either misidentified or not identified at the species level was the sea squirt, *Molgula manhattensis*.

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 93.9% to 100%, with an average value of 97.2%. The index for the majority of laboratories (5 of 8) was above 95% and three of the participating laboratories would have achieved 'excellent' sample flags if the NMBAQC / UK NMMP standards were applied. Further details of each participating laboratory's performance are given in Section 6: Comments on Individual Laboratories.

3.1.4 Biomass determinations

A comparison of the estimates of the biomass made by the participating laboratories and Unicomarine Ltd. broken down by major taxonomic group for the MB13 circulation is presented in Table 3. Two laboratories did not supply biomass data. The average difference between the two weight values was 9.9%, 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 –12.7% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +62.8% (measurements by laboratory were greater than those made by Unicomarine Ltd.). The average difference between estimations varied greatly between faunal groups, ranging from –3.2% to +23.3% (from molluscs to polychaetes, respectively).

3.1.5 Uniformity of samples

The faunal content of the samples distributed as MB13 is shown in Table 4. Data received from the participating laboratories were fairly similar showing natural variation often encountered in subtidal coastal marine 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-seven selected samples were received from nineteen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS29, OS30 and OS31 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 25 ml to 8 L of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 1 to 127, and the number of individuals from 1 to 3598. Nineteen of the twenty-four laboratories participating in this exercise returned all three Own Samples; eight of these Own Samples have been audited externally by Aquatic Environments due to

Unicomarine Ltd. being responsible for the initial sample processing; one laboratory (LB1218) supplied three Own Samples without sorted residues.

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-three samples (58% of all samples) the number of taxa recorded by the participating laboratories was identical to that obtained by Unicomarine Ltd. (column 4). In the twenty-four exceptions, the difference was at most twelve 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 49%. The average difference was 3.5% (sixteen samples exceeded this average). Twenty-five of the fifty-four comparable samples (three samples were supplied without residue) reported showed 100% extraction of fauna from the residue (column 12), and in fifteen samples various numbers of individuals (but no new taxa) were missed during sorting (column 11). The remaining eleven samples contained taxa in the residue which were not previously extracted, the worst example being eleven new taxa found in the residue (column 10). In the worst instance residue was found to contain five hundred and eighty-eight 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 twenty-four, 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-four (42%) of the fifty-seven samples re-analysed. An average of 1.3 taxonomic differences per laboratory were recorded; in the worst instance seven 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 49% to 100%, with an average figure of 96%. Five samples from five different laboratories achieved a similarity figure of less than 90% (excluding samples supplied without residue). Ten samples produced a similarity figure of 100%; these were submitted by seven different laboratories (LB1202, LB1203, LB1208, LB1209, LB1216, LB1219 and LB1226). The best overall results were achieved by laboratories LB1216 (results comprised 98.84%, 100% and 100%) and LB1221 (99.26%, 99.65% and 99.91%), both averaged 99.61% similarity. The worst overall results were achieved by laboratory LB1201, whose results comprised 49.37%, 96.54% and 96.32%. 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; nineteen samples were not supplied with species biomass data; four samples were reported to five decimal places (4 decimal places is required). Consequently, only thirty-eight of the fifty-seven samples received have been used for comparative analysis. Table 7 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. The total biomass values obtained by the participating laboratories varied greatly with those obtained by Unicomarine Ltd. The average was a +7.2% difference between the two sets of results (*i.e.* heavier than Unicomarine Ltd.); the range was from –44.4% to +46.7%. 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 -2.6% for polychaetes, +7.1% for oligochaetes, +6.7% for nemerteans, +6.3% for Chelicerata, +3.1% for crustaceans, +15.2% for echinoderms, +2.6% for molluscs and -3.7% 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 PS26, nine out of eleven participating laboratories returned data (including laboratories with grouped results); two laboratories did not provide data, one of which notified non-participation. For PS27, nine out of the eleven participating laboratories returned data; two laboratories did not provide data, one of which notified non-participation. Detailed results for each exercise have been reported to the participating laboratories (Hall, 2005 & 2006b), additional comments are added below.

3.3.2 Analysis of sample replicates

Replicate samples of the sediment used for the two PS distributions were analysed using 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 PS26; the shape of the distribution curves was very similar for the two analytical techniques and they were closely grouped with the laser curves differing by showing the presence of some very coarse sand and less coarse to medium sand particles. This sample had a low percentage of sediment in the fine fraction (average of 3.36% <63µm). The figures for %<63µm varied significantly between the two techniques with laser analysis producing an average figure of 4.31% and sieve and pipette producing approximately 44% less (2.41%). Consequently, the derived statistic for median particle size (ϕ) were also slightly different between the two techniques. The average median particle size from laser analyses was 1.49ϕ, compared with 1.37ϕ 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 PS27 was of a muddy sediment (average of 97.60% <63µm) and the cumulative distribution curves differed markedly between the two techniques, particularly for the composition of silt/clay particles. The sieve and pipette technique indicated that approximately 50% of the sample was clay material; this figure was just 15% for the laser data. The figures for % <63µm produced by two techniques were different due to the laser records of more fine and very fine sand particles; laser analysis produced an average of 96.09% and sieve and pipette produced 99.11%. 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.

One laboratory, which normally sub-contract their particle size analysis to another laboratory (also participating), elected to utilise the results from this laboratory for PS26 and PS27; 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 PS26 and PS27 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-sixth distribution – PS26

There was generally good agreement for PS26 between the results from the analysis of *replicates* and those from the majority of participating laboratories. The results for two laboratories (LB1203 and LB1224) were adrift due to a higher estimation of the silt/clay component; another two laboratories (LB1212 and LB1217) recorded at least 50% more very coarse sand than the other participants. The difference between the analytical techniques was less marked than has been seen for other PS circulations (see Figure 1), however all participating laboratories used laser methodologies. Table 10 shows the variation in data received from the participating laboratories. The derived statistic for %silt/clay ranged from 0.84% to 13.4%, with the majority of laboratories producing figures slightly higher than the *replicate* analyses produced by Unicomarine Ltd.

3.3.3.2 Twenty-seventh distribution – PS27

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 Figure 2). All participating laboratories used laser methodologies. The results for one laboratory (LB1202) were adrift due to a higher estimation of the coarse fractions; another two laboratories (LB1203 and LB1201) recorded less coarse silt and sand material than the other participants. Table 11 shows the variation in data received from the participating laboratories. The derived statistic for %silt/clay ranged from 76.95% to 99.46%, with the majority of laboratories producing figures slightly lower than the *replicate* analyses produced by Unicomarine Ltd.

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

3.4.1 General comments

The implementation of this part of the Scheme was the same as previous years, however this year an additional exercise was added to specifically address the identification of fish from transitional waters. All three RT circulations were accompanied by details of each specimen's habitat details (depth, salinity, substratum, and geographical location). A number of laboratories use these modules of the Scheme for training purposes and have selected them preferentially over other modules. UK NMMP laboratories are required to participate in this component though it is not used when assigning 'pass' or 'fail' flags. Three circulations of twenty-five specimens were made. For RT26 the species were 'targeted' upon the most misidentified invertebrate taxa from the previous twenty-five ring test circulations. For RT27 twenty-five specimens from a variety of invertebrate Phyla were circulated. RT28 'targeted' fish species for circulation to slightly fewer laboratories that routinely identify fish. Other aspects of the three circulations, in particular the method of scoring results, were the same as for previous circulations. Participating laboratories were permitted to retain the RT28 fish specimens as part of their in-house reference collections. In total twenty-one laboratories were distributed with RT26 specimens; seventeen laboratories received RT27 specimens; fifteen laboratories received RT28 fish specimens. For RT26, fourteen laboratories returned data; four laboratories specified non-participation for this exercise; three did not supply data or indicate non-participation. For RT27, fifteen laboratories returned data; three laboratories specified non-participation for this exercise; three did not supply data or indicate non-participation. For RT28, thirteen laboratories returned data; one laboratory specified non-participation for this exercise; one 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 taxon, *e.g. Sphaeroma hookeri* for *Lekanesphaera hookeri*.
- Simple mis-spelling of a name*, e.g. Sternapsis scutata* for *Sternaspis scutata*.

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

Tables 12, 13 and 14, respectively, present the identifications made by each of the participating laboratories for each of the twenty-five specimens in RT circulations RT26, RT27 and RT28. For clarity the name is given only in those instances where the generic or specific name given by the laboratory differed from the AQC identification. Where it was considered that the name referred to the same species as the AQC identification but differed for one of the reasons indicated above, then the name is presented in brackets "[name]". Errors of spelling or the use of a different synonym are not bracketed in this way if the species to which the laboratory was referring was not the same as the AQC identification. A dash, "-", in the Tables indicates that the name of the genus (and / or species) given by the laboratory was considered to be the same as the AQC identification. A pair of zeros, "0 0", in the Tables indicates that the subscribing laboratory did not return data.

3.4.2.1 Scoring of RT results

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

3.4.3 Ring Test distribution results

The RT component of the Scheme mirrored that of 2004/05 as there was only a single 'standard' exercise (RT27). RT26 was covertly targeted on 'problem taxa from previous ring tests'. RT28 was targeted on fish from transitional waters. The RT circulations are designed as a learning exercise to discover where particular difficulties lie within specific common taxa. Results were forwarded to the participating laboratories as soon as practicable. Each participant also received a ring test bulletin (RTB26, RTB27 and RTB28), 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'. The fish specimens circulated as RT28 were donated for inclusion in each participant laboratories in-house reference collection or for future in-house training.

3.4.3.1 Twenty-sixth distribution – RT26

RT26 contained twenty-five 'problem taxa from previous ring tests'. The results from the circulation are presented in Table 12 in the same manner as for all previous RT circulations. Eleven of the twenty-five specimens circulated were molluscs; seven were polychaetes; five were crustaceans; and two were oligochaete specimens. The agreement at the generic level was relatively poor; sixty errors (from a potential three hundred and fifty) were recorded from the fourteen participating laboratories. Agreement at the specific level was also poor; one hundred and fifty-six errors were recorded. Ten of the specimens circulated were incorrectly identified by at least half of the participants. These taxa, responsible for the majority of differences, are described briefly below.

The bulk of the errors recorded could be attributed to ten specimens. *Potamopyrgus antipodarum, Lekanesphaera hookeri, Corophium insidiosum, Lacuna parva, Idotea granulosa, Thyasira sarsi, Diastylis rathkei, Gibbula cineraria, Odostomia turrita* and *Chaetozone christiei* accounted for a total

of 30% of all generic and 62% of all the specific differences recorded. Only one of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Limapontia depressa)*, when this specimen was originally circulated in 1999 (RT14) it produced three generic and ten specific errors from sixteen participating laboratories. Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB26 – Hall & Worsfold, 2005a) which was circulated to each laboratory that supplied results for this exercise. Following the bulletin, several requests for further explanatory information were received; these were addressed by means of **further notes and images** in an additional comments document that was circulated to all RT26 participants (RTB26 additional comments – Hall & Worsfold, 2005b).

3.4.3.2 Twenty-seventh distribution – RT27

Table 13 presents the results for the RT27. One of the specimens was donated by Carol Milner (SEPA, Dingwall). Nine of the twenty-five specimens circulated were polychaetes; seven were crustaceans; five were molluscs; one was an oligochaete; one was a sipunculan; one was a sea spider; and one was an echinoderm specimen. The agreement at the generic level was relatively good; forty-four errors (from a potential three hundred and seventy-five) were recorded from the fifteen participating laboratories. Agreement at the specific level was also relatively good; eighty-one errors were recorded. Four of the specimens circulated were incorrectly identified by at least half of the participants. These taxa, responsible for the majority of differences, are described briefly below.

Five of the ring test specimens caused problems for several laboratories; specifically *Mya truncata* (small / medium specimens)*, Lekanesphaera hookeri* (medium specimens), *Neanthes succinea* (medium / small specimens), *Scolelepis tridentata* (small, poor specimens) and *Ampelisca diadema* (medium specimens). These taxa accounted for 32% of the generic and 53% of the specific differences recorded. Five of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Calocaris macandreae, Sternaspis scutata, Hyala vitrea, Nephtys incisa, Amphiura chiajei* and *Mesopodopsis slabberi*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB27 - Hall & Worsfold, 2006) which was circulated to each laboratory that supplied results for this exercise.

3.4.3.3 Twenty-eighth distribution – RT28

RT28 contained twenty-five fish specimens. Five of the specimens were donated by Myles O'Reilly (SEPA, East Kilbride); one specimen was donated by Henk van Rein (EHS, Lisburn). The results from the circulation are presented in Table 14 in the same manner as for the other circulations. The agreement at the generic level was very good; just twenty-two errors (from a potential three hundred and twenty-five) were recorded from the thirteen participating laboratories. Agreement at the specific level was relatively good; forty errors were recorded. The majority of participating laboratories correctly identified each of the specimens. Only a few of the taxa were responsible for the majority of differences and these are described briefly below.

The bulk of the errors recorded could be attributed to five specimens. *Syngnathus rostellatus* (12-14cm specimen)*, Ammodytes marinus* (9-11cm specimen)*, Pomatoschistus microps* (4-5cm specimen)*, Pomatoschistus minutus* (7-8cm specimen) and *Pleuronectes platessa* (10-13cm specimen) accounted for a total of 41% of all generic and 60% of all the specific differences recorded. Nine of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Agonus cataphractus, Lumpenus lumpretaeformis, Limanda limanda, Clupea harengus, Entelurus aequoreus, Sprattus sprattus, Pholis gunnellus, Osmerus eperlanus* and a second smaller *Sprattus sprattus*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB28 – Hall & Dyson, 2006) which was circulated to all RT28 participants.

3.4.4 Differences between participating laboratories

Figures 7, 8 and 9 present the number of differences recorded at the level of genus and species for each of the participating laboratories, for RT circulations RT26, RT27 and RT28 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 RT26 and RT27 were of molluscs. Mollusc specimens (sixteen specimens in total) were responsible for 40% of generic differences and 34% of the total number of specific differences. Sixteen of the total fifty specimens circulated were polychaetes and these produced 36% of the generic and 27% of the specific differences recorded. Crustacean specimens (twelve specimens in total) were responsible for 13% of generic differences and 32% of the total number of specific differences. Three of the specimens circulated were oligochaetes and these produced 7% of the generic and 5% of the specific differences recorded. One of the specimens circulated was a sipunculan and produced 3% of the generic and 1% of the specific differences recorded. One of the specimens circulated was a sea spider and produced 1% of the generic differences recorded. One of the specimens circulated was an echinoderm, which produced no generic or specific differences.

3.5 Laboratory Reference (LR)

3.5.1 *General comments*

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

3.5.2 *Returns from participating laboratories*

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

4. Discussion of Results

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

4.1 Macrobenthic Analyses

The sample distributed as MB13 comprised a relatively undiverse and sparsely populated coastal sandy sample. The extraction of fauna from the sediment was straightforward with little organic 'float' material to mask the fauna. The dominant taxa recorded in the majority of samples were *Nephtys cirrosa / Nephtys* sp. juv. and *Eumida bahusiensis*. Five of the participating laboratories extracted all the countable material from the residue (LB1201, LB1204, LB1208, LB1221 and LB1224); just one individual was not extracted in each of the three remaining samples. Identification of the extracted fauna caused very few if any problems for participants. Five laboratories (LB1202, LB1204, LB1208, LB1221 and LB1224) correctly identified all their extracted fauna. There were a total of just four taxonomic mistakes from all eight participants, the majority (3) of these involved *Molgula manhattensis*. All eight returning laboratories attained a Bray-Curtis similarity higher than 90%. The highest Bray-Curtis similarity index achieved was 100% (LB1204, LB1221 and LB1224). The average Bray-Curtis figure achieved was 97%. This represents the highest figure for the MB exercise, to date; the average for MB12 was 77%, 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 (MB13). The area sampled was well uniformed in its faunal composition. The samples were typical of the area and showed only slight natural variation. All samples were of relatively equal volume and sediment characteristics.

The 'blot-drying' procedure employed by Unicomarine Ltd. for the determination of biomass was as specified in the Green Book, *i.e.* avoiding excessive pressure when blotting specimens dry. However, there remains a considerable variation between the estimates of total biomass made by the participating laboratories and Unicomarine Ltd. Six laboratories provided biomass data; two provided data that was lighter in total than Unicomarine Ltd.; four supplied data that was heavier than Unicomarine Ltd. estimations. The extremes recorded were 12.7% lighter (LB1221) and 62.8% heavier (LB1207) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories and Unicomarine Ltd. was 9.9% (*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 2.2% heavier (MB12). It seems likely that the main reasons for the observed differences between the measurements are more thorough, or less consistent, drying by participating laboratories prior to weighing. A similar observation was made in previous years of the Scheme. The average percentage difference between Unicomarine Ltd. and participating laboratories biomass figures for MB11 was -3.1%, MB10 was -13.3%, MB09 was –14.6%, MB08 it was +4.9%, MB07 it was –1.67%, MB06 it was +26%, MB05 it was +32% and for MB04 it was +20%. There are likely to be several reasons for the differences between years, though the nature of the fauna in the distributed samples is likely to 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 equally well in the OS exercise and the MB13 exercise. The average value of the index was 96% for the OS, compared with 97% for MB13. Both components have produced several good results and some instances of excellent sample processing.

There were fifty-seven samples submitted for this module, including eight samples that have been processed by the Scheme's external auditor. One laboratory (LB1218) supplied three Own Samples without sorted residues, these samples have been excluded from the summary statistics below. The high number of returns was facilitated by the distribution of timely reminders. Approximately 91% of the fifty-four comparable samples reported exceeded the 90% Bray-Curtis pass mark and approximately 81% of the samples exceeded 95% Bray-Curtis similarity. The average Bray-Curtis similarity index achieved was 96%. These figures are consistent with the high quality results from previous OS exercises. In the 2004/05 Scheme year eleven (OS26, 27 and 28) the average Bray-Curtis figure was 96%, and 94% (of the fifty-four samples received) achieved more than 90% Bray-Curtis results. In the 2003/04 Scheme year ten (OS 23, 24 and 25) the average Bray-Curtis figure was 94%, and 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 seventy-seven admissible samples have been received (OS01-31), with an average Bray-Curtis similarity figure of 92.87%. Ninety-six samples have fallen below the 90% pass mark (20%). Fifty-seven samples have achieved a similarity figure of 100% (12% of all returns). Extraction of fauna is an area in which several participating laboratories could review their efficiency. All countable fauna must be extracted to record a truly representative sample, although this is rarely the case due to time restraints or inefficient methods used. A sample that has been poorly picked stands high possibility of being unrepresentative regardless of the quality of subsequent faunal identifications, and should the sorted residue be disposed, this cannot be rectified. Laboratories should study their detailed OS and MB reports and target the particular taxon or groups of taxa that are being commonly overlooked during the picking stages of sample analysis. It must be resolved whether the individuals are either not recognised as countable or not scanned using the extraction methods employed. If it is the former, then training is appropriate. If the latter is the case then a review of current extraction methods should be conducted.

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

4.3 Particle Size Analyses

The difference between the two main techniques employed for analysis of the samples (laser and sieve) was again evident in the results from the analysis of the replicates samples. The sample distributed as PS26 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 two laboratories (LB1203 and LB1224) indicated much higher proportions of silt/clay and less very coarse sand than the other data returns for PS26, hence these two sets of results are displaced in the cumulative curve figure (Figure 3).

PS27 showed a distinct difference in size distribution curves produced by laser or sieve and pipette methods (Figure 2). There was also a significant amount of scatter in the results for PS27 from participating laboratories (Figure 4) despite all these data being derived from laser analysis. Figure 6 shows the z-scores for each of the major statistics supplied by the participating laboratories. The data received from one laboratory (LB1202) indicated a lower silt-clay fraction compared to the *replicate* sample data produced prior to the exercise. In Scheme year 10 a series of experiments deduced that the replicates distributed as PS23 (muddy sample) 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 PS26 and PS27 samples prior to analysis. The results varied considerably and some were extremely descriptive (Table 16, final column). Participating laboratories were also instructed to describe the sediment using the Folk triangle after analysis. Data were provided by six laboratories for PS26 and eight laboratories for PS27. Three of the six laboratories, that submitted data using the Folk triangle, described PS26 as 'sand'; one recorded 'sandy mud'; one recorded 'muddy sand'; and one described 'moderately sorted fine skewed coarse sand'. Five of the seven laboratories, that submitted data using the Folk triangle, described PS27 as 'mud'; one laboratory recorded 'sandy mud'; and one recorded 'silt'.

It is essential that analytical methods are 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 all returned data 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 inclusion at taxonomic workshops. The ring test bulletins (RTB), which detail specifically the reasons for any identification errors, have further emphasised the learning aspect of this component. RT26 identified discrepancies with literature used by some participating laboratories for their identification of the *Tharyx* Type A, *Tubificoides* cf. *galiciensis*, *Psammoryctides barbatus, Protocirrineris chrysoderma, Chaetozone christiei* and *Pseudarachna hirsuta* specimens. RT27 identified discrepancies with literature used by some participating laboratories for their identification of the *Neanthes succinea* and *Scolelepis tridentata* specimens. One Laboratory (LB1204) identified all twenty-five specimens correctly. RT28 identified discrepancies with literature used by some participating laboratories for their identification of the *Pomatoschistus microps* and *P. minutus* specimens. Three laboratories (LB1220, LB1221 and LB1224) correctly identified all twenty-five RT28 specimens. All participating laboratories have been made aware of the variety of problems encountered for these ring tests via the ring test bulletins (RTB26, RTB26 extra comments, RTB27 and RTB28).

4.5 Laboratory Reference

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

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

5. Application of NMBAQC Scheme Standards

One of the key roles of the Invertebrate and Particle Size components of the NMBAQC Scheme is to assess the reliability of data collected as part of the UK National Marine Monitoring Programme (UK NMMP). With this aim performance target standards were defined for certain Scheme exercises and applied in Scheme year three (1996/97). These standards were the subject of a review in 2001 (Unicomarine, 2001) and were altered in Scheme year eight; each performance standard is described in detail in Appendix 2: Description of the Scheme Standards. Laboratories meeting or exceeding the required standard for a given exercise would be considered to have performed satisfactorily for that particular exercise. A flag indicating a 'Pass' or 'Fail' would be assigned to each laboratory for each of the exercises concerned. It should be noted that, as in previous years, only the OS and PS exercise have been used in 'flagging' for the purposes of assessing data for the UK NMMP.

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

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

5.1 Laboratory Performance

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

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

It can be seen from Table 15 (columns 4, 13 and 22) that for the OS exercise the majority of laboratories are considered to have met or exceeded the required standard for three of the OS targets - the enumeration of taxa and individuals and the Bray-Curtis comparison. Overall 98% of the comparisons were considered to have passed the enumeration of taxa standard; 96% exceeded the enumeration of individuals standard and 91% passed the Bray-Curtis comparison standard. NMBAQC Scheme / UK NMMP sample flags have been applied to each of the Own Samples in accordance with the performance flagging criteria introduced in Scheme year eight (Table 15, column 23); two of the fifty-four applicable samples are flagged as 'Fail - Bad'; three are flagged as 'Fail - Poor'; five are flagged as 'Pass - Acceptable'; thirty-four are flagged as 'Pass - Good'; and ten are flagged as 'Pass - Excellent' for achieving 100% Bray-Curtis similarity indices. Some laboratories have already addressed their 'failing' samples by undertaking remedial action (see 5.4 Remedial Action below).

Performance with respect to the biomass standard was slightly poorer (Table 15, column 19) with only 71% of the eligible samples meeting the required standard. It should be noted that there were laboratories for which the results from the biomass exercise should be considered unsuitable for comparison with the standard (expressed as five decimal places instead of the requested four, and fauna rendered dry or damaged by initial biomass procedures).

Application of the new PS exercise standards, introduced in Scheme year nine, (See Appendix 2: Description of the Scheme Standards) is shown in Table 16. The upper section of Table 16 shows the results for the PS26 exercise. Two laboratories (LB1207 and LB1224, excluding centralised results) failed to meet the standard for %< 63μm; one laboratory (LB1203) failed to meet the standard for median (ϕ); all participating laboratories passed the standard for mean (ϕ); two laboratories (LB1202 and LB1224) failed to meet the standard for sorting; and one laboratory (LB1224) 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 PS27 exercise. One laboratory (LB1202) failed to meet the standard for %< 63μm; two laboratories (LB1202 and LB1203) failed to meet the standard for median (ϕ); one laboratory (LB1203) failed to meet the standard for mean (ϕ); all participating laboratories passed the standard for sorting; two laboratories (LB1203 and LB1221) failed to meet the standard for IGS(SKi). Six laboratories passed all standards.

5.2 Statement of Performance

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

5.3 Comparison with Results from Previous Years

A comparison of the overall results for recent years is presented in Table 17. The Table shows the number of laboratories assigned 'Pass' and 'Fail' flags for the OS exercises over the past eleven years based upon the current NMBAQC Scheme standards (See Appendix 2: Description of the Scheme standards for each component). This year's fifty-four comparable Own Samples resulted in the third highest percentage pass rate, 91% (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 results for each participating laboratory over the past eleven years (the '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 improve upon the flagged data. The revised NMBAQC Scheme OS standards, introduced in Scheme year eight, give clear methods for discerning the level of remedial action required (See Appendix 2: Description of the Scheme Standards). A failing Own Sample is categorised by the achievement of a Bray-Curtis similarity indices of <90%. The performance indicators used to determine the level of remedial action required are %taxa in residue, %taxonomic errors, %individuals in residue (see Table 15, columns 7, 10 and 16) and %count variance. Own Samples not achieving the required standards are monitored by the NMBAQC committee. The participating laboratories are expected to initiate remedial action and notify the NMBAQC Scheme Contract Manager when this has been completed. Any remedial action undertaken should be audited externally where required. The NMBAQC Contract Manager and Scheme's contractor, Unicomarine Ltd., will provide clarification on specific details of remedial action or consider appeals relating to the remedial action process.

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

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

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

NMMP samples

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

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

Non-NMMP samples

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

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

For Year 12, remedial action, outlined below, was required for associated replicates of the following Own Samples:

NMMP samples

LB1206 OS31- Review of *Pholoe baltica / P. assimilis* identifications – currently being undertaken by an external expert (Dr Mary Petersen).
Remedial Action - deemed completed (18/10/2006).

LB1207 OS30- Reprocess *Nucula nitidosa / N. nucleus* and *Amphiura chiajei* identifications for remaining replicates;
Review methods for estimation of abundance.
Remedial Action – completed (27/07/2006).

LB1209 OS30- Review methods for estimation of abundance.
Remedial Action – completed (11/05/2007).

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

Non-NMMP samples

LB1201 OS29- Reprocess residues for remaining replicate samples;

Review identifications of *Pholoe inornata*, *Monocorophium sextonae, Eumida sanguinea* and *Malmgreniella arenicolae.*
Remedial Action - status unknown.

One participating laboratory responsible for NMMP samples, LB1218, supplied three Own Samples without their associated sorted residues. In this instance the samples have been processed, but excluded from inapplicable derived statistics within this report. In future samples not supplied in the correct format will be rejected.

6. Comments on Individual Laboratories

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

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

Where possible these are noted for each laboratory listed below.

Also in the comments below, the results for RT26, RT27 and RT28 are expressed in terms of their position relative to the results from all laboratories. The overall range of differences at the level of genus and species was used to define three categories according to the number of differences: **Low**, **Mid** and **High** (based on the number of differences with the Unicomarine identifications, *i.e.* **Low** = relatively good agreement with Unicomarine identifications). Each laboratory has been placed into a group for information only, on this basis.

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

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

Laboratory – LB1201

Macrobenthos (Training Exercise)

MB13 – Coastal sample. Two taxonomic differences (*Molgula manhattensis* and *Spio martinensis*). All individuals extracted from the residue. Bray-Curtis similarity index of 93.94%. No biomass data supplied. Residue/fauna not stained. Laboratory policy stated as not extracting nematodes, bryozoans, hydroids or copepods.

Ring Test (Training Exercise)

RT26 – Six generic and eleven specific differences. Number of AQC identifications in Mid group.
RT27 – Two generic and four specific differences. Number of AQC identifications in Mid group.
RT28 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Fail, 'Bad'.
Seven taxonomic differences (*Malmgreniella arenicolae, Pholoe inornata, Anaitides maculata, Eumida sanguinea, Eulalia ornata/viridis, Monocorophium sextonae* and *Ophiura albida*). Five hundred and eighty-eight individuals not extracted from the residue, including eleven previously unpicked taxa (*Cliona* sp., *Perophora listeri, Balanus crenatus,* Turbellaria, *Branchiomma bombyx, Sphaerosyllis taylori, Callipallene* sp., *Polycarpa pomaria, Doto* sp., *Cuthona* sp. and *Pleurocrypta* sp.). Count variance of three individuals. Bray-Curtis similarity index of 49.4%. No biomass data supplied.

OS30 – NMBAQCS sample flag – Pass, 'Good'.
Three taxonomic differences (*Golfingia elongata, Amphictene auricoma* and *Gari fervensis*). Nine individuals not extracted from the residue, including one previously unpicked taxon (*Paradoneis lyra*). Bray-Curtis similarity index of 96.5%. No biomass data supplied.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Abra nitida*). Two individuals not extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 96.3%. No biomass data supplied.

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

PS26 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. No sediment descriptions provided.
PS27 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve displaced to the right of the majority of curves. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.

Laboratory – LB1202

Macrobenthos (Training Exercise)

MB13 – Coastal sample. All individuals correctly identified (*Molgula manhattensis* identified as *Molgula* sp.). One individual not picked from the residue, this was a previously unpicked taxon (Decapoda zoea). Bray-Curtis similarity index of 97.96%. Biomass on average 2.28% lighter than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Exercise)

RT26 – Five generic and sixteen specific differences. Number of AQC identifications in High group.
RT27 – Five generic and seven specific differences. Number of AQC identifications in High group.
RT28 – Two generic and three specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 18.28% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
Three taxonomic differences (*Malmgeniella arenicolae, Chamelea striatula* and *Eulima glabra*). All individuals extracted from the residue. Bray-Curtis similarity index of 95.9%. Biomass on average 0.02% heavier than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, 'Good'.

One taxonomic difference (*Thyasira polygona*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 98.9%. Biomass on average 13.8% heavier than Unicomarine Ltd.

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

PS26 – All NMBAQCS standards passed except sorting standard (marginally failed).
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'very slightly muddy (yellow) sand (oolitic?)' prior to analysis; described as 'sand' using the Folk triangle.
PS27 – NMBAQCS standards for %silt/clay and median failed. All remaining NMBAQCS standards passed.

Laser diffraction analysis conducted. Size distribution curve significantly displaced to the left of the other curves, indicating a larger proportion of coarser sand material. Sediment described as 'black, anoxic, slightly sandy mud + organic fragments' prior to analysis; described as 'sandy mud' using the Folk triangle.

Laboratory – LB1203

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Three generic and eight specific differences. Number of AQC identifications in Mid group.
RT27 – One generic and five specific differences. Number of AQC identifications in Mid group.
RT28 – Four generic and five specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified (one taxon repeated – *Praxillella affinis*). All individuals extracted from the residue. Bray-Curtis similarity index of 99.3%. No biomass by species data available.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. One individual not extracted from the residue, this was a previously unpicked taxon (*Crepidula fornicata* juv.). Bray-Curtis similarity index of 98.6%. No biomass by species data available.
OS31 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass by species data available.

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

PS26 – NMBAQCS standard for median failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve displaced to the right (finer) of the majority of curves. Sediment described as 'sand' prior to analysis; described as 'sand' using the Folk triangle.
PS27 – NMBAQCS standards for median, mean and IGS(SKi) failed. NMBAQCS standards for %silt/clay and sorting passed.
Laser diffraction analysis conducted. Size distribution curve displaced to the right of the majority of curves. The lack of data above 9phi would have caused the IGS(SKi) standard failure. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.

Laboratory – LB1204

Macrobenthos (Training Exercise)

MB13 – Coastal sample. All specimens correctly identified (*Molgula manhattensis* identified as Molgulidae sp. indet.). All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 4.55% heavier than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups except aquatic insects.

Ring Test (Training Exercise)

RT26 – Three generic and eleven specific differences. Number of AQC identifications in Mid group.
RT27 – All specimens correctly identified. Number of AQC identifications in Low group.
RT28 – Four generic and eight specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – Not participating in this exercise.
OS30 – Not participating in this exercise.
OS31 – Not participating in this exercise.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1205

Macrobenthos (Training Exercise)

MB13 - Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 - Not participating in this exercise.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 98.6%. Biomass on average 23.08% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
Two taxonomic differences (*Abra nitida* and *Eulimella laevis*). One individual not picked from the residue. Count variance of seven individuals. Bray-Curtis similarity index of 97.9%. Biomass on average 7.53% heavier than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
Three taxonomic differences (*Magelona alleni, Nebalia herbstii* and *Dosinia lupinus*). All individuals extracted from residue. Count variance of three individuals. Bray-Curtis similarity index of 98.9%. Biomass on average 4.01% heavier than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1206

Macrobenthos (Training Exercise)

MB13 – Coastal sample. One taxonomic difference (*Molgula manhattensis*). One individual not picked from the residue, this was a previously unpicked taxon (*Hydrobia ulvae*). Bray-Curtis similarity index of 93.88%. Biomass on average 2.57% heavier than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Exercise)

RT26 – Two generic and ten specific differences. Number of AQC identifications in Mid group.
RT27 – Three generic and four specific differences. Number of AQC identifications in Mid group.
RT28 – One generic and one specific difference. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Retusa umbilicata*). Twenty-six individuals not picked from the residue. Count variance of five individuals. Bray-Curtis similarity index of 97.6%. Biomass on average 3.96% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Acceptable'.
One taxonomic difference (*Tubificoides pseudogaster* agg.). Seven individuals not picked from the residue. Count variance of four individuals. Bray-Curtis similarity index of 92.0%. Biomass on average 10.12% lighter than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, following Remedial Action (tentative 'Poor' original flag); audit result under review, specimens with external expert..
Six taxonomic differences (*Glycera alba/rouxi, Paradoneis lyra, Pholoe baltica* (under review), *Thracia convexa, Polinices* sp. juv. and *Semierycina nitida*). Ten individuals not extracted from the residue, including one previously unpicked taxon (*Alcyonidium parasiticum*). Count variance of five individuals. Bray-Curtis similarity index of 87.6%. Biomass data supplied to 5 decimal places; not 4 as requested. Biomass on average 1.91% lighter than Unicomarine Ltd. Remedial action conducted: taxonomic error under review by Dr Mary Petersen (October 2006).

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

PS26 – NMBAQCS standard for %silt/clay failed. All remaining NMBAQCS standards passed.
Data from centralised analysis. Laser diffraction analysis conducted. Size distribution curve showing less silt/clay than the majority of curve data. Sediment described as 'sand' prior to analysis; described as 'sand' using the Folk triangle.
PS27 – All NMBAQCS standards passed.
Data from centralised analysis. Laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed results provided above 8.5phi. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.

Laboratory – LB1207

Macrobenthos (Training Exercise)

MB13 – Coastal sample. One taxonomic difference (*Molgula manhattensis*). One individual not picked from the residue, this was a previously unpicked taxon (*Hydrobia ulvae*). Bray-Curtis similarity index of 94.34%. Biomass on average 62.8% heavier than Unicomarine Ltd, primarily due to a single transcription error. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Exercise)

RT26 – Two generic and nine specific differences. Number of AQC identifications in Mid group.
RT27 – One generic and five specific differences. Number of AQC identifications in Mid group.
RT28 – Two generic and three specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 97.0%. Biomass on average 46.67% heavier than Unicomarine Ltd., primarily due to a transcription error.
OS30 – NMBAQCS sample flag – Pass, following Remedial Action ('Poor' original flag).
Five taxonomic differences (*Gammaropsis maculata, Abra nitida, Nuculoma tenuis, Nucula nucleus* and *Amphiura chiajei*). Thirteen individuals not extracted from the residue, including two previously unpicked taxa (Nematoda and *Autolytus* sp.). Two additional taxa found within extracted fauna (*Laonice bahusiensis* and *Nuculoma tenuis)*. Bray-Curtis similarity index of 85.11%. Biomass on average 5.79% heavier than Unicomarine Ltd. Remedial action conducted: taxonomic errors reviewed for all remaining replicates (27th July 2006).
OS31 – NMBAQCS sample flag – Pass, 'Acceptable'.
Seven taxonomic differences (*Golfingia elongata, Galathowenia oculata, Semierycina nitida, Abra nitida, Dosinia lupinus, Amphipholis squamata* and *Thracia convexa*). Four additional taxa found within extracted fauna (*Golfingia elongata*, *Semierycina nitida, Thracia* sp. juv. and Actiniaria). Three individuals not extracted from the residue. Count variance of six individuals. Bray-Curtis similarity index of 90.7%. Biomass on average 8.52% heavier than Unicomarine Ltd.

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

PS26 – NMBAQCS standard for %silt/clay failed. All remaining NMBAQCS standards passed.
NMBAQCS standard for %silt/clay failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve showing less silt/clay than the majority of curve data. Sediment described as 'sand' prior to analysis; described as 'sand' using the Folk triangle.
PS27 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve, although no detailed results provided above 8.5phi. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.

Laboratory – LB1208

Macrobenthos (Training Exercise)

MB13 - Coastal sample. All 'countable' individuals correctly identified (an empty *Nucula nitidosa* shell was counted as live and identified as *Nucula nucleus*). All individuals extracted from the residue. Count variance of one individual (empty *Nucula nitidosa*). Bray-Curtis similarity index of 97.30%. No biomass data supplied. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups except copepods and aquatic insects.

Ring Test (Training Exercise)

RT26 – One generic and ten specific differences. Number of AQC identifications in Mid group.
RT27 – Three generic and five specific differences. Number of AQC identifications in Mid group.
RT28 – Two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS30 – NMBAQCS sample flag – Pass, 'Acceptable'.
Two taxonomic differences (*Heterochaeta costata* and *Neomysis integer*). Four individuals not picked from the residue. Bray-Curtis similarity index of 91.8%. No biomass data supplied.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Heterochaeta costata*). Two individuals not extracted from residue. Bray-Curtis similarity index of 99.2%. No biomass data supplied.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1209

Macrobenthos (Training Exercise)

MB13 – No data received.

Ring Test (Training Exercise)

RT26 – No data received.
RT27 – No data received.
RT28 – Five generic and six specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Exercise)

LR10 – No specimens received.

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

OS29 – NMBAQCS sample flag – Pass, 'Excellent' (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 44.44% lighter than Aquatic Environments.
OS30 – NMBAQCS sample flag – Pass, following Remedial Action ('Bad' original flag). (External audit by Aquatic Environments).
All individuals correctly identified. One individual not picked from the residue, this was a previously unpicked taxon (*Levinsenia gracilis*). Bray-Curtis similarity index of 80.0%. Biomass on average 5.56% lighter than Aquatic Environments.
OS31 – NMBAQCS sample flag – Pass, 'Excellent' (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 7.95% lighter than Aquatic Environments.

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

PS26 – No data received. All NMBAQCS standards deemed failed.
PS27 – No data received. All NMBAQCS standards deemed failed.

Laboratory – LB1210

Macrobenthos (Training Exercise)

MB13 - Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – No data received.

RT27 – No data received.
RT28 – No data received.

Laboratory Reference (Training Exercise)

LR10 – No specimens received.

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

OS29 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS30 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS31 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1211 (left the Scheme; email notification dated 27/02/06)

Macrobenthos (Training Exercise)

MB13 - Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – Not participating in this exercise.
OS30 – Not participating in this exercise.
OS31 – Not participating in this exercise.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1212

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LB09 – Not participating in this exercise.

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

OS29 – Not participating in this exercise.
OS30 – Not participating in this exercise.
OS31 – Not participating in this exercise.

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

PS26 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'sandy' prior to analysis; no description provided using the Folk triangle (post-analysis).
PS27 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'mud' prior to analysis; no description provided using the Folk triangle (post-analysis).

Laboratory – LB1213

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Fourteen generic and twenty specific differences. Number of AQC identifications in High group.
RT27 – Six generic and ten specific differences. Number of AQC identifications in High group.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS30 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS31 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1214

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Two individuals not extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 99.7%. No biomass data supplied.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Four individuals not extracted from the residue. Count variance of nineteen individuals. Bray-Curtis similarity index of 99.8%. No biomass data supplied.
OS31 – NMBAQCS sample flag – Pass, 'Good'.

All individuals correctly identified. Four individuals not extracted from the residue. Count variance of three individuals. Bray-Curtis similarity index of 98.5%. No biomass data supplied.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1215

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 –One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Good' (External audit by Aquatic Environments).
All individuals correctly identified. Four individuals not extracted from the residue, including one previously unpicked taxon (*Leptochiton asellus*). Bray-Curtis similarity index of 99.7%. Biomass on average 2.14% heavier than Aquatic Environments.
OS30 – NMBAQCS sample flag – Pass, 'Good' (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Count variance of seven individuals. Bray-Curtis similarity index of 99.8%. Biomass on average 8.88% heavier than Aquatic Environments.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Six individuals not extracted from residue, including one previously unpicked taxon (*Arenicola* sp. juv.). Count variance of seven individuals. Bray-Curtis similarity index of 99.0%. Biomass on average 6.98% heavier than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1216

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Four generic and ten specific differences. Number of AQC identifications in Mid group.
RT27 – Two generic and two specific differences. Number of AQC identifications in Low group.
RT28 – Two generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.

One taxonomic difference (*Polinice catena* juv.). All individuals extracted from the residue. Bray-Curtis similarity index of 98.8%. Biomass data supplied to 5 decimal places; not 4 as requested. Biomass on average 14.93% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass data supplied to 5 decimal places; not 4 as requested. Biomass on average 11.13% lighter than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass data supplied to 5 decimal places; not 4 as requested. Biomass on average 9.75% heavier than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1217

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS30 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS31 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.

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

PS26 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. Size distribution curve displaced slightly to the left of the majority of curves. Sediment described as 'muddy, coarse sand' prior to analysis; described as 'moderately sorted fine skewed coarse sand' using the Folk triangle.
PS27 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'silt' prior to analysis; described as 'silt' using the Folk triangle.

Laboratory – LB1218

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – NMBAQCS sample flag – Not Applicable, sample residue not supplied for audit.
Three taxonomic differences (*Philine* sp., *Prionospio fallax* and *Abra nitida*). Count variance of eight individuals. Bray-Curtis similarity index of 92.1%. Biomass on average 9.87% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Not Applicable, sample residue not supplied for audit.
Three taxonomic differences (*Chaetoderma nitidulum, Aphelochaeta vivipara* and *Diaphana minuta*). Two additional taxa found within the extracted fauna (*Tubificoides* cf. *galiciensis* and *Diaphana minuta*). Count variance of twelve individuals. Bray-Curtis similarity index of 93.9%. Biomass on average 42.81% heavier than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Not Applicable, sample residue not supplied for audit.
Three taxonomic differences (*Spio martinensis,* Enchytraeidae and *Tubificoides* cf. *galiciensis*). One additional taxon found within the extracted fauna (*Spio martinensis*). Count variance of thirteen individuals. Bray-Curtis similarity index of 86.2%. Biomass on average 36.12% heavier than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1219

Macrobenthos (Training Exercise)

MB13 - Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Ten individuals not extracted from the residue. Bray-Curtis similarity index of 98.0%. No biomass data supplied.
OS31 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. No biomass data supplied.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1220

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Seven generic and seventeen specific differences. Number of AQC identifications in High group.

RT27 – Four generic and seven specific differences. Number of AQC identifications in Mid group.
RT28 – All twenty-five specimens correctly identified. Number of AQC identifications in Low group.

Laboratory Reference (Training Exercise)

LR10 - Not participating in this exercise.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 99.1%. Biomass on average 24.48% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 98.0%. Biomass on average 10.69% heavier than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Vesicularia spinosa*). Eight individuals not extracted from the residue. Bray-Curtis similarity index of 99.1%. Biomass on average 31.83% heavier than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1221

Macrobenthos (Training Exercise)

MB13 – Coastal sample. All individuals correctly identified (*Molgula manhattensis* identified as *Molgula* spp.; Podocopida identified as Ostracoda spp.). All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 12.7% lighter than Unicomarine Ltd. Residue/fauna stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Eight generic and eleven specific differences. Number of AQC identifications in High group.
RT28 – All twenty-five specimens correctly identified. Number of AQC identifications in Low group.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Good' (External audit by Aquatic Environments).
All individuals correctly identified. All individuals extracted from the residue. Count variance of twelve individuals. Bray-Curtis similarity index of 99.3%. Biomass on average 1.84% lighter than Aquatic Environments.
OS30 – NMBAQCS sample flag – Pass, 'Good' (External audit by Aquatic Environments).
All individuals correctly identified. One individual not extracted from the residue (*Balanus crenatus*). Count variance of seven individuals. Bray-Curtis similarity index of 99.7%. Biomass on average 1.19% heavier than Aquatic Environments.
OS31 – NMBAQCS sample flag – Pass, 'Good' (External audit by Aquatic Environments).

All individuals correctly identified. Two individuals not extracted from the residue, including one previously unpicked taxon (*Parvicardium exiguum*). Count variance of one individual. Bray-Curtis similarity index of 99.9%. Biomass on average 0.06% lighter than Aquatic Environments.

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

PS26 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'medium sand' prior to analysis; described as 'sandy mud' using the Folk triangle.
PS27 – NMBAQCS standard for IGS (SKi) failed. All remaining NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'fine mud' prior to analysis; described as 'mud' using the Folk triangle.

Laboratory – LB1222

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Four generic and ten specific differences. Number of AQC identifications in Mid group.
RT27 – Five generic and seven specific differences. Number of AQC identifications in Mid group.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – NMBAQCS sample flag – Pass, 'Acceptable'.
Six taxonomic differences (*Tubificoides* cf. *galiciensis, Cerastoderma edule, Sphaerodoropsis minuta?* and *Cossura pygodactyla*). One hundred and sixty-five individuals not extracted from the residue, including five previously unpicked taxa (*Bicellariella cilliata, Carcinus maenas* juv., *Scrupocellaria repans*, *Nolella* sp. and Campanulariidae). One additional taxon found within the extracted fauna (*Microprotopus maculatus*). Count variance of forty-eight individuals. Bray-Curtis similarity index of 93.6%. Biomass on average 1.48% lighter than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
Four taxonomic differences (*Websterineris glauca, Exogone naidina, Bodotria scorpioides, Cerastoderma edule, Caulleriella zetlandica* and *Tubificoides* cf. *galiciensis*). Four hundred and nine individuals not extracted from the residue, including five previously unpicked taxa (*Gibbula* sp. juv., Porifera, *Nolella* sp., Campanulariidae and *Hydrobia ulvae*). Five additional taxa found within the extracted fauna (Actiniaria, *Dendrodoa grossularia, Acanthochitona crinita, Cryptosula pallasiana* and Turbellaria). Count variance of one hundred and twenty individuals. Bray-Curtis similarity index of 96.2%. Biomass on average 31.34% lighter than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Seven individuals not extracted from the residue. Count variance of fourteen individuals. Bray-Curtis similarity index of 99.7%. Biomass on average 12.90% heavier than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1223

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – One generic and six specific differences. Number of AQC identifications in Low group.
RT27 – Two specific differences. Number of AQC identifications in Low group.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Specimens reviewed and returned.

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

OS29 – Not participating in this exercise.
OS30 – Not participating in this exercise.
OS31 – Not participating in this exercise.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1224

Macrobenthos (Training Exercise)

MB13 – Coastal sample. All individuals correctly identified (*Molgula manhattensis* identified *Molgula* sp.). All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 4.6% heavier than Unicomarine Ltd. Residue/fauna not stained. Laboratory policy stated as extracting all faunal groups.

Ring Test (Training Exercise)

RT26 – Three specific differences. Number of AQC identifications in Low group.
RT27 – Two specific differences. Number of AQC identifications in Low group.
RT28 – All twenty-five specimens correctly identified. Number of AQC identifications in Low group.

Laboratory Reference (Training Exercise)

LR10 – No specimens received.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Chamelea striatula*). All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 99.4%. Biomass on average 27.12% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
One taxonomic difference (*Nucula nitidosa*). All individuals extracted from the residue. Bray-Curtis similarity index of 95.7%. Biomass on average 1.66% lighter than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 97.9%. No biomass data supplied.

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

PS26 – NMBAQCS standard for %silt/clay, sorting and IGS (SKi) failed. NMBAQCS standards for median and mean passed.
Laser diffraction analysis conducted. Size distribution curve displaced to the right of the majority of curves and beneath all the other curves from 3.5 to 10phi, indicating a larger proportion of fine silt and clay material. Sediment described as 'muddy sand' prior to analysis; described as 'muddy sand' using the Folk triangle.

PS27 – All NMBAQCS standards passed.
Laser diffraction analysis conducted. No major differences in size distribution curve. Sediment described as 'mud' prior to analysis; described as 'mud' using the Folk triangle.

Laboratory – LB1225

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Eight generic and fifteen specific differences. Number of AQC identifications in High group.
RT27 – Four generic and ten specific differences. Number of AQC identifications in High group.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – Not participating in this exercise.
OS30 – Not participating in this exercise.
OS31 – Not participating in this exercise.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1226

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – NMBAQCS sample flag – Pass, 'Acceptable'.
All individuals correctly identified. Twelve individuals not extracted from the residue, including two previously unpicked taxa (Nematoda and *Anoplodactylus petiolatus*). Count variance of ten individuals. Bray-Curtis similarity index of 93.6%. Biomass on average 28.99% heavier than Unicomarine Ltd.
OS30 – NMBAQCS sample flag – Pass, 'Excellent'.
All individuals correctly identified. All individuals extracted from the residue. Bray-Curtis similarity index of 100%. Biomass on average 6.48% lighter than Unicomarine Ltd.
OS31 – NMBAQCS sample flag – Fail, 'Poor'; Remedial action status unknown.
One taxonomic difference (*Bathyporeia elegans*). Two individuals not extracted from the residue, including one previously unpicked taxon (*Mytilus edulis* juv.). Bray-Curtis similarity index of 87.5%. Biomass on average 0.35% lighter than Unicomarine Ltd.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1227

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS30 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.
OS31 – Sample not received. NMBAQCS sample flag – 'Deemed Fail'.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

Laboratory – LB1228

Macrobenthos (Training Exercise)

MB13 – Not participating in this exercise.

Ring Test (Training Exercise)

RT26 – Not participating in this exercise.
RT27 – Not participating in this exercise.
RT28 – Not participating in this exercise.

Laboratory Reference (Training Exercise)

LR10 – Not participating in this exercise.

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

OS29 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 99.2%. No biomass data supplied.
OS30 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. Four individuals not extracted from the residue, including two previously unpicked taxa (*Mendicula ferruginosa* and *M. pygmaea*). Bray-Curtis similarity index of 95.9%. No biomass data supplied.
OS31 – NMBAQCS sample flag – Pass, 'Good'.
All individuals correctly identified. One individual not extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 96.3%. No biomass data supplied.

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

PS26 – Not participating in this exercise.
PS27 – Not participating in this exercise.

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. Many of the interim results are now provided as secure PDF documents. E-mail capabilities must be made a prerequisite for participation in the Scheme. All primary correspondence for Scheme year thirteen will continue to be conducted via e-mail; hard copies of data sheets will be provided only where appropriate or specifically requested. The Scheme website should be fully utilised for reporting Scheme components.
3. Laboratories involved in UK NMMP data submission should endeavour to return data on **ALL** necessary components of the Scheme in the format requested. This will be required to allow the setting of performance "flags". Non-return of data will result in assignment of a "Fail" flag. For NMMP laboratories this deemed "Fail" for no submitted data is to be perceived as far worse than a participatory "Fail" flag.
4. A minority of participating laboratories have received 'deemed fail' flags as a result of not informing Unicomarine Ltd. of their intentions to abstain from particular exercises. The RT exercises are directly influenced by the number of participants, *i.e.* fewer participants enable less abundantly encountered taxa to be circulated. Some laboratories receive RT material but do not return data; 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 as soon as possible.
5. There were continued problems associated with the measurement of biomass for individual species. In this and the previous Scheme year several laboratories, despite using blotted wet weight biomass techniques, rendered some of their specimens too damaged to be re-identified. Some laboratories 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. A standardised protocol and reporting format for UK NMMP analysis is to be developed via the NMBAQC Scheme.
6. The particle size exercises (PS) once again show differences in the results obtained by different analytical methods (*e.g.* laser, sieve). 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 is to be developed through the NMBAQC Scheme for UK NMMP. The final draft will accommodate consultation and feedback from all significant parties.
7. The maintenance of a comprehensive reference collection has numerous benefits for improving identification ability, maintaining consistency of identification between surveys and access to growth series material. The Laboratory Reference exercise (LR) can be used as a means of verifying reference specimens. Laboratories are strongly recommended to implement and expand in-house reference collections of fauna. The inclusion of growth series material is extremely useful for certain faunal groups, *e.g.* identifying certain molluscs. All surveys should have an associated reference collection to enable ease of cross-checking or adopting future taxonomic developments.

8. Differences in the literature used for identification of invertebrates have been highlighted by the RT, MB and OS exercises. Unpublished keys from Scheme workshops, *etc.* could be posted on the Scheme's website. The Scheme has produced a UK Standard Taxonomic Literature List database. Laboratories are encouraged to review the content and give details of additions wherever possible.

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

10. There are still some problems of individuals and taxa missed at the sorting stage of Own Sample analysis. This is an area that is often the major contributing factor in samples with 'fail' flags or low Bray-Curtis similarity indices. In the MB13 exercise there was a significant improvement upon the previous year's results; unlike in the previous exercise this sample was relatively straightforward to sort and extract all the fauna. The situation was slightly worse for the OS samples where a maximum of 11 taxa and up to 15% of the taxa were not extracted. In the worst instances 588 individuals were not picked from the residue and up to 49% of the total individuals remained in the residue. On average for the OS exercise 0.7 taxa were not extracted compared with 0.52, 0.84, 1.73, 1.98, 2.04, 1.25, 1.48, 0.45 and 1.39 taxa from last nine 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 UK 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 are being developed through the NMBAQC Scheme, to standardise the faunal groups to be extracted from NMMP samples and reasonable levels of identification for all taxa likely to be encountered, participating laboratories will be required to provided comments prior to the production of the final draft.

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

13. 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.

8. References

Folk, R.L. (1974) *The Petrology of Sedimentary Rocks*. Hemphill Publishing Co. Texas

Hall, D.J. (2005) *National Marine Biological Analytical Quality Control Scheme. Particle Size Results: PS26.* Report to the NMBAQC Scheme participants. Unicomarine Report NMBAQCps26, October 2005.

Hall, D.J. (2006a) *National Marine Biological Analytical Quality Control Scheme. Macrobenthic Exercise Results – MB13.* Report to the NMBAQC Scheme participants. Unicomarine report NMBAQCmb13, June 2006.

Hall, D.J. (2006b) *National Marine Biological Analytical Quality Control Scheme. Particle Size Results: PS27.* Report to the NMBAQC Scheme participants. Unicomarine Report NMBAQCps27, May 2006.

Hall, D.J. & Worsfold, T.M. (2002) *National Marine Biological Analytical Quality Control Scheme. Oligochaeta Questionnaire Report: Including provisional NMMP standard policy for oligochaete identification.* Report to the NMBAQC Committee and Scheme participants. Unicomarine report NMBAQColigquest, July 2002.

Hall, D.J. & Worsfold, T.M. (2005a) *National Marine Biological Analytical Quality Control Scheme. Ring Test Bulletin – RTB#26.* Report to the NMBAQC Scheme participants. Unicomarine report NMBAQCrt26, October 2005.

Hall, D.J. & Worsfold, T.M. (2005b) *National Marine Biological Analytical Quality Control Scheme. Ring Test Bulletin – RTB#26 Additional Comments.* Report to the NMBAQC Scheme participants. Unicomarine report NMBAQCrt26extra, November 2005.

Hall, D.J. & Worsfold, T.M. (2006) *National Marine Biological Analytical Quality Control Scheme. Ring Test Bulletin – RTB#27.* Report to the NMBAQC Scheme participants. Unicomarine report NMBAQCrt27, May 2006.

Hall, D.J. & Dyson, J. D. (2006) *National Marine Biological Analytical Quality Control Scheme. Ring Test Bulletin – RTB#28.* Report to the NMBAQC Scheme participants. Unicomarine report NMBAQCrt28, May 2006.

Howson, C.M. & Picton, B.E. (eds) (1997) *The species directory of the marine fauna and flora of the British Isles and surrounding seas.* Ulster Museum and The Marine Conservation Society, Belfast and Ross-on-Wye.

Unicomarine (1995) *National Marine Biological Quality Control Scheme. Annual Report (Year one).* Report to the NMBAQC Committee and Scheme participants. September 1995.

Unicomarine (1996) *National Marine Biological Quality Control Scheme. Annual Report (Year two).* Report to the NMBAQC Committee and Scheme participants. September 1996.

Unicomarine (2001) *National Marine Biological Analytical Quality Control Scheme. Own Sample Format and Standards Review: Current Problems and Proposed Solutions.* Report to the NMBAQC Committee. April 2001.

Worsfold, T.M. & Hall, D.J. (2001) *National Marine Biological Analytical Quality Control Scheme. Sorting Methods Questionnaire*. Report to the NMBAQC Committee and Scheme participants. Unicomarine report NMBAQCsortmeth, August 2001.

Tables

Table 1. Results from the analysis of Macrobenthic sample MB13 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
LB1201	13	13	0	0.0	33	33	0	0.0	0	0	0.0	0	93.94	2
LB1202	11	12	-1	8.3	24	25	-1	4.0	1	1	4.0	0	97.96	0
LB1204	9	9	0	0.0	16	16	0	0.0	0	0	0.0	0	100.00	0
LB1206	11	12	-1	8.3	24	25	-1	4.0	1	1	4.0	0	93.88	1
LB1207	13	14	-1	7.1	26	27	-1	3.7	1	1	3.7	0	94.34	1
LB1208	11	10	1	9.1	18	17	1	5.6	0	0	0.0	1	97.30	0
LB1209	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1221	9	9	0	0.0	20	20	0	0.0	0	0	0.0	0	100.00	0
LB1224	14	14	0	0.0	31	31	0	0.0	0	0	0.0	0	100.00	0

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 MB13.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1201	UM count	-	24	4	-	2	-	2	1	33
	PL missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1202	UM count	-	18	-	-	4	-	2	1	25
	PL missed	-	0	-	-	1	-	0	0	1
	%missed	-	0.0	-	-	25.0	-	0.0	0.0	4.0
LB1204	UM count	-	11	-	-	2	-	2	1	16
	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1206	UM count	-	19	-	-	3	-	2	1	25
	PL missed	-	0	-	-	0	-	1	0	1
	%missed	-	0.0	-	-	0.0	-	50.0	0.0	4.0
LB1207	UM count	-	21	-	-	3	-	2	1	27
	PL missed	-	0	-	-	0	-	1	0	1
	%missed	-	0.0	-	-	0.0	-	50.0	0.0	3.7
LB1208	UM count	-	11	-	-	3	-	2	1	17
	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1209	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1221	UM count	-	14	-	-	3	-	2	1	20
	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1224	UM count	-	26	-	-	2	-	2	1	31
	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0

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 MB13. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1201	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1202	PL	-	0.04045	-	-	0.01241	-	0.13616	0.03185	0.22087
	UM	-	0.0377	-	-	0.0119	-	0.1357	0.0406	0.2259
	%diff.	-	6.8	-	-	4.1	-	0.3	-27.5	-2.277358
LB1204	PL	-	0.049	-	-	0.0099	-	0.1781	0.0116	0.2486
	UM	-	0.0366	-	-	0.0095	-	0.1806	0.0106	0.2373
	%diff.	-	25.3	-	-	4.0	-	-1.4	8.6	4.5454545
LB1206	PL	-	0.04993	-	-	0.13958	-	0.14810	0.04884	0.38645
	UM	-	0.0506	-	-	0.1379	-	0.1441	0.0439	0.3765
	%diff.	-	-1.3	-	-	1.2	-	2.7	10.1	2.5747186
LB1207	PL	-	0.6607	-	-	0.017	-	0.1485	0.1189	0.9451
	UM	-	0.0864	-	-	0.0117	-	0.148	0.1052	0.3513
	%diff.	-	86.9	-	-	31.2	-	0.3	11.5	62.8
LB1208	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1209	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB1221	PL	-	0.0346	-	-	0.0067	-	0.1544	0.0046	0.2003
	UM	-	0.0302	-	-	0.0055	-	0.1865	0.0035	0.2257
	%diff.	-	12.7	-	-	17.9	-	-20.8	23.9	-12.7
LB1224	PL	-	0.0973	-	-	0.0065	-	0.1091	0.174	0.3869
	UM	-	0.0881	-	-	0.0066	-	0.1094	0.165	0.3691
	%diff.	-	9.5	-	-	-1.5	-	-0.3	5.2	4.6

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

Table 4. Variation in faunal content of samples distributed as MB13.

Taxa*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total taxa
LB1201	0	8	1	0	1	0	2	1	13
LB1202	0	6	0	0	3	0	2	1	12
LB1204	0	5	0	0	1	0	2	1	9
LB1206	0	7	0	0	2	0	2	1	12
LB1207	0	9	0	0	2	0	2	1	14
LB1208	0	4	0	0	2	0	2	1	9
LB1209	-	-	-	-	-	-	-	-	-
LB1221	0	4	0	0	2	0	2	1	9
LB1224	0	10	0	0	1	0	2	1	14
Mean	0	7	0	0	2	0	2	1	12
Max	0	10	1	0	3	0	2	1	14
Min	0	4	0	0	1	0	2	1	9

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

Individuals*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total Ind.
LB1201	0	24	4	0	2	0	2	1	33
LB1202	0	18	0	0	4	0	2	1	25
LB1204	0	11	0	0	2	0	2	1	16
LB1206	0	19	0	0	3	0	2	1	25
LB1207	0	21	0	0	3	0	2	1	27
LB1208	0	11	0	0	3	0	2	1	17
LB1209	-	-	-	-	-	-	-	-	-
LB1221	0	14	0	0	3	0	2	1	20
LB1224	0	26	0	0	2	0	2	1	31
Mean	0	18	1	0	3	0	2	1	24
Max	0	26	4	0	4	0	2	1	33
Min	0	11	0	0	2	0	2	1	16

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

Table 5. Results from the analysis of Own Samples (OS29 to OS31) 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
LB1201	OS29	72	84	-12	14.3	612	1203	-591	49.1	11	588	48.9	-3	49.37	7	No biomass data
LB1201	OS30	58	58	0	0.0	212	221	-9	4.1	1	9	4.1	0	96.54	3	No biomass data
LB1201	OS31	33	32	1	3.0	149	150	-1	0.7	0	2	1.3	1	96.32	1	No biomass data
LB1202	OS29	1	1	0	0.0	7	7	0	0.0	0	0	0.0	0	100.00	0	-
LB1202	OS30	48	47	1	2.1	307	321	-14	4.4	0	0	0.0	-14	95.86	3	-
LB1202	OS31	34	33	1	2.9	131	130	1	0.8	0	0	0.0	1	98.85	1	-
LB1203	OS29	41	40	1	2.4	134	134	0	0.0	0	0	0.0	0	99.25	0	No spp. biomass data
LB1203	OS30	19	20	-1	5.0	36	37	-1	2.7	1	1	2.7	0	98.63	0	No spp. biomass data
LB1203	OS31	23	23	0	0.0	74	74	0	0.0	0	0	0.0	0	100.00	0	No spp. biomass data
LB1205	OS29	12	12	0	0.0	72	70	2	2.8	0	0	0.0	2	98.59	0	-
LB1205	OS30	41	42	-1	2.4	487	481	6	1.2	0	1	0.2	7	97.93	2	-
LB1205	OS31	50	50	0	0.0	519	516	3	0.6	0	0	0.0	3	98.94	3	-
LB1206	OS29	61	60	1	1.6	664	685	-21	3.1	0	26	3.8	5	97.55	1	-
LB1206	OS30	22	23	-1	4.3	129	140	-11	7.9	0	7	5.0	-4	91.97	1	-
LB1206	OS31	103	104	-1	1.0	1510	1525	-15	1.0	1	10	0.7	-5	87.61	6	Biomass to 5 decimal places; ext review ongoing
LB1207	OS29	10	10	0	0.0	17	16	1	5.9	0	0	0.0	1	96.97	0	-
LB1207	OS30	43	47	-4	8.5	184	192	-8	4.2	2	13	6.8	5	85.11	5	Remedial Action completed 12/07/06
LB1207	OS31	45	49	-4	8.2	238	247	-9	3.6	0	3	1.2	-6	90.72	7	-
LB1208	OS29	7	7	0	0.0	107	107	0	0.0	0	0	0.0	0	100.00	0	No biomass data
LB1208	OS30	8	8	0	0.0	181	185	-4	2.2	0	4	2.2	0	91.80	2	No biomass data
LB1208	OS31	8	7	1	12.5	263	265	-2	0.8	0	2	0.8	0	99.24	1	No biomass data
LB1209	OS29	1	1	0	0.0	1	1	0	0.0	0	0	0.0	0	100.00	0	External audit
LB1209	OS30	2	3	-1	33.3	2	3	-1	33.3	1	1	33.3	0	80.00	0	External audit; Remedial Action completed 11/05/07
LB1209	OS31	3	3	0	0.0	3	3	0	0.0	0	0	0.0	0	100.00	0	External audit
LB1210	OS29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1210	OS30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1210	OS31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1212	OS29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1212	OS30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1212	OS31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1213	OS29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1213	OS30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1213	OS31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1214	OS29	20	20	0	0.0	910	911	-1	0.1	0	2	0.2	1	99.73	0	No biomass data
LB1214	OS30	24	24	0	0.0	3242	3227	15	0.5	0	4	0.1	19	99.77	0	No biomass data
LB1214	OS31	12	12	0	0.0	168	169	-1	0.6	0	4	2.4	3	98.52	0	No biomass data
LB1215	OS29	60	61	-1	1.6	621	625	-4	0.6	1	4	0.6	0	99.69	0	External audit
LB1215	OS30	60	60	0	0.0	1912	1905	7	0.4	0	0	0.0	7	99.77	0	External audit
LB1215	OS31	19	20	-1	5.0	470	469	1	0.2	1	6	1.3	7	99.04	0	-
LB1216	OS29	17	17	0	0.0	86	86	0	0.0	0	0	0.0	0	98.84	1	Biomass to 5 decimal places
LB1216	OS30	21	21	0	0.0	95	95	0	0.0	0	0	0.0	0	100.00	0	Biomass to 5 decimal places
LB1216	OS31	14	14	0	0.0	33	33	0	0.0	0	0	0.0	0	100.00	0	Biomass to 5 decimal places
LB1217	OS29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1217	OS30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1217	OS31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1218	OS29	31	31	0	0.0	1686	1678	8	0.5	-	-	-	-	(92.08)	3	NO RESIDUE SUPPLIED
LB1218	OS30	13	15	-2	13.3	159	171	-12	7.0	-	-	-	-	(93.94)	3	NO RESIDUE SUPPLIED
LB1218	OS31	24	25	-1	4.0	386	373	13	3.4	-	-	-	-	(86.12)	3	NO RESIDUE SUPPLIED
LB1219	OS29	11	11	0	0.0	46	46	0	0.0	0	0	0.0	0	100.00	0	No biomass data
LB1219	OS30	26	26	0	0.0	240	250	-10	4.0	0	10	4.0	0	97.97	0	No biomass data
LB1219	OS31	19	19	0	0.0	189	189	0	0.0	0	0	0.0	0	100.00	0	No biomass data
LB1220	OS29	7	7	0	0.0	55	56	-1	1.8	0	0	0.0	-1	99.12	0	-
LB1220	OS30	9	9	0	0.0	50	48	2	4.0	0	0	0.0	2	98.00	0	-
LB1220	OS31	19	19	0	0.0	573	581	-8	1.4	0	8	1.4	0	99.14	1	-
LB1221	OS29	12	12	0	0.0	946	934	12	1.3	0	0	0.0	12	99.26	0	External audit
LB1221	OS30	43	43	0	0.0	1149	1143	6	0.5	0	1	0.1	7	99.65	0	External audit
LB1221	OS31	68	69	-1	1.4	1660	1661	-1	0.1	1	2	0.1	1	99.91	0	External audit
LB1222	OS29	117	127	-10	7.9	3237	3598	-361	10.0	5	409	11.4	48	93.61	6	-
LB1222	OS30	82	88	-6	6.8	2403	2448	-45	1.8	5	165	6.7	120	96.23	4	-
LB1222	OS31	10	10	0	0.0	1417	1410	7	0.5	0	7	0.5	14	99.68	0	-
LB1224	OS29	24	24	0	0.0	232	231	1	0.4	0	0	0.0	1	99.35	1	-
LB1224	OS30	8	8	0	0.0	23	23	0	0.0	0	0	0.0	0	95.65	1	-
LB1224	OS31	5	5	0	0.0	23	24	-1	4.2	0	0	0.0	-1	97.87	0	No biomass data
LB1226	OS29	12	13	-1	7.7	109	111	-2	1.8	2	12	10.8	10	93.64	0	-
LB1226	OS30	3	3	0	0.0	13	13	0	0.0	0	0	0.0	0	100.00	0	-
LB1226	OS31	4	5	-1	20.0	15	17	-2	11.8	1	2	11.8	0	87.50	1	-
LB1227	OS29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1227	OS30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1227	OS31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1228	OS29	20	20	0	0.0	61	60	1	1.6	0	0	0.0	1	99.19	0	No biomass data
LB1228	OS30	20	22	-2	9.1	71	75	-4	5.3	2	4	5.3	0	95.89	0	No biomass data
LB1228	OS31	18	18	0	0.0	22	24	-2	8.3	0	1	4.2	-1	96.30	0	No biomass data

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

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS29-31).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1201	UM count	2	326	-	6	290	29	496	54	1203
OS29	PL missed	1	56	-	4	22	12	447	46	588
	%missed	50.0	17.2	-	66.7	7.6	41.4	90.1	85.2	48.9
LB1201	UM count	4	88	-	-	25	54	36	14	221
OS30	PL missed	0	3	-	-	0	0	1	5	9
	%missed	0.0	3.4	-	-	0.0	0.0	2.8	35.7	4.1
LB1201	UM count	5	70	-	-	2	2	70	1	150
OS31	PL missed	0	0	-	-	0	0	2	0	2
	%missed	0.0	0.0	-	-	0.0	0.0	2.9	0.0	1.3
LB1202	UM count	-	-	-	-	-	7	-	-	7
OS29	PL missed	-	-	-	-	-	0	-	-	0
	%missed	-	-	-	-	-	0.0	-	-	0.0
LB1202	UM count	3	71	-	-	3	3	237	4	321
OS30	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1202	UM count	5	66	-	-	7	-	52	-	130
OS31	PL missed	0	0	-	-	0	-	0	-	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	-	0.0
LB1203	UM count	-	36	-	1	22	6	64	5	134
OS29	PL missed	-	0	-	0	0	0	0	0	0
	%missed	-	0.0	-	0.0	0.0	0.0	0.0	0.0	0.0
LB1203	UM count	-	29	-	-	7	-	1	-	37
OS30	PL missed	-	0	-	-	0	-	1	-	1
	%missed	-	0.0	-	-	0.0	-	100.0	-	2.7
LB1203	UM count	-	69	-	-	2	-	3	-	74
OS31	PL missed	-	0	-	-	0	-	0	-	0
	%missed	-	0.0	-	-	0.0	-	0.0	-	0.0
LB1205	UM count	-	20	5	-	12	2	31	-	70
OS29	PL missed	-	0	0	-	0	0	0	-	0
	%missed	-	0.0	0.0	-	0.0	0.0	0.0	-	0.0
LB1205	UM count	4	334	-	-	28	15	93	6	480
OS30	PL missed	0	0	-	-	1	0	0	0	1
	%missed	0.0	0.0	-	-	3.6	0.0	0.0	0.0	0.2
LB1205	UM count	5	364	3	-	44	11	72	17	516
OS31	PL 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
LB1206	UM count	5	258	-	-	33	6	380	3	685
OS29	PL missed	0	1	-	-	0	0	25	0	26
	%missed	0.0	0.4	-	-	0.0	0.0	6.6	0.0	3.8
LB1206	UM count	-	64	20	-	1	1	48	6	140
OS30	PL missed	-	4	0	-	0	0	3	0	7
	%missed	-	6.3	0.0	-	0.0	0.0	6.3	0.0	5.0
LB1206	UM count	45	934	-	-	71	51	384	40	1525
OS31	PL missed	0	3	-	-	1	1	5	0	10
	%missed	0.0	0.3	-	-	1.4	2.0	1.3	0.0	0.7

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS29-31).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1207	UM count	-	9	-	-	2	-	4	1	16
OS29	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB1207	UM count	2	127	-	-	28	6	27	2	192
OS30	PL missed	0	4	-	-	5	0	2	2	13
	%missed	0.0	3.1	-	-	17.9	0.0	7.4	100.0	6.8
LB1207	UM count	2	40	-	-	1	96	97	11	247
OS31	PL missed	0	1	-	-	0	0	2	0	3
	%missed	0.0	2.5	-	-	0.0	0.0	2.1	0.0	1.2
LB1208	UM count	-	51	48	-	-	-	-	8	107
OS29	PL missed	-	0	0	-	-	-	-	0	0
	%missed	-	0.0	0.0	-	-	-	-	0.0	0.0
LB1208	UM count	-	125	41	-	7	-	-	12	185
OS30	PL missed	-	1	2	-	0	-	-	1	4
	%missed	-	0.8	4.9	-	0.0	-	-	8.3	2.2
LB1208	UM count	-	2	122	-	73	-	10	58	265
OS31	PL missed	-	0	1	-	0	-	0	1	2
	%missed	-	0.0	0.8	-	0.0	-	0.0	1.7	0.8
LB1209	AE count	-	1	-	-	-	-	-	-	1
OS29	UM missed	-	0	-	-	-	-	-	-	0
	%missed	-	0.0	-	-	-	-	-	-	0.0
LB1209	AE count	-	3	-	-	-	-	-	-	3
OS30	UM missed	-	1	-	-	-	-	-	-	1
	%missed	-	33.3	-	-	-	-	-	-	33.3
LB1209	AE count	1	1	-	-	-	-	1	-	3
OS31	UM missed	0	0	-	-	-	-	0	-	0
	%missed	0.0	0.0	-	-	-	-	0.0	-	0.0
LB1214	UM count	-	830	66	-	4	-	11	-	911
OS29	PL missed	-	1	1	-	0	-	0	-	2
	%missed	-	0.1	1.5	-	0.0	-	0.0	-	0.2
LB1214	UM count	-	3040	141	-	4	-	21	21	3227
OS30	PL missed	-	4	0	-	0	-	0	0	4
	%missed	-	0.1	0.0	-	0.0	-	0.0	0.0	0.1
LB1214	UM count	-	74	93	-	-	-	2	-	169
OS31	PL missed	-	1	3	-	-	-	0	-	4
	%missed	-	1.4	3.2	-	-	-	0.0	-	2.4
LB1215	AE count	-	361	83	-	101	-	64	16	625
OS29	UM missed	-	1	1	-	0	-	2	0	4
	%missed	-	0.3	1.2	-	0.0	-	3.1	0.0	0.6
LB1215	AE count	1	1071	59	2	62	1	60	649	1905
OS30	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
LB1215	UM count	-	67	321	-	25	-	16	40	469
OS31	PL missed	-	4	1	-	0	-	0	1	6
	%missed	-	6.0	0.3	-	0.0	-	0.0	2.5	1.3

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS29-31).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1216	UM count	-	38	-	-	4	3	41	-	86
OS29	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1216	UM count	-	51	-	-	3	10	31	-	95
OS30	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1216	UM count	-	19	-	-	6	2	6	-	33
OS31	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB1217	UM count	-	-	-	-	-	-	-	-	0
OS29	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1217	UM count	-	-	-	-	-	-	-	-	0
OS30	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1217	UM count	-	-	-	-	-	-	-	-	0
OS31	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1218	UM count	-	-	-	-	-	-	-	-	0
OS29	PL missed	-	SAMPLE RESIDUE NOT SUPPLIED						-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1218	UM count	-	-	-	-	-	-	-	-	0
OS30	PL missed	-	SAMPLE RESIDUE NOT SUPPLIED						-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1218	UM count	-	-	-	-	-	-	-	-	0
OS31	PL missed	-	SAMPLE RESIDUE NOT SUPPLIED						-	0
	%missed	-	-	-	-	-	-	-	-	-
LB1219	UM count	-	20	-	-	23	3	-	-	46
OS29	PL missed	-	0	-	-	0	0	-	-	0
	%missed	-	0.0	-	-	0.0	0.0	-	-	0.0
LB1219	UM count	1	200	-	-	6	6	29	8	250
OS30	PL missed	0	0	-	-	0	0	10	0	10
	%missed	0.0	0.0	-	-	0.0	0.0	34.5	0.0	4.0
LB1219	UM count	-	164	-	-	1	1	22	1	189
OS31	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1220	UM count	-	3	53	-	-	-	-	-	56
OS29	PL missed	-	0	0	-	-	-	-	-	0
	%missed	-	0.0	0.0	-	-	-	-	-	0.0
LB1220	UM count	-	5	37	-	-	-	6	-	48
OS30	PL missed	-	0	0	-	-	-	0	-	0
	%missed	-	0.0	0.0	-	-	-	0.0	-	0.0
LB1220	UM count	-	467	38	-	31	-	13	32	581
OS31	PL missed	-	6	0	-	0	-	1	1	8
	%missed	-	1.3	0.0	-	0.0	-	7.7	3.1	1.4

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS29-31).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1221	AE count	-	58	783	-	11	-	79	3	934
OS29	UM missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB1221	AE count	-	564	253	3	180	-	134	9	1143
OS30	UM missed	-	0	0	0	1	-	0	0	1
	%missed	-	0.0	0.0	0.0	0.6	-	0.0	0.0	0.1
LB1221	AE count	2	489	2	-	486	2	649	31	1661
OS31	UM missed	0	0	0	-	0	0	2	0	2
	%missed	0.0	0.0	0.0	-	0.0	0.0	0.3	0.0	0.1
LB1222	UM count	19	1942	35	5	403	8	376	810	3598
OS29	PL missed	3	116	1	1	41	0	27	220	409
	%missed	15.8	6.0	2.9	20.0	10.2	0.0	7.2	27.2	11.4
LB1222	UM count	4	1378	29	9	242	-	555	231	2448
OS30	PL missed	0	65	0	1	20	-	55	24	165
	%missed	0.0	4.7	0.0	11.1	8.3	-	9.9	10.4	6.7
LB1222	UM count	-	1	1370	-	1	-	-	38	1410
OS31	PL missed	-	0	7	-	0	-	-	0	7
	%missed	-	0.0	0.5	-	0.0	-	-	0.0	0.5
LB1224	UM count	3	54	-	-	16	43	108	7	231
OS29	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1224	UM count	-	19	-	-	-	-	3	1	23
OS30	PL missed	-	0	-	-	-	-	0	0	0
	%missed	-	0.0	-	-	-	-	0.0	0.0	0.0
LB1224	UM count	-	17	1	-	-	-	5	1	24
OS31	PL missed	-	0	0	-	-	-	0	0	0
	%missed	-	0.0	0.0	-	-	-	0.0	0.0	0.0
LB1226	UM count	-	10	2	1	8	-	89	1	111
OS29	PL missed	-	0	0	1	3	-	7	1	12
	%missed	-	0.0	0.0	100.0	37.5	-	7.9	100.0	10.8
LB1226	UM count	-	-	1	-	12	-	-	-	13
OS30	PL missed	-	-	0	-	0	-	-	-	0
	%missed	-	-	0.0	-	0.0	-	-	-	0.0
LB1226	UM count	-	2	-	-	13	-	2	-	17
OS31	PL missed	-	0	-	-	0	-	2	-	2
	%missed	-	0.0	-	-	0.0	-	100.0	-	11.8
LB1228	UM count	1	30	-	-	6	1	21	1	60
OS29	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB1228	UM count	-	45	-	-	4	2	24	-	75
OS30	PL missed	-	0	-	-	0	0	4	-	4
	%missed	-	0.0	-	-	0.0	0.0	16.7	-	5.3
LB1228	UM count	-	14	-	-	1	-	2	7	24
OS31	PL missed	-	0	-	-	0	-	0	1	1
	%missed	-	0.0	-	-	0.0	-	0.0	14.3	4.2

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 OS29-OS31.

		Sample OS29								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1201	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1202	PL	-	-	-	-	-	0.0093	-	-	0.0093
	UM	-	-	-	-	-	0.0076	-	-	0.0076
	%diff.	-	-	-	-	-	18.3	-	-	18.3
LB1203	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1205	PL	-	0.3429	0.0006	-	0.0024	0.8756	0.0563	-	1.2778
	UM	-	0.2850	0.0003	-	0.0014	0.6349	0.0613	-	0.9829
	%diff.	-	16.9	50.0	-	41.7	27.5	-8.9	-	23.1
LB1206	PL	0.0049	3.8274	-	-	0.0275	0.0505	1.9046	0.0005	5.8154
	UM	0.0059	3.5529	-	-	0.0287	0.0535	1.9438	0.0004	5.5852
	%diff.	-20.4	7.2	-	-	-4.4	-5.9	-2.1	20.0	4.0
LB1207	PL	-	0.4065	-	-	1.8989	-	0.4348	0.0217	2.7619
	UM	-	0.3814	-	-	0.6470	-	0.4249	0.0197	1.4730
	%diff.	-	6.2	-	-	65.9	-	2.3	9.2	46.7
LB1208	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1209	UM	-	0.0081	-	-	-	-	-	-	0.0081
	AE	-	0.0117	-	-	-	-	-	-	0.0117
	%diff.	-	-44.4	-	-	-	-	-	-	-44.4
LB1214	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1215	UM	0.0001	4.6567	0.0186	-	0.0520	-	43.6198	0.0002	48.3474
	AE	0.0001	4.4674	0.0158	-	0.0506	-	42.7801	0.0002	47.3142
	%diff.	0.0	4.1	15.1	-	2.7	-	1.9	0.0	2.1
LB1216	PL	-	0.02691	-	-	0.00558	0.11608	0.19598	-	0.34455
	UM	-	0.0535	-	-	0.0015	0.0301	0.2080	-	0.2931
	%diff.	-	-98.8	-	-	73.1	74.1	-6.1	-	14.9
LB1218	PL	0.0081	1.3074	0.1161	-	0.0001	-	0.3280	0.0001	1.7598
	UM	0.0069	1.1178	0.1479	-	0.0001	-	0.3133	0.0001	1.5861
	%diff.	14.8	14.5	-27.4	-	0.0	-	4.5	0.0	9.9
LB1219	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1220	PL	-	0.0106	0.0086	-	-	-	-	-	0.0192
	UM	-	0.0082	0.0063	-	-	-	-	-	0.0145
	%diff.	-	22.6	26.7	-	-	-	-	-	24.5
LB1221	UM	-	4.5296	0.8513	-	0.0139	-	0.0275	0.0001	5.4224
	AE	-	4.6311	0.8549	-	0.0132	-	0.0230	0.0001	5.5223
	%diff.	-	-2.2	-0.4	-	5.0	-	16.4	0.0	-1.8
LB1222	PL	-	3.1700	0.0021	-	0.0113	-	48.3027	0.0182	51.5043
	UM	-	3.9363	0.0025	-	0.0128	-	48.2884	0.0272	52.2672
	%diff.	-	-24.2	-19.0	-	-13.3	-	0.0	-49.5	-1.5
LB1224	PL	0.0031	0.3486	-	-	0.0062	2.7000	2.3447	0.0008	5.4034
	UM	0.0004	0.2681	-	-	0.0038	1.4209	2.2435	0.0014	3.9381
	%diff.	87.1	23.1	-	-	38.7	47.4	4.3	-75.0	27.1
LB1226	PL	-	0.0565	0.0011	-	0.0182	-	0.0163	-	0.0921
	UM	-	0.0336	0.0004	-	0.0087	-	0.0227	-	0.0654
	%diff.	-	40.5	63.6	-	52.2	-	-39.3	-	29.0
LB1228	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

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 OS29-OS31.

		Sample OS30								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1201	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1202	PL	0.2352	0.5282	-	-	0.0031	0.1274	6.2711	0.0124	7.1774
	UM	0.2263	0.4512	-	-	0.0027	0.1135	6.3703	0.0120	7.1760
	%diff.	3.8	14.6	-	-	12.9	10.9	-1.6	3.2	0.0
LB1203	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1205	PL	0.0608	3.6163	-	-	0.0468	2.7398	5.1525	0.0017	11.6179
	UM	0.0581	3.1313	-	-	0.0278	2.5020	5.0229	0.0013	10.7434
	%diff.	4.4	13.4	-	-	40.6	8.7	2.5	23.5	7.5
LB1206	PL	-	0.0767	0.0011	-	0.0015	0.0001	0.1211	0.0001	0.2006
	UM	-	0.0862	0.0013	-	0.0012	0.0001	0.1320	0.0001	0.2209
	%diff.	-	-12.4	-18.2	-	20.0	0.0	-9.0	0.0	-10.1
LB1207	PL	0.0116	3.4364	-	-	0.0540	0.2126	200.3770	-	204.0916
	UM	0.0116	3.4414	-	-	0.0652	0.2260	188.5404	-	192.2846
	%diff.	0.0	-0.1	-	-	-20.7	-6.3	5.9	-	5.8
LB1208	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1209	UM	-	0.0036	-	-	-	-	-	-	0.0036
	AE	-	0.0038	-	-	-	-	-	-	0.0038
	%diff.	-	-5.6	-	-	-	-	-	-	-5.6
LB1214	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1215	UM	0.0002	3.2367	0.0051	0.0003	0.1319	0.0001	0.1731	0.5788	4.1262
	AE	0.0002	2.9714	0.0045	0.0003	0.1212	0.0001	0.1589	0.5031	3.7597
	%diff.	0.0	8.2	11.8	0.0	8.1	0.0	8.2	13.1	8.9
LB1216	PL	-	0.02768	-	-	0.00210	0.06318	0.16349	-	0.25645
	UM	-	0.0448	-	-	0.0034	0.0694	0.1674	-	0.2850
	%diff.	-	-61.8	-	-	-61.9	-9.8	-2.4	-	-11.1
LB1218	PL	-	0.1608	0.0010	-	0.0014	-	0.0078	-	0.1710
	UM	-	0.0913	0.0004	-	0.0005	-	0.0056	-	0.0978
	%diff.	-	43.2	60.0	-	64.3	-	28.2	-	42.8
LB1219	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1220	PL	-	0.0004	0.0045	-	-	-	0.0297	-	0.0346
	UM	-	0.0005	0.0036	-	-	-	0.0268	-	0.0309
	%diff.	-	-25.0	20.0	-	-	-	9.8	-	10.7
LB1221	UM	-	0.7567	0.0251	0.0016	0.1672	-	27.4272	0.0003	28.3781
	AE	-	0.6702	0.0260	0.0014	0.1511	-	27.1907	0.0003	28.0397
	%diff.	-	11.4	-3.6	12.5	9.6	-	0.9	0.0	1.2
LB1222	PL	0.0004	0.4608	0.0004	-	0.0190	-	1.2348	0.0010	1.7164
	UM	0.0005	0.6890	0.0009	-	0.0335	-	1.5294	0.0011	2.2544
	%diff.	-25.0	-49.5	-125.0	-	-76.3	-	-23.9	-10.0	-31.3
LB1224	PL	-	0.2934	-	-	-	-	0.5779	0.0116	0.8829
	UM	-	0.2982	-	-	-	-	0.5890	0.0104	0.8976
	%diff.	-	-1.6	-	-	-	-	-1.9	10.3	-1.7
LB1226	PL	-	-	0.0001	-	0.1171	-	-	-	0.1172
	UM	-	-	0.0001	-	0.1247	-	-	-	0.1248
	%diff.	-	-	0.0	-	-6.5	-	-	-	-6.5
LB1228	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

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 OS29-OS31.

		Sample OS31								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB1201	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1202	PL	0.0089	0.4054	-	-	0.0260	-	0.0817	-	0.5220
	UM	0.0066	0.3591	-	-	0.0190	-	0.0690	-	0.4537
	%diff.	25.8	11.4	-	-	26.9	-	15.5	-	13.1
LB1203	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1205	PL	0.3427	4.55743	0.0004	-	0.0599	1.8216	4.0598	0.2057	11.04753
	UM	0.3341	4.4261	0.0003	-	0.0403	1.6792	3.9552	0.1692	10.6044
	%diff.	2.5	2.9	25.0	-	32.7	7.8	2.6	17.7	4.0
LB1206	PL	0.02450	2.05939	-	-	0.18098	0.28583	1.49448	0.01192	4.05710
	UM	0.0235	2.1947	-	-	0.2027	0.2850	1.4181	0.0106	4.1346
	%diff.	4.1	-6.6	-	-	-12.0	0.3	5.1	11.1	-1.9
LB1207	PL	0.0118	2.2749	-	-	0.0001	3.9126	18.5877	0.4370	25.2241
	UM	0.0108	2.1147	-	-	0.0003	3.7256	16.8138	0.4097	23.0749
	%diff.	8.5	7.0	-	-	-200.0	4.8	9.5	6.2	8.5
LB1208	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1209	UM	0.0385	0.0102	-	-	-	-	0.0016	-	0.0503
	AE	0.0405	0.0122	-	-	-	-	0.0016	-	0.0543
	%diff.	-5.2	-19.6	-	-	-	-	0.0	-	-8.0
LB1214	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1215	PL	-	0.1239	0.0427	-	0.0556	-	0.0127	0.0674	0.3023
	UM	-	0.1148	0.0350	-	0.0590	-	0.0124	0.0600	0.2812
	%diff.	-	7.3	18.0	-	-6.1	-	2.4	11.0	7.0
LB1216	PL	-	0.03650	-	-	0.00308	0.19265	1.00180	-	1.23403
	UM	-	0.0608	-	-	0.0045	0.0661	0.9823	-	1.1137
	%diff.	-	-66.6	-	-	-46.1	65.7	1.9	-	9.8
LB1218	PL	-	0.7622	0.0145	-	-	-	0.0419	0.0001	0.8187
	UM	-	0.4901	0.0085	-	-	-	0.0243	0.0001	0.5230
	%diff.	-	35.7	41.4	-	-	-	42.0	0.0	36.1
LB1219	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1220	PL	-	0.4633	0.0043	-	0.0617	-	0.0493	0.0007	0.5793
	UM	-	0.3069	0.0047	-	0.0396	-	0.0432	0.0005	0.3949
	%diff.	-	33.8	-9.3	-	35.8	-	12.4	28.6	31.8
LB1221	UM	0.0030	6.5199	0.0001	-	0.1554	0.0005	21.7394	0.7979	29.2162
	AE	0.0030	6.4477	0.0001	-	0.1366	0.0005	21.8354	0.8090	29.2323
	%diff.	0.0	1.1	0.0	-	12.1	0.0	-0.4	-1.4	-0.1
LB1222	PL	-	0.0001	0.5484	-	0.0001	-	-	0.0002	0.5488
	UM	-	0.0001	0.4774	-	0.0001	-	-	0.0004	0.4780
	%diff.	-	0.0	12.9	-	0.0	-	-	-100.0	12.9
LB1224	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB1226	PL	-	0.0135	-	-	0.0148	-	-	-	0.0283
	UM	-	0.0135	-	-	0.0149	-	-	-	0.0284
	%diff.	-	0.0	-	-	-0.7	-	-	-	-0.4
LB1228	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Table 8. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS26.

PS26	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS26 - 42 - laser	6.21	1.52	1.67	1.25	0.290
PS26 - 43 - laser	3.31	1.49	1.60	1.02	0.180
PS26 - 44 - laser	4.80	1.50	1.64	1.12	0.230
PS26 - 45 - laser	4.35	1.46	1.60	1.09	0.230
PS26 - 46 - laser	3.65	1.48	1.60	1.04	0.200
PS26 - 47 - laser	4.52	1.50	1.62	1.07	0.220
PS26 - 48 - laser	3.33	1.45	1.57	1.03	0.190
PS26 - 35 - sieve	2.69	1.44	1.56	0.94	0.26
PS26 - 36 - sieve	2.13	1.38	1.48	0.89	0.25
PS26 - 37 - sieve	2.49	1.37	1.49	0.92	0.28
PS26 - 38 - sieve	2.42	1.30	1.43	0.89	0.30
PS26 - 39 - sieve	2.18	1.37	1.47	0.88	0.26
PS26 - 40 - sieve	2.74	1.39	1.51	0.93	0.27
PS26 - 41 - sieve	2.20	1.33	1.45	0.88	0.28

Table 9. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS27.

PS27	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS27 - 42 - laser	95.49	6.99	7.01	1.93	0.030
PS27 - 43 - laser	95.98	6.94	6.99	1.92	0.050
PS27 - 44 - laser	96.85	6.94	7.01	1.90	0.080
PS27 - 45 - laser	97.18	6.94	7.01	1.88	0.080
PS27 - 46 - laser	95.98	6.93	7.01	1.95	0.070
PS27 - 47 - laser	95.20	6.93	6.98	1.98	0.060
PS27 - 48 - laser	95.95	6.95	7.00	1.93	0.050
PS27 - 35 - sieve	98.77	-	-	-	-
PS27 - 36 - sieve	99.36	-	-	-	-
PS27 - 37 - sieve	99.30	-	-	-	-
PS27 - 38 - sieve	99.09	-	-	-	-
PS27 - 39 - sieve	99.07	-	-	-	-
PS27 - 40 - sieve	99.16	-	-	-	-
PS27 - 41 - sieve	99.01	-	-	-	-

Table 10. Summary of the particle size information received from participating laboratories and replicate analysis laboratories for the twenty-sixth particle size distribution - PS26.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB1201	DS/L	3.65	0.74	0.93	1.09	0.38
LB1202	WS/DS/FD/L	3.78	0.99	1.37	1.30	0.43
LB1203	DS/WS/L	5.79	1.91	2.087	1.10	0.346
LB1206*	L	0.84	0.89	1.00	0.89	0.19
LB1207	L	0.84	0.89	1.00	0.89	0.19
LB1212	L	3.97	1.07	0.90	1.02	-0.20
LB1217	L	3.30	0.99	0.82	0.96	0.170
LB1221	L	4.05	1.12	1.18	0.96	-0.25
LB1224	L	13.4	1.67	2.04	1.86	-0.6

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 calculations
"-" - No data. See Section 6, for details.
Shaded cells - maximum and minimum values for each derived statistic.

Table 11. Summary of the particle size information received from participating laboratories and replicate analysis laboratories for the twenty-seventh particle size distribution - PS27.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB1201	L	97.61	6.60	6.44	1.24	-0.27
LB1202	WS/DS/L	76.95	5.21	5.31	1.90	0.140
LB1203	L	99.46	8	7.70	1.18	-0.4231
LB1206*	L	93.11	6.66	6.37	1.51	-0.28
LB1207	L	93.11	6.66	6.37	1.51	-0.28
LB1212	L	94.06	6.48	5.62	1.58	0.01
LB1217	L	94.96	6.16	5.45	1.61	-0.160
LB1221	L	95.93	6.78	6.74	1.59	3.54
LB1224	L	97.31	6.78	6.71	1.50	0.04

Key to methods:

L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette
L* - data for this laboratory not included in calculations.
"-" - No data. See Section 6, for details.
Shaded cells - maximum and minimum values for each derived statistic (replicate data not shown).

Table 12. The identifications of the fauna made by participating laboratories for RT26. Names are given only where different from the AQC identification.

RT26	Taxon	LB1201	LB1203	LB1206	LB1208	LB1210
RT2601	Sabella pavonina	- -	- -	- -	- -	0 0
RT2602	Potamopyrgus antipodarum	Pusillina sarsi	Pseudamnicola confusa	Pseudamnicola confusa	- -	0 0
RT2603	Tharyx A	- -	- -	- -	- -	0 0
RT2604	Mytilus edulis	Modiolus modiolus	- -	- -	- -	0 0
RT2605	Lekanesphaera hookeri	Sphaeroma monodi	[Sphaeroma] monodi	[Sphaeroma] rugicauda	[Sphaeroma] rugicauda	0 0
RT2606	Limapontia depressa	- -	- -	- -	- -	0 0
RT2607	Manayunkia aestuarina	- -	Fabriciola cf. berkeleyi	- -	- -	0 0
RT2608	Tubificoides cf. galiciensis	- swirencoides	- insularis	- [galiciencis]	- [galiciensis]	0 0
RT2609	Paramphinome jeffreysii	- -	- -	- -	- -	0 0
RT2610	Onoba aculeus	- -	- -	- -	- semicostata	0 0
RT2611	Corophium insidiosum	- ascherusicum	- -	- acherusicum	- acherusicum	0 0
RT2612	Psammoryctides barbatus	- -	- -	- -	- -	0 0
RT2613	Aricidea catherinae	- -	- -	- -	- cerrutii	0 0
RT2614	Lacuna parva	Lacuninae sp. Juv.	- -	- pallidula	- pallidula	0 0
RT2615	Chamelea striatula	Circomphalus casina	- -	[Venus] -	Clausinella fasciata	0 0
RT2616	Idotea granulosa	- pelagica	- pelagica	- pelagica	- -	0 0
RT2617	Thyasira sarsi	- -	- -	- equalis	- flexuosa	0 0
RT2618	Diastylis rathkei	- lucifera	- lucifera	- lucifera	- lucifera	0 0
RT2619	Gibbula cineraria	- tumida	- -	- -	- umbilicalis	0 0
RT2620	Ventrosia ventrosa	Hydrobia neglecta	[Hydrobia] -	- -	- -	0 0
RT2621	Protocirrineris chrysoderma	[cf. Protocirrineris] -	Cirriformia tentaculata	- -	[Protocirrinereis] -	0 0
RT2622	Odostomia turrita	- -	- plicata	- plicata	- plicata	0 0
RT2623	Chaetozone christiei	- -	- -	- setosa	- [christei]	0 0
RT2624	Obtusella intersecta	- -	- -	Paludinella litorina	- -	0 0
RT2625	Pseudarachna hirsuta	- -	- -	- -	- -	0 0

RT26	Taxon	LB1202	LB1204	LB1207	LB1209	LB1211
RT2601	Sabella pavonina	- flabellata	- spallanzanii	- -	0 0	0 0
RT2602	Potamopyrgus antipodarum	Rissoella opalina	- [jenkinsii]	Hydrobia ulvae	0 0	0 0
RT2603	Tharyx A	- killariensis	- -	- -	0 0	0 0
RT2604	Mytilus edulis	- [edulis juv.]	- -	- -	0 0	0 0
RT2605	Lekanesphaera hookeri	[Sphaeroma] rugicauda	[Sphaeroma] rugicauda	[Sphaeroma] rudicauda	0 0	0 0
RT2606	Limapontia depressa	- -	- -	- -	0 0	0 0
RT2607	Manayunkia aestuarina	- -	Fabricia stellaris	- -	0 0	0 0
RT2608	Tubificoides cf. galiciensis	- -	- -	- insularis	0 0	0 0
RT2609	Paramphinome jeffreysii	- -	- -	- -	0 0	0 0
RT2610	Onoba aculeus	- -	- -	- -	0 0	0 0
RT2611	Corophium insidiosum	- bonnellii	- -	- -	0 0	0 0
RT2612	Psammoryctides barbatus	- -	- -	- -	0 0	0 0
RT2613	Aricidea catherinae	- -	- -	- -	0 0	0 0
RT2614	Lacuna parva	- pallidula	- pallidula	- pallidula	0 0	0 0
RT2615	Chamelea striatula	Myrtea spinifera	- -	- -	0 0	0 0
RT2616	Idotea granulosa	- pelagica	- pelagica	- neglecta	0 0	0 0
RT2617	Thyasira sarsi	- flexuosa	- flexuosa	- -	0 0	0 0
RT2618	Diastylis rathkei	- lucifera	- lucifera	- lucifera	0 0	0 0
RT2619	Gibbula cineraria	- umbilicalis	- -	- tumida	0 0	0 0
RT2620	Ventrosia ventrosa	Hydrobia neglecta	[Hydrobia] -	[Hydrobia] -	0 0	0 0
RT2621	Protocirrineris chrysoderma	Cirriformia tentaculata	Cirriformia tentaculata	- -	0 0	0 0
RT2622	Odostomia turrita	- plicata	- plicata	Rissoa interrupta	0 0	0 0
RT2623	Chaetozone christiei	- setosa	- C	- setosa	0 0	0 0
RT2624	Obtusella intersecta	- -	Rissoella opalina	- -	0 0	0 0
RT2625	Pseudarachna hirsuta	Corophium crassicorne	- -	- -	0 0	0 0

Table 12. The identifications of the fauna made by participating laboratories for RT26. Names are given only where different from the AQC identification.

RT26	Taxon	LB1213	LB1217	LB1222	LB1224
RT2601	Sabella pavonina	- spallanzanii	0 0	- -	- -
RT2602	Potamopyrgus antipodarum	Mercuria confusa	0 0	- -	- -
RT2603	Tharyx A	Cirratulus filiformis	0 0	- -	- -
RT2604	Mytilus edulis	Modiolula phaseolina	0 0	- -	- -
RT2605	Lekanesphaera hookeri	- rugicauda	0 0	Sphaeroma monodi	- -
RT2606	Limapontia depressa	- -	0 0	- -	- -
RT2607	Manayunkia aestuarina	- -	0 0	- -	- -
RT2608	Tubificoides cf. galiciensis	Carinoma armandi	0 0	- [galiciensis]	- -
RT2609	Paramphinome jeffreysii	Scalibregma inflatum	0 0	Pseudeurythoe hemuli	- -
RT2610	Onoba aculeus	- -	0 0	- -	- -
RT2611	Corophium insidiosum	Colomastix pusilla	0 0	- -	- bonnellii
RT2612	Psammoryctides barbatus	Capitella capitata	0 0	- -	- -
RT2613	Aricidea catherinae	Scolelepis foliosa	0 0	- cerrutii	[Aricidea (Acmira)] -
RT2614	Lacuna parva	Polynices montagui	0 0	- vincta	[Lacuna (Epheria)] vincta
RT2615	Chamelea striatula	Venus casina	0 0	- -	- -
RT2616	Idotea granulosa	- pelagica	0 0	- pelagica	- -
RT2617	Thyasira sarsi	- croulinensis	0 0	- -	- -
RT2618	Diastylis rathkei	- rugosa	0 0	[Daistylis] lucifera	- [rathkei typica]
RT2619	Gibbula cineraria	- tumida	0 0	- umbilicalis	[Gibbula (Steromphala)] -
RT2620	Ventrosia ventrosa	[Hydrobia] -	0 0	Hydrobia neglecta	- -
RT2621	Protocirrineris chrysoderma	Drilonereis filum	0 0	[Protocirrinereis] -	[Protocirrineis] [cf. chrysoderma]
RT2622	Odostomia turrita	- -	0 0	- -	- plicata
RT2623	Chaetozone christiei	Cirratulus filiformis	0 0	- setosa	- -
RT2624	Obtusella intersecta	Rissoella diaphana	0 0	Lacuna parva	- -
RT2625	Pseudarachna hirsuta	Gnathia vorax	0 0	- -	- -

RT26	Taxon	LB1216	LB1220	LB1223	LB1225
RT2601	Sabella pavonina	- -	- crassicornis	- -	- -
RT2602	Potamopyrgus antipodarum	Hydrobia ulvae	- -	- -	- -
RT2603	Tharyx A	Caulleriella zetlandica	- -	Chaetozone gibber	Chaetozone gibber
RT2604	Mytilus edulis	- -	- -	- -	Modiolus modiolus
RT2605	Lekanesphaera hookeri	[Sphaeroma] ruguicauda	Sphaeroma monodi	[Sphaeroma] -	[Sphaeroma] -
RT2606	Limapontia depressa	- -	- -	- -	- -
RT2607	Manayunkia aestuarina	- -	- -	- -	- -
RT2608	Tubificoides cf. galiciensis	- -	- -	- insularis	- swirencoides
RT2609	Paramphinome jeffreysii	- -	Nephtyidae sp. Juv.	- -	- -
RT2610	Onoba aculeus	- -	- -	- semicostata	- -
RT2611	Corophium insidiosum	- acherusicum	- acherusicum	- -	- ascherusicum
RT2612	Psammoryctides barbatus	Tubificoides heterochaetus	- -	- -	Enchytraeidae -
RT2613	Aricidea catherinae	- minuta	- cerruti	- -	- cerruti
RT2614	Lacuna parva	- pallidula	- pallidula	- -	Velutina velutina
RT2615	Chamelea striatula	- -	Myrtea spinifera	- -	Circomphalus casina
RT2616	Idotea granulosa	- pelagica	- pelagica	- emarginata	- -
RT2617	Thyasira sarsi	- -	- flexuosa	- -	- flexuosa
RT2618	Diastylis rathkei	- lucifera	- lucifera	- lucifera	- lucifera
RT2619	Gibbula cineraria	- -	- tumida	- -	- tumida
RT2620	Ventrosia ventrosa	- -	Potamopyrgus antipodarum	- -	Hydrobia neglecta
RT2621	Protocirrineris chrysoderma	[Protocirinereis] -	Cirriformia tentaculata	- -	- -
RT2622	Odostomia turrita	Brachystomia eulimoides	- sp.	- unidentata	Rissoella diaphana
RT2623	Chaetozone christiei	- [christei]	- setosa agg.	- -	- setosa agg.
RT2624	Obtusella intersecta	[Otusella] -	Rissoella sp. Juv.	- -	- -
RT2625	Pseudarachna hirsuta	- -	Munna? sp.	- -	Pleurogonium rubicundum

Table 13. The identifications of the fauna made by participating laboratories for RT27. Names are given only where different from the AQC identification.

RT27	Taxon	LB1201	LB1203	LB1206	LB1208	LB1210
RT2701	Calocaris macandreae	- -	- -	- -	- -	0 0
RT2702	Donax vittatus	- -	- -	- -	- -	0 0
RT2703	Sternaspis scutata	- -	- -	[Sternapsis] -	- -	0 0
RT2704	Thysanocardia procera	- -	- -	Golfingia margaritacea	- -	0 0
RT2705	Aristias neglectus	- -	- -	- -	Perrierella audouiniana	0 0
RT2706	Branchiura sowerbyi	- -	- -	- -	- -	0 0
RT2707	Hyala vitrea	- -	- -	- -	- -	0 0
RT2708	Corophium curvispinum	- -	- -	- -	- -	0 0
RT2709	Mya truncata	- -	- arenaria	- -	- -	0 0
RT2710	Nephtys incisa	- -	- -	- -	- -	0 0
RT2711	Lekanesphaera hookeri	- -	[Sphaeroma] rugicauda	[Sphaeroma] -	- -	0 0
RT2712	Monticellina dorsobranchialis	- -	- -	Aphelochaeta A	- -	0 0
RT2713	Nephtys kersivalensis	- -	- -	- -	- -	0 0
RT2714	Neanthes succinea	Hediste diversicolor	- -	Hediste diversicolor	Hediste diversicolor	0 0
RT2715	Leitoscoloplos mammosus	Scoloplos armiger	- -	- -	Scoloplos armiger	0 0
RT2716	Amphiura chiajei	- -	- -	- -	- -	0 0
RT2717	Anoplodactylus petiolatus	- -	- -	- -	- -	0 0
RT2718	Scolelepis tridentata	- cf. gilchristi	- cf. gilchristi	- -	- -	0 0
RT2719	Timoclea ovata	- -	- -	- -	- -	0 0
RT2720	Gammarus locusta	- -	- -	- -	- -	0 0
RT2721	Mesopodopsis slabberi	- -	- -	- -	- -	0 0
RT2722	Magelona minuta	- -	- -	- -	- -	0 0
RT2723	Petricola pholadiformis	- -	Barnea candida	- -	- -	0 0
RT2724	Ampelisca diadema	- spinipes	- spinipes	- spinipes	- spinipes	0 0
RT2725	Scolelepis bonnieri	- -	- -	- -	- squamata	0 0

RT27	Taxon	LB1202	LB1204	LB1207	LB1209	LB1211
RT2701	Calocaris macandreae	- -	- -	- -	0 0	0 0
RT2702	Donax vittatus	- -	- -	- -	0 0	0 0
RT2703	Sternaspis scutata	- -	- -	- [scutatus]	0 0	0 0
RT2704	Thysanocardia procera	- -	- -	[Golfingia] -	0 0	0 0
RT2705	Aristias neglectus	Acidostoma nodiferum	- -	- -	0 0	0 0
RT2706	Branchiura sowerbyi	Nais elinguis	- -	- -	0 0	0 0
RT2707	Hyala vitrea	- -	- -	- -	0 0	0 0
RT2708	Corophium curvispinum	- -	- -	- -	0 0	0 0
RT2709	Mya truncata	- -	- -	- arenaria	0 0	0 0
RT2710	Nephtys incisa	- -	- -	- -	0 0	0 0
RT2711	Lekanesphaera hookeri	- rugicauda	[Sphaeroma] -	[Sphaeroma] rugicauda	0 0	0 0
RT2712	Monticellina dorsobranchialis	- -	- -	- -	0 0	0 0
RT2713	Nephtys kersivalensis	- -	- -	- cirrosa	0 0	0 0
RT2714	Neanthes succinea	Hediste diversicolor	- -	Nereis diversicolor	0 0	0 0
RT2715	Leitoscoloplos mammosus	Scoloplos armiger	- -	- -	0 0	0 0
RT2716	Amphiura chiajei	- -	- -	- -	0 0	0 0
RT2717	Anoplodactylus petiolatus	- -	- -	- -	0 0	0 0
RT2718	Scolelepis tridentata	- cf. gilchristi	- -	- -	0 0	0 0
RT2719	Timoclea ovata	Laevicardium crassum	- -	- -	0 0	0 0
RT2720	Gammarus locusta	- -	- -	- -	0 0	0 0
RT2721	Mesopodopsis slabberi	- -	- -	- -	0 0	0 0
RT2722	Magelona minuta	- -	- -	- -	0 0	0 0
RT2723	Petricola pholadiformis	- -	- -	- -	0 0	0 0
RT2724	Ampelisca diadema	- -	- -	- spinipes	0 0	0 0
RT2725	Scolelepis bonnieri	- -	- -	- -	0 0	0 0

Table 13. The identifications of the fauna made by participating laboratories for RT27. Names are given only where different from the AQC identification.

RT27	Taxon	LB1213	LB1220	LB1222	LB1224
RT2701	Calocaris macandreae	- -	- -	- -	- -
RT2702	Donax vittatus	- -	Mya arenaria	- -	- -
RT2703	Sternaspis scutata	- -	- -	[Sternapsis] [scutatus]	- -
RT2704	Thysanocardia procera	- -	- -	Echiura echiura	- -
RT2705	Aristias neglectus	- -	- -	Socarnes erythropthalamus	- -
RT2706	Branchiura sowerbyi	[Brachiura] -	- -	- -	- -
RT2707	Hyala vitrea	- -	- -	[Hyalia] -	- -
RT2708	Corophium curvispinum	- volutator	- -	- -	- -
RT2709	Mya truncata	0 0	Tellimya ferruginosa	- arenaria	- -
RT2710	Nephtys incisa	- -	- -	- -	- -
RT2711	Lekanesphaera hookeri	[Sphaeroma] rugicaudata	[Sphaeroma] rugicauda	- rugicauda	- rugicauda
RT2712	Monticellina dorsobranchialis	Aphelochaeta A	- -	Aphelochaeta marioni	- -
RT2713	Nephtys kersivalensis	- caeca	- -	- -	- -
RT2714	Neanthes succinea	Hediste diversicolor	[Nereis] -	Hediste diversicolor	- -
RT2715	Leitoscoloplos mammosus	- -	- -	- -	- -
RT2716	Amphiura chiajei	- -	- -	- -	- -
RT2717	Anoplodactylus petiolatus	- -	Nymphon gracile	- -	- -
RT2718	Scolelepis tridentata	Spionidae -	- gilchristi	Malacoceros ?	[Parascolelepis] c.f. korsuni
RT2719	Timoclea ovata	Laevicardium crassum	Cardiacea juv. -	- -	- -
RT2720	Gammarus locusta	Maera grossima	- -	- -	- -
RT2721	Mesopodopsis slabberi	- -	- -	- -	- -
RT2722	Magelona minuta	- -	- -	- -	- -
RT2723	Petricola pholadiformis	- -	- -	[Perticola] -	- -
RT2724	Ampelisca diadema	- tenuicornis	- aequicornis	- -	- -
RT2725	Scolelepis bonnieri	- -	- -	- -	- -

RT27	Taxon	LB1216	LB1221	LB1223	LB1225
RT2701	Calocaris macandreae	- -	- -	- -	- -
RT2702	Donax vittatus	- -	- -	- -	- -
RT2703	Sternaspis scutata	- -	- -	- -	- -
RT2704	Thysanocardia procera	- -	Golfingia margaritacea	- -	- -
RT2705	Aristias neglectus	- -	Ambasia atlantica	- -	Socarnes erythropthalmus
RT2706	Branchiura sowerbyi	Nais elinguis	- -	- -	Capitellides giardi
RT2707	Hyala vitrea	- -	- -	- -	- -
RT2708	Corophium curvispinum	- -	- multisetosum	- -	- insidiosum
RT2709	Mya truncata	- -	- arenaria	- arenaria	- -
RT2710	Nephtys incisa	- -	- -	- -	- -
RT2711	Lekanesphaera hookeri	- -	[Sphaeroma] -	- -	- rugicauda
RT2712	Monticellina dorsobranchialis	- -	Cirriformia tentaculata	- -	- -
RT2713	Nephtys kersivalensis	- -	- -	- -	- -
RT2714	Neanthes succinea	Nereis zonata	Platynereis dumerilii	- -	- -
RT2715	Leitoscoloplos mammosus	- -	Scoloplos armiger	- -	Scoloplos armiger
RT2716	Amphiura chiajei	- -	- -	- -	- -
RT2717	Anoplodactylus petiolatus	- -	- -	- -	- -
RT2718	Scolelepis tridentata	- -	Aonides oxycephala	- -	- gilchristi
RT2719	Timoclea ovata	- -	Glycymeris glycymeris	- -	- -
RT2720	Gammarus locusta	- -	- -	- -	- -
RT2721	Mesopodopsis slabberi	- -	- -	- -	- -
RT2722	Magelona minuta	- -	[Megalona] -	- -	- filiformis
RT2723	Petricola pholadiformis	- -	Sphenia binghami	- -	Gari costulata
RT2724	Ampelisca diadema	- -	- spinipes	- spinipes	- tenuicornis
RT2725	Scolelepis bonnieri	- -	- -	- -	- squamata

Table 14. The identifications of the fauna made by participating laboratories for RT28. Names are given only where different from the AQC identification.

RT28	Taxon	LB1201	LB1203	LB1206	LB1208	LB1210
RT2801	Arnoglossus laterna	- -	Lepidorhombus whiffagonis	Lepidorhombus whiffiagonis	- -	0 0
RT2802	Buglossidium luteum	- -	Solea solea	- -	- -	0 0
RT2803	Agonus cataphractus	- -	- -	- -	- -	0 0
RT2804	Echiichthys vipera	Trachinus draco	- -	- -	- -	0 0
RT2805	Dicentrarchus labrax	- -	- -	- -	- punctatus	0 0
RT2806	Lumpenus lumpretaeformis	- [lampretaeformis]	- [lampretaeformis]	- -	- -	0 0
RT2807	Limanda limanda	- -	- -	- -	- -	0 0
RT2808	Clupea harengus	- -	- -	- -	- -	0 0
RT2809	Syngnathus rostellatus	- typhle	- acus	- -	- -	0 0
RT2810	Entelurus aequoreus	- -	- [aequoraeus]	- -	- -	0 0
RT2811	Platichthys flesus	[Platichtlys] -	- -	- -	- -	0 0
RT2812	Sprattus sprattus	- -	- -	- -	- -	0 0
RT2813	Pholis gunnellus	- -	- -	- -	- -	0 0
RT2814	Ammodytes marinus	- tobianus	- -	- -	- -	0 0
RT2815	Pomatoschistus microps	- -	[Pomatschistus] -	- -	- -	0 0
RT2816	Pomatoschistus minutus	- microps	[Pomatschistus] -	- -	- -	0 0
RT2817	Gobius niger	- -	- -	- -	- -	0 0
RT2818	Pleuronectes platessa	- -	Limanda limanda	- -	- -	0 0
RT2819	Hippoglossoides platessoides	- -	- -	- -	- -	0 0
RT2820	Ammodytes tobianus	- -	- -	- -	- marinus	0 0
RT2821	Solea solea	- -	- -	- -	- -	0 0
RT2822	Scomber scombrus	- -	- -	- -	- -	0 0
RT2823	Osmerus eperlanus	- -	- -	- -	- -	0 0
RT2824	Sprattus sprattus	- -	- -	- -	- -	0 0
RT2825	Pleuronectes platessa	- -	Glyptocephalus cynoglossus	- -	- -	0 0

RT28	Taxon	LB1202	LB1204	LB1207	LB1209	LB1215
RT2801	Arnoglossus laterna	- -	- -	- -	- -	- -
RT2802	Buglossidium luteum	- -	- -	- -	- -	- -
RT2803	Agonus cataphractus	- -	- -	- -	[Agonis] -	- -
RT2804	Echiichthys vipera	- -	- -	[Echiichtys] -	- -	- -
RT2805	Dicentrarchus labrax	- -	- -	- -	[Diecentrarchus] -	[Morone] -
RT2806	Lumpenus lumpretaeformis	- -	- -	- -	- [lampretaeformis]	- [lampretaeformis]
RT2807	Limanda limanda	- -	- -	- -	- -	- -
RT2808	Clupea harengus	- -	- -	[Clupeea] -	- -	- -
RT2809	Syngnathus rostellatus	- acus	- acus	- -	- acus	- -
RT2810	Entelurus aequoreus	- -	- -	- -	[Entellurus] [aquoreus]	- -
RT2811	Platichthys flesus	- -	- -	- -	Pluronectes platessa	- -
RT2812	Sprattus sprattus	- -	- -	- -	- -	- -
RT2813	Pholis gunnellus	- -	- -	- -	- -	- -
RT2814	Ammodytes marinus	- -	- tobianus	Gymnammodytes semisquamatus	Hyperoplus lanceolatus	- tobianus
RT2815	Pomatoschistus microps	Aphia minuta	- pictus	- pictus	- -	- pictus
RT2816	Pomatoschistus minutus	- -	Gobiusculus flavescens	- -	- -	- pictus
RT2817	Gobius niger	- -	- -	- -	- -	- -
RT2818	Pleuronectes platessa	Limanda limanda	Limanda limanda	- -	Limanda limanda	- -
RT2819	Hippoglossoides platessoides	- -	- -	- -	- -	Limanda limanda
RT2820	Ammodytes tobianus	- -	Hyperoplus immaculatus	- -	Hyperoplus lanceolatus	- -
RT2821	Solea solea	- -	- -	Microchirus variegatus	- -	- -
RT2822	Scomber scombrus	- -	- japonicus	- -	- -	- -
RT2823	Osmerus eperlanus	- -	- -	- -	- -	- -
RT2824	Sprattus sprattus	- -	- -	- -	- -	- -
RT2825	Pleuronectes platessa	- -	Platichthys flesus	- -	Hippoglossoides platessoides	- -

Table 14. The identifications of the fauna made by participating laboratories for RT28. Names are given only where different from the AQC identification.

RT28	Taxon	LB1216	LB1221
RT2801	Arnoglossus laterna	- -	- -
RT2802	Buglossidium luteum	- -	- -
RT2803	Agonus cataphractus	- -	- -
RT2804	Echiichthys vipera	- -	- -
RT2805	Dicentrarchus labrax	- -	- -
RT2806	Lumpenus lumpretaeformis	- [lampretaeformis]	- -
RT2807	Limanda limanda	- -	- -
RT2808	Clupea harengus	- -	- -
RT2809	Syngnathus rostellatus	- -	- -
RT2810	Entelurus aequoreus	- -	- -
RT2811	Platichthys flesus	- -	- -
RT2812	Sprattus sprattus	- -	- -
RT2813	Pholis gunnellus	- -	- -
RT2814	Ammodytes marinus	Gymnammodytes semisquamatus	- -
RT2815	Pomatoschistus microps	- pictus	- -
RT2816	Pomatoschistus minutus	- microps	- -
RT2817	Gobius niger	Thorogobius ephippiatus	- -
RT2818	Pleuronectes platessa	- -	- -
RT2819	Hippoglossoides platessoides	- -	- -
RT2820	Ammodytes tobianus	- -	- -
RT2821	Solea solea	- -	- -
RT2822	Scomber scombrus	- -	- -
RT2823	Osmerus eperlanus	- -	- -
RT2824	Sprattus sprattus	- -	- -
RT2825	Pleuronectes platessa	- -	- -

RT28	Taxon	LB1220	LB1224
RT2801	Arnoglossus laterna	- -	- -
RT2802	Buglossidium luteum	- -	- -
RT2803	Agonus cataphractus	- -	- -
RT2804	Echiichthys vipera	- -	- -
RT2805	Dicentrarchus labrax	- -	- -
RT2806	Lumpenus lumpretaeformis	- -	- -
RT2807	Limanda limanda	- -	- -
RT2808	Clupea harengus	- -	- -
RT2809	Syngnathus rostellatus	- -	- -
RT2810	Entelurus aequoreus	- -	- -
RT2811	Platichthys flesus	- -	- -
RT2812	Sprattus sprattus	- -	- -
RT2813	Pholis gunnellus	- [gennellus]	- -
RT2814	Ammodytes marinus	- -	- -
RT2815	Pomatoschistus microps	[Potamoschistus] -	- -
RT2816	Pomatoschistus minutus	[Potamoschistus] -	- -
RT2817	Gobius niger	- -	- -
RT2818	Pleuronectes platessa	- -	- -
RT2819	Hippoglossoides platessoides	- -	- -
RT2820	Ammodytes tobianus	- -	- -
RT2821	Solea solea	- -	- -
RT2822	Scomber scombrus	- -	- -
RT2823	Osmerus eperlanus	- -	- -
RT2824	Sprattus sprattus	- -	- -
RT2825	Pleuronectes platessa	- -	- -

Table 15. Summary of the performance of participating laboratories in the Own Sample (OS) exercises 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.	Min	Max	Target	Flag	Missed	% Missed	Remedial Action	Lab.	%	Remedial Action	Lab.	Min	Max	Target	Flag	Missed	% Missed	Remedial Action	Lab.	Target	Flag	Target	Lab.	Flag	
LB1201	OS29	72	75.6	92.4	75.6 - 92.4	Fail	11	13.1	Reprocess	7	9.6	Review	612	1082.7	1323.3	1082.7 - 1323.3	Fail	588	48.9	Reprocess	-	-	-	90.0	49.37	Fail	Fail-Bad
LB1201	OS30	58	52.2	63.8	52.2 - 63.8	PASS	1	1.7		3	5.3		212	198.9	243.1	198.9 - 243.1	PASS	9	4.1		-	-	-	90.0	96.54	PASS	Pass-Good
LB1201	OS31	33	28.8	35.2	28.8 - 35.2	PASS	0	0.0		1	3.1		149	135.0	165.0	135.0 - 165.0	PASS	2	1.3		-	-	-	90.0	96.32	PASS	Pass-Good
LB1202	OS29	1	-1.0	3.0	-1.0 - 3.0	PASS	0	0.0		0	0.0		7	5.0	9.0	5.0 - 9.0	PASS	0	0.0		0.0093	0.0061 - 0.0091	Fail	90.0	100.00	PASS	Pass-Excellent
LB1202	OS30	48	42.3	51.7	42.3 - 51.7	PASS	0	0.0		3	6.4		307	288.9	353.1	288.9 - 353.1	PASS	0	0.0		7.1774	5.7408 - 8.6112	PASS	90.0	95.86	PASS	Pass-Good
LB1202	OS31	34	29.7	36.3	29.7 - 36.3	PASS	0	0.0		1	3.0		131	117.0	143.0	117.0 - 143.0	PASS	0	0.0		0.5220	0.3630 - 0.5444	PASS	90.0	98.85	PASS	Pass-Good
LB1203	OS29	41	36.0	44.0	36.0 - 44.0	PASS	0	0.0		0	0.0		134	120.6	147.4	120.6 - 147.4	PASS	0	0.0		-	-	-	90.0	99.25	PASS	Pass-Good
LB1203	OS30	19	18.0	22.0	18.0 - 22.0	PASS	1	5.0		0	0.0		36	33.3	40.7	33.3 - 40.7	PASS	1	2.7		-	-	-	90.0	98.63	PASS	Pass-Good
LB1203	OS31	23	20.7	25.3	20.7 - 25.3	PASS	0	0.0		0	0.0		74	66.6	81.4	66.6 - 81.4	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1205	OS29	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		72	63.0	77.0	63.0 - 77.0	PASS	0	0.0		1.2778	0.7863 - 1.1795	Fail	90.0	98.59	PASS	Pass-Good
LB1205	OS30	41	37.8	46.2	37.8 - 46.2	PASS	0	0.0		2	4.8		487	432.9	529.1	432.9 - 529.1	PASS	1	0.2		11.6179	8.5947 - 12.8921	PASS	90.0	97.93	PASS	Pass-Good
LB1205	OS31	50	45.0	55.0	45.0 - 55.0	PASS	0	0.0		3	6.0		519	464.4	567.6	464.4 - 567.6	PASS	0	0.0		11.0475	8.4835 - 12.7253	PASS	90.0	98.94	PASS	Pass-Good
LB1206	OS29	61	54.0	66.0	54.0 - 66.0	PASS	0	0.0		1	1.7		664	616.5	753.5	616.5 - 753.5	PASS	26	3.8		5.8154	4.4682 - 6.7022	PASS	90.0	97.55	PASS	Pass-Good
LB1206	OS30	22	20.7	25.3	20.7 - 25.3	PASS	0	0.0		1	4.3		129	126.0	154.0	126.0 - 154.0	PASS	7	5.0		0.2006	0.1767 - 0.2651	PASS	90.0	91.97	PASS	Pass-Acceptable
LB1206	OS31	103	93.6	114.4	93.6 - 114.4	PASS	1	1.0		6	5.8	Review	1510	1372.5	1677.5	1372.5 - 1677.5	PASS	10	0.7		4.0571	3.3077 - 4.9615	PASS	90.0	87.61	Fail	Fail-Poor
LB1207	OS29	10	8.0	12.0	8.0 - 12.0	PASS	0	0.0		0	0.0		17	14.0	18.0	14.0 - 18.0	PASS	0	0.0		2.7619	1.1784 - 1.7676	Fail	90.0	96.97	PASS	Pass-Good
LB1207	OS30	43	42.3	51.7	42.3 - 51.7	PASS	2	4.3		5	11.1	Reprocess	184	172.8	211.2	172.8 - 211.2	PASS	13	6.8	Review	204.0916	153.8277 - 230.7415	PASS	90.0	85.11	Fail	Fail-Poor
LB1207	OS31	45	44.1	53.9	44.1 - 53.9	PASS	0	0.0		7	14.3		238	222.3	271.7	222.3 - 271.7	PASS	3	1.2		25.2241	18.4599 - 27.6899	PASS	90.0	90.72	PASS	Pass-Acceptable
LB1208	OS29	7	5.0	9.0	5.0 - 9.0	PASS	0	0.0		0	0.0		107	96.3	117.7	96.3 - 117.7	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1208	OS30	8	6.0	10.0	6.0 - 10.0	PASS	0	0.0		2	25.0		181	166.5	203.5	166.5 - 203.5	PASS	4	2.2		-	-	-	90.0	91.80	PASS	Pass-Acceptable
LB1208	OS31	8	5.0	9.0	5.0 - 9.0	PASS	0	0.0		1	14.3		263	238.5	291.5	238.5 - 291.5	PASS	2	0.8		-	-	-	90.0	99.24	PASS	Pass-Good
LB1209	OS29	1	-1.0	3.0	-1.0 - 3.0	PASS	0	0.0		0	0.0		1	-1.0	3.0	-1.0 - 3.0	PASS	0	0.0		0.0081	0.0094 - 0.0140	Fail	90.0	100.00	PASS	Pass-Excellent
LB1209	OS30	2	1.0	5.0	1.0 - 5.0	PASS	1	33.3	Review	0	0.0		2	1.0	5.0	1.0 - 5.0	PASS	1	33.3	Review	0.0036	0.0030 - 0.0046	PASS	90.0	80.00	Fail	Fail-Bad
LB1209	OS31	3	1.0	5.0	1.0 - 5.0	PASS	0	0.0		0	0.0		3	1.0	5.0	1.0 - 5.0	PASS	0	0.0		0.0503	0.0434 - 0.0652	PASS	90.0	100.00	PASS	Pass-Excellent
LB1210	OS29	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1210	OS30	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1210	OS31	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1212	OS29	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1212	OS30	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1212	OS31	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1213	OS29	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1213	OS30	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1213	OS31	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1214	OS29	20	18.0	22.0	18.0 - 22.0	PASS	0	0.0		0	0.0		910	819.9	1002.1	819.9 - 1002.1	PASS	2	0.2		-	-	-	90.0	99.73	PASS	Pass-Good
LB1214	OS30	24	21.6	26.4	21.6 - 26.4	PASS	0	0.0		0	0.0		3242	2904.3	3549.7	2904.3 - 3549.7	PASS	4	0.1		-	-	-	90.0	99.77	PASS	Pass-Good
LB1214	OS31	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		168	152.1	185.9	152.1 - 185.9	PASS	4	2.4		-	-	-	90.0	98.52	PASS	Pass-Good
LB1215	OS29	60	54.9	67.1	54.9 - 67.1	PASS	1	1.6		0	0.0		621	562.5	687.5	562.5 - 687.5	PASS	4	0.6		48.3474	37.8514 - 56.7770	PASS	90.0	99.69	PASS	Pass-Good
LB1215	OS30	60	54.0	66.0	54.0 - 66.0	PASS	0	0.0		0	0.0		1912	1714.5	2095.5	1714.5 - 2095.5	PASS	0	0.0		4.1262	3.0078 - 4.5116	PASS	90.0	99.77	PASS	Pass-Good
LB1215	OS31	19	18.0	22.0	18.0 - 22.0	PASS	1	5.0		0	0.0		470	422.1	515.9	422.1 - 515.9	PASS	6	1.3		0.3023	0.2250 - 0.3374	PASS	90.0	99.04	PASS	Pass-Good
LB1216	OS29	17	15.0	19.0	15.0 - 19.0	PASS	0	0.0		1	5.9		86	77.4	94.6	77.4 - 94.6	PASS	0	0.0		0.3446	0.2345 - 0.3517	PASS	90.0	98.84	PASS	Pass-Good
LB1216	OS30	21	18.9	23.1	18.9 - 23.1	PASS	0	0.0		0	0.0		95	85.5	104.5	85.5 - 104.5	PASS	0	0.0		0.2565	0.2280 - 0.3420	PASS	90.0	100.00	PASS	Pass-Excellent
LB1216	OS31	14	12.0	16.0	12.0 - 16.0	PASS	0	0.0		0	0.0		33	29.7	36.3	29.7 - 36.3	PASS	0	0.0		1.2340	0.8910 - 1.3364	PASS	90.0	100.00	PASS	Pass-Excellent
LB1217	OS29	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1217	OS30	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1217	OS31	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1218	OS29	31	27.9	34.1	27.9 - 34.1	PASS	-	-		3	9.7		1686	1510.2	1845.8	1510.2 - 1845.8	PASS	-	-		1.7598	1.2689 - 1.9033	PASS	90.0	92.08	PASS	Not Applicable
LB1218	OS30	13	13.0	17.0	13.0 - 17.0	PASS	-	-		3	20.0		159	153.9	188.1	153.9 - 188.1	PASS	-	-		0.1710	0.0782 - 0.1174	Fail	90.0	93.94	PASS	Not Applicable
LB1218	OS31	24	22.5	27.5	22.5 - 27.5	PASS	-	-		3	12.0	Reprocess	386	335.7	410.3	335.7 - 410.3	PASS	-	-		0.8187	0.4184 - 0.6276	Fail	90.0	86.17	Fail	Not Applicable
LB1219	OS29	11	9.0	13.0	9.0 - 13.0	PASS	0	0.0		0	0.0		46	41.4	50.6	41.4 - 50.6	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1219	OS30	26	23.4	28.6	23.4 - 28.6	PASS	0	0.0		0	0.0		240	225.0	275.0	225.0 - 275.0	PASS	10	4.0		-	-	-	90.0	97.97	PASS	Pass-Good
LB1219	OS31	19	17.0	21.0	17.0 - 21.0	PASS	0	0.0		0	0.0		189	170.1	207.9	170.1 - 207.9	PASS	0	0.0		-	-	-	90.0	100.00	PASS	Pass-Excellent
LB1220	OS29	7	5.0	9.0	5.0 - 9.0	PASS	0	0.0		0	0.0		55	50.4	61.6	50.4 - 61.6	PASS	0	0.0		0.0192	0.0116 - 0.0174	Fail	90.0	99.12	PASS	Pass-Good
LB1220	OS30	9	7.0	11.0	7.0 - 11.0	PASS	0	0.0		0	0.0		50	43.2	52.8	43.2 - 52.8	PASS	0	0.0		0.0346	0.0247 - 0.0371	PASS	90.0	98.00	PASS	Pass-Good
LB1220	OS31	19	17.0	21.0	17.0 - 21.0	PASS	0	0.0		1	5.3		573	522.9	639.1	522.9 - 639.1	PASS	8	1.4		0.5793	0.3159 - 0.4739	Fail	90.0	99.14	PASS	Pass-Good
LB1221	OS29	12	10.0	14.0	10.0 - 14.0	PASS	0	0.0		0	0.0		946	840.6	1027.4	840.6 - 1027.4	PASS	0	0.0		5.4224	4.4178 - 6.6268	PASS	90.0	99.26	PASS	Pass-Good
LB1221	OS30	43	38.7	47.3	38.7 - 47.3	PASS	0	0.0		0	0.0		1149	1028.7	1257.3	1028.7 - 1257.3	PASS	1	0.1		28.3781	22.4318 - 33.6476	PASS	90.0	99.65	PASS	Pass-Good
LB1221	OS31	68	62.1	75.9	62.1 - 75.9	PASS	1	1.4		0	0.0		1660	1494.9	1827.1	1494.9 - 1827.1	PASS	2	0.1		29.2162	23.3858 - 35.0788	PASS	90.0	99.91	PASS	Pass-Good
LB1222	OS29	117	114.3	139.7	114.3 - 139.7	PASS	5	3.9		6	4.9		3237	3238.2	3957.8	3238.2 - 3957.8	Fail	409	11.4		51.5043	41.8138 - 62.7206	PASS	90.0	93.61	PASS	Pass-Acceptable
LB1222	OS30	82	79.2	96.8	79.2 - 96.8	PASS	5	5.7		4	4.8		2403	2203.2	2692.8	2203.2 - 2692.8	PASS	165	6.7		1.7164	1.8035 - 2.7053	Fail	90.0	96.23	PASS	Pass-Good
LB1222	OS31	10	8.0	12.0	8.0 - 12.0	PASS	0	0.0		0	0.0		1417	1269.0	1551.0	1269.0 - 1551.0	PASS	7	0.5		0.5488	0.3824 - 0.5736	PASS	90.0	99.68	PASS	Pass-Good
LB1224	OS29	24	21.6	26.4	21.6 - 26.4	PASS	0	0.0		1	4.2		232	207.9	254.1	207.9 - 254.1	PASS	0	0.0		5.4034	3.1505 - 4.7257	Fail	90.0	99.35	PASS	Pass-Good
LB1224	OS30	8	6.0	10.0	6.0 - 10.0	PASS	0	0.0		1	12.5		23	20.7	25.3	20.7 - 25.3	PASS	0	0.0		0.8829	0.7181 - 1.0771	PASS	90.0	95.65	PASS	Pass-Good
LB1224	OS31	5	3.0	7.0	3.0 - 7.0	PASS	0	0.0		0	0.0		23	21.6	26.4	21.6 - 26.4	PASS	0	0.0		-	-	-	90.0	97.87	PASS	Pass-Good
LB1226	OS29	12	11.0	15.0	11.0 - 15.0	PASS	2	15.4		0	0.0		109	99.9	122.1	99.9 - 122.1	PASS	12	10.8		0.0921	0.0523 - 0.0785	Fail	90.0	93.64	PASS	Pass-Acceptable
LB1226	OS30	3	1.0	5.0	1.0 - 5.0	PASS	0	0.0		0	0.0		13	11.0	15.0	11.0 - 15.0	PASS	0	0.0		0.1172	0.0998 - 0.1498	PASS	90.0	100.00	PASS	Pass-Excellent
LB1226	OS31	4	3.0	7.0	3.0 - 7.0	PASS	1	20.0	Review	1	25.0	Review	15	15.0	19.0	15.0 - 19.0	PASS	2	11.8	Review	0.0283	0.0227 - 0.0341	PASS	90.0	87.50	Fail	Fail-Poor
LB1227	OS29	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1227	OS30	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1227	OS31	-	-	-	-		-	-		-	-		-	-	-	-		-	-		-	-	-	90.0	-		
LB1228	OS29	20	18.0	22.0	18.0 - 22.0	PASS	0	0.0		0	0.0		61	54.0	66.0	54.0 - 66.0	PASS	0	0.0		-	-	-	90.0	99.19	PASS	Pass-Good
LB1228	OS30	20	19.8	24.2	19.8 - 24.2	PASS	2	9.1		0	0.0		71	67.5	82.5	67.5 - 82.5	PASS	4	5.3		-	-	-	90.0	95.89	PASS	Pass-Good
LB1228	OS31	18	16.0	20.0	16.0 - 20.0	PASS	0	0.0		0	0.0		22	21.6	26.4	21.6 - 26.4	PASS	1	4.2		-	-	-	90.0	96.30	PASS	Pass-Good

Table 16. Z-score results for the derived statistics supplied by participating laboratories for the particle size (PS) exercises - PS26 and PS27 - NMBAQC / UK NMMP standards applied.

PS26

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	4.31	0.42	PASS	1.49	1.04	PASS	1.61	0.76	PASS	1.09	0.29	PASS	0.220	0.33	PASS	-
SieveRepAv	2.41	-1.56	PASS	1.37	0.61	PASS	1.48	0.43	PASS	0.90	-1.21	PASS	0.271	0.55	PASS	sand/sand
LB1201	3.65	-0.27	PASS	0.74	-1.65	PASS	0.93	-0.98	PASS	1.09	0.30	PASS	0.380	1.01	PASS	-/-
LB1202	3.78	-0.13	PASS	0.99	-0.75	PASS	1.37	0.14	PASS	1.30	2.00	Fail	0.43	1.22	PASS	v.sl.muddy (yellow) sand (oolitic?)/sand
LB1203	5.8	1.96	PASS	1.91	2.57	Fail	2.087	1.96	PASS	1.10	0.40	PASS	0.346	0.86	PASS	sand/sand
LB1206*	0.84	-3.20	Fail	0.89	-1.11	PASS	1.00	-0.80	PASS	0.89	-1.32	PASS	0.19	0.21	PASS	sand/sand
LB1207	0.84	-3.20	Fail	0.89	-1.11	PASS	1.00	-0.80	PASS	0.89	-1.32	PASS	0.190	0.21	PASS	sand/sand
LB1209	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1212	3.97	0.07	PASS	1.07	-0.46	PASS	0.90	-1.05	PASS	1.02	-0.27	PASS	-0.200	-1.44	PASS	sandy/-
LB1217	3.30	-0.63	PASS	0.99	-0.75	PASS	0.82	-1.26	PASS	0.96	-0.75	PASS	0.170	0.12	PASS	muddy,coarse sand/mod sorted fine skewed coarse sand
LB1221	4.05	0.15	PASS	1.12	-0.28	PASS	1.18	-0.34	PASS	0.96	-0.75	PASS	-0.250	-1.65	PASS	medium sand/sM
LB1224	13.4	9.90	Fail	1.67	1.70	PASS	2.04	1.84	PASS	1.86	6.54	Fail	-0.6	-3.12	Fail	muddy sand/muddy sand

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

PS27

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description
LaserRepAv	96.09	0.03	PASS	6.95	1.24	PASS	7.00	1.14	PASS	1.93	1.89	PASS	0.060	0.74	PASS	Unspecified
SieveRepAv	99.11	1.57	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1201	97.61	0.81	PASS	6.60	-0.12	PASS	6.44	0.18	PASS	1.24	-1.65	PASS	-0.270	-1.21	PASS	Mud/Mud
LB1202	76.95	-9.68	Fail	5.21	-5.57	Fail	5.31	-1.75	PASS	1.90	1.74	PASS	0.140	1.22	PASS	Black,anoxic,slightly sandy mud + org. frags/Sandy mud
LB1203	99.46	1.74	PASS	8	5.38	Fail	7.70	2.34	Fail	1.18	-1.96	PASS	-0.4231	-2.11	Fail	Mud/Mud
LB1206*	93.11	-1.48	PASS	6.66	0.12	PASS	6.37	0.06	PASS	1.51	-0.26	PASS	-0.28	-1.27	PASS	Mud/Mud
LB1207	93.11	-1.48	PASS	6.66	0.12	PASS	6.37	0.06	PASS	1.51	-0.26	PASS	-0.280	-1.27	PASS	Mud/Mud
LB1209	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB1212	94.06	-1.00	PASS	6.48	-0.59	PASS	5.62	-1.22	PASS	1.58	0.10	PASS	0.010	0.45	PASS	Mud/-
LB1217	94.96	-0.54	PASS	6.16	-1.84	PASS	5.45	-1.51	PASS	1.61	0.25	PASS	-0.160	-0.56	PASS	Silt/Silt
LB1221	95.93	-0.05	PASS	6.78	0.59	PASS	6.74	0.70	PASS	1.59	0.15	PASS	3.54	21.32	Fail	Fine Mud/Mud
LB1224	97.31	0.65	PASS	6.78	0.59	PASS	6.71	0.64	PASS	1.50	-0.32	PASS	0.040	0.63	PASS	Mud/Mud

"-" 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 2005/06 with respect to the NMBAQC / UK NMMP standards. Initial OS results excluding remedial action.

Scheme Year	Exercise	Pass (>90% BCSI)	Fail (<90% BCSI)	% Pass
02 (1995/96)	01	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
12 (2005/06)*	29, 30, 31	49	5	91

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 12 (2005/06).

	Scheme Year 2	Scheme Year 3			Scheme Year 4			Scheme Year 5			Scheme Year 6			Scheme Year 7			Scheme Year 8			Scheme Year 9			Scheme Year 10			Scheme Year 11			Scheme Year 12		
LabCode	**OS01**	**OS02**	**OS03**	**OS04**	**OS05**	**OS06**	**OS07**	**OS08**	**OS09**	**OS10**	**OS11**	**OS12**	**OS13**	**OS14**	**OS15**	**OS16**	**OS17**	**OS18**	**OS19**	**OS20**	**OS21**	**OS22**	**OS23**	**OS24**	**OS25**	**OS26**	**OS27**	**OS28**	**OS29**	**OS30**	**OS31**
LB1201	-	-	-	-	95.75	92.56	96.37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	98.21	96.45	90.77	49.37	96.54	96.32
LB1202	-	-	-	-	89.9	-	-	-	-	-	95.8	49.56	67.28	72.73	89.52	70.87	55.86	71.28	90.77	72.58	98.56	99.61	95.89	95.82	97.62	100	98.9	98.52	100	95.86	98.85
LB1203	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.68	91.36	93.63	98.66	96.44	92.46	100	98.46	98	99.45	95.08	100	99.25	98.63	100
LB1204	-	-	-	-	-	-	-	-	-	-	97.92	84.85	97.29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1205	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.22	90.00	93.85	98.59	97.93	98.94
LB1206	100	100	100	100	98.88	100	100	97.46	100	83.33	89.29	95.65	94.48	76.92	92.82	95.43	92.68	96.68	97.43	96.91	93.74	91.23	93.29	97.35	94.12	98.82	91.48	90.48	97.55	91.97	87.61
LB1207	97.91	96.3	85.8	89.82	75.29	95.44	74.89	73.3	97.33	93.01	73.02	99.5	90.5	93.13	94.57	90.32	96.67	94.12	90.39	94.27	96.43	96.77	83.74	90.72	96.77	100	96.42	94.55	96.97	85.11	90.72
LB1208	-	-	-	-	-	-	-	-	-	-	-	-	-	92.09	96.52	82.22	91.5	99.34	97.22	84.94	76.92	80.46	89.16	99.83	96.18	98.04	100	100	100	91.8	99.24
LB1209	-	-	-	-	60	62.5	83.82	87.5	93.5	94.12	74.21	76.6	70.98	74.02	81.74	78.47	78.95	90.36	100	70.25	94.68	78.57	98.11	100	100	100	100	96.3	100	80.00	100
LB1210	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	-	-	-
LB1211	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	-	-	-	-	-	-	-	-	-
LB1212	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1213	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1214	98.18	100	83.33	95.77	100	100	94.74	-	-	-	98.21	97.79	100	-	-	-	-	-	-	97.52	99.43	92.86	98.76	92.31	99.5	99.02	100	99.40	99.73	99.77	98.52
LB1215	99.44	98.39	100	100	100	99.31	99.75	98.59	98.59	100	98.14	66.26	88.78	96.95	99.09	98.95	98.99	84.62	91.09	99.37	99.24	98.67	96.48	97.92	99.37	99.7	100	98.92	99.69	99.77	99.04
LB1216	92.83	94.19	99.04	97.96	99.45	99.03	95.72	100	99.66	99.79	100	70	75.56	83.58	77.62	99.71	98.39	95.87	100	100	100	95.24	96.85	90.26	96.55	98.49	97.73	99.44	98.84	100	100
LB1217	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1218	97.17	98.93	96.58	98.4	100	98.8	98.04	91.32	98.8	98.35	99.23	90.38	98.13	99.21	91.1	96.22	99.55	93.98	95.24	99.07	96.69	98.14	96.68	92.27	77.38	82.37	98.44	71.38	92.08	93.94	86.17
LB1219	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	97.97	100
LB1220	98.54	-	-	-	99.68	99.87	90.2	91.73	43.85	35.71	97.27	98.7	97.56	94.12	97.4	98.08	96.94	95.4	98.84	-	-	-	98.26	96.21	98.72	98.62	98.78	98.00	99.12	98	99.14
LB1221	97.94	-	92.08	-	74.34	94.64	96.43	71.03	96.48	99.17	98.32	97.65	96.3	96.67	98.21	96.96	92.41	96.74	89.86	98.54	98.2	99.54	99.6	97.85	98.86	99.46	100	97.33	99.26	99.65	99.91
LB1222		73.15	68.7	96.12	-	-	-	93.33	90.46	93.1	87.15	98.56	98.24	95.9	92.57	91.22	-	-	-	86.15	98.43	96.78	95.23	96.92	95.97	98.48	96.15	98.62	93.61	96.23	99.68
LB1223	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	96.89	72.07	56.22	-	-	-	-	-	-	-	-	-	-	-	-
LB1224	-	-	-	-	-	-	-	95.08	53.66	60.42	-	-	-	-	-	-	84.32	100	80.31	-	-	-	93.7	83.94	91.23	-	-	-	99.35	95.65	97.87
LB1225	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB1226	-	-	-	-	-	-	-	-	-	-	100	98.96	85.71	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	93.64	100	87.5
LB1227	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	92.5	92.07	100	95.58	91.49	70.95	-	-	-
LB1228	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	88.89	43.32	83.72	99	94.6	85.11	94.74	95.89	96.43	99.19	95.89	96.3

Key: Shaded cells = 'Fail' flag irrespective of subsequent remedial action.
Red text = no sample residue supplied
- = 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 PS26. Seven samples analysed by sieve and seven samples analysed by Laser.

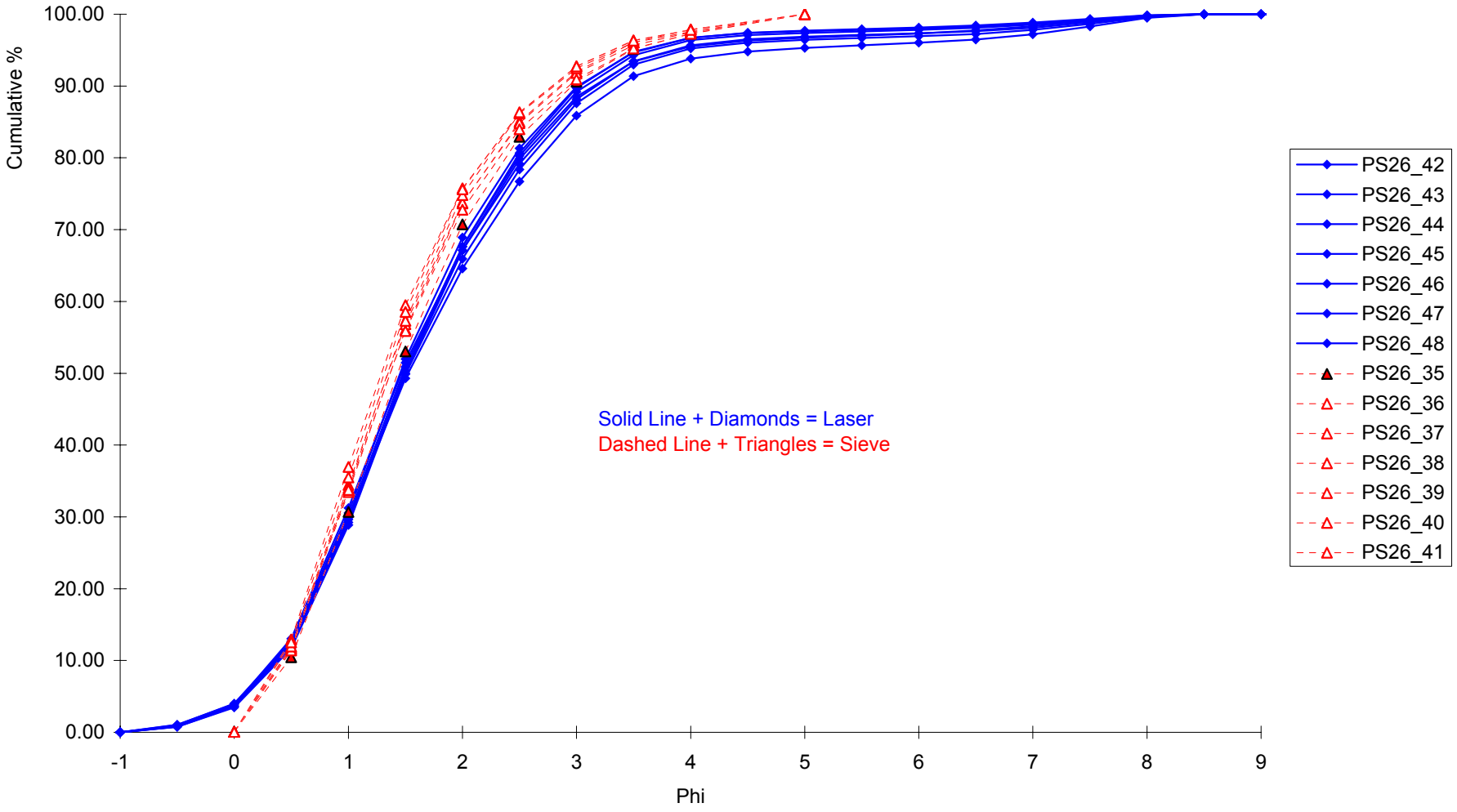


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS27. Seven samples analysed by sieve and seven samples analysed by Laser.

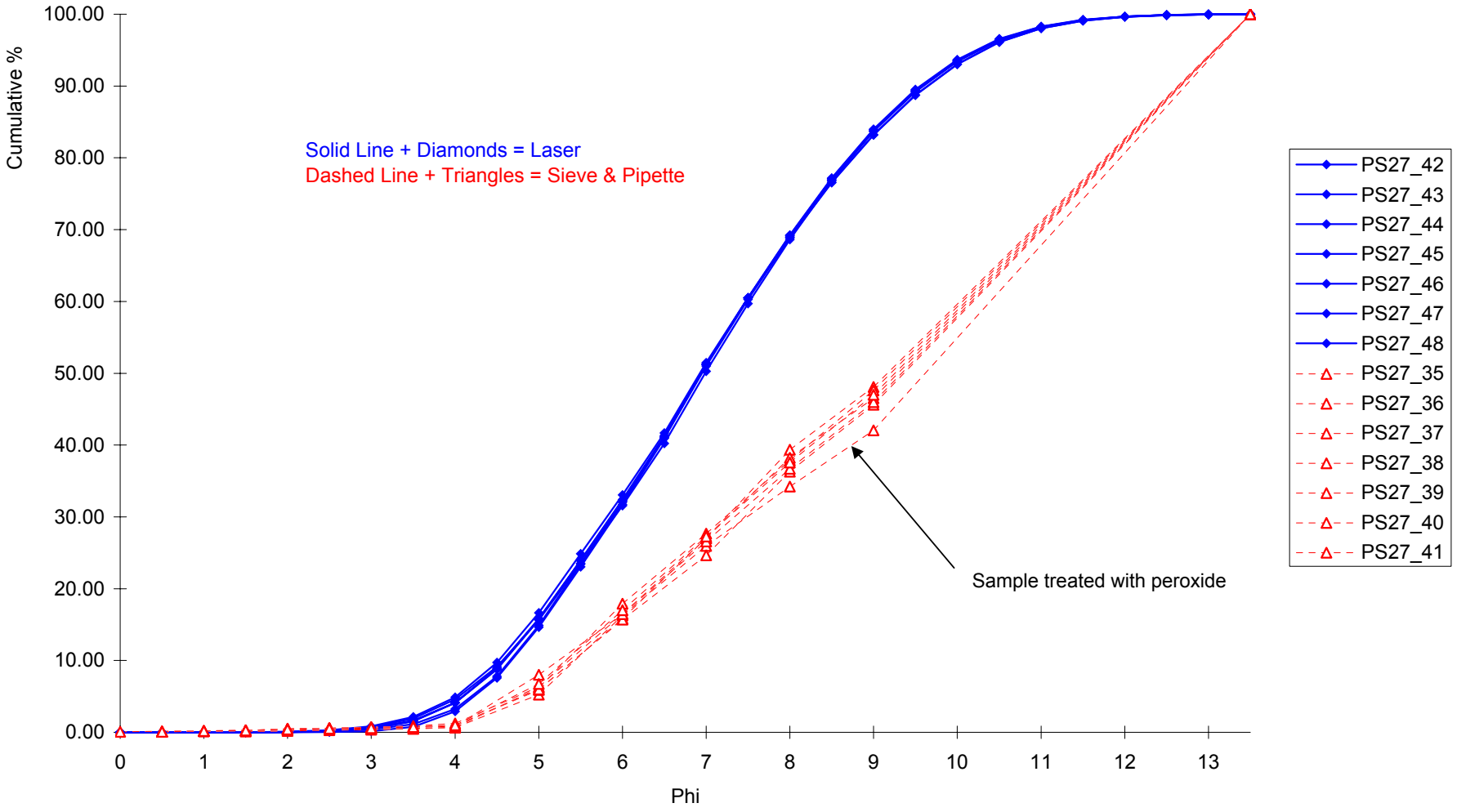


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS26.

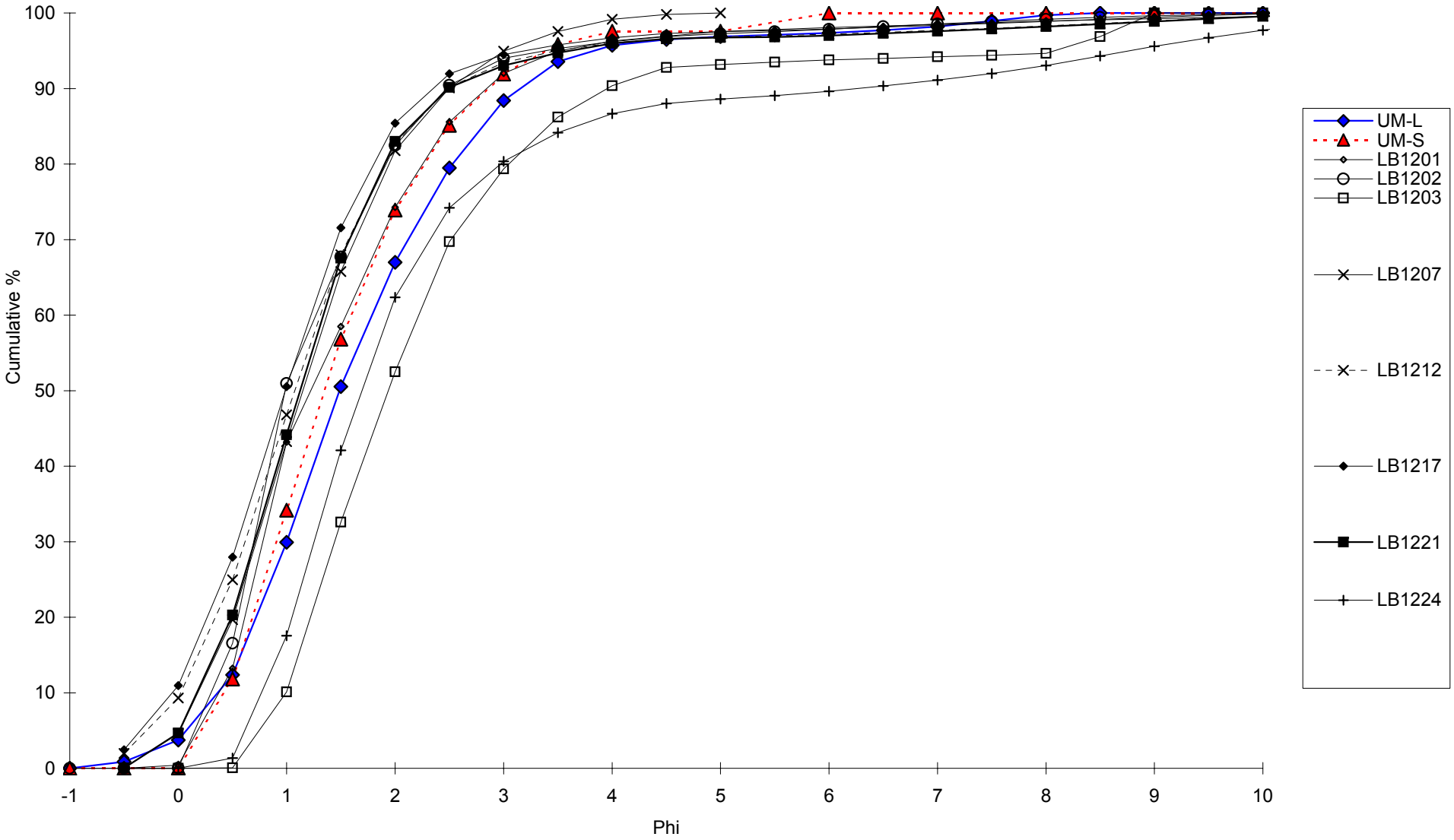


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS27.

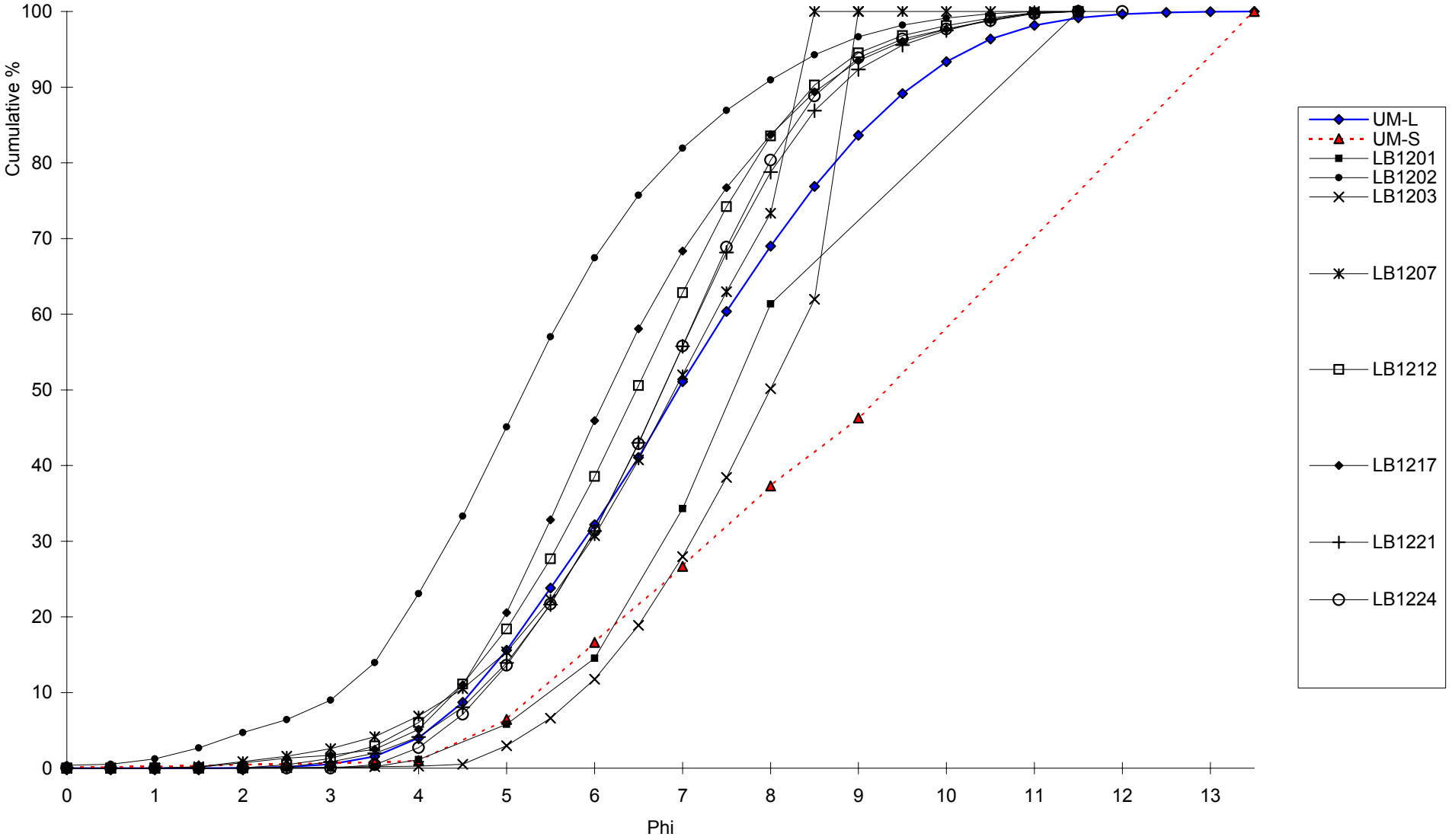


Figure 5. Z-scores for PS26 derived statistics (replicated data not displayed).

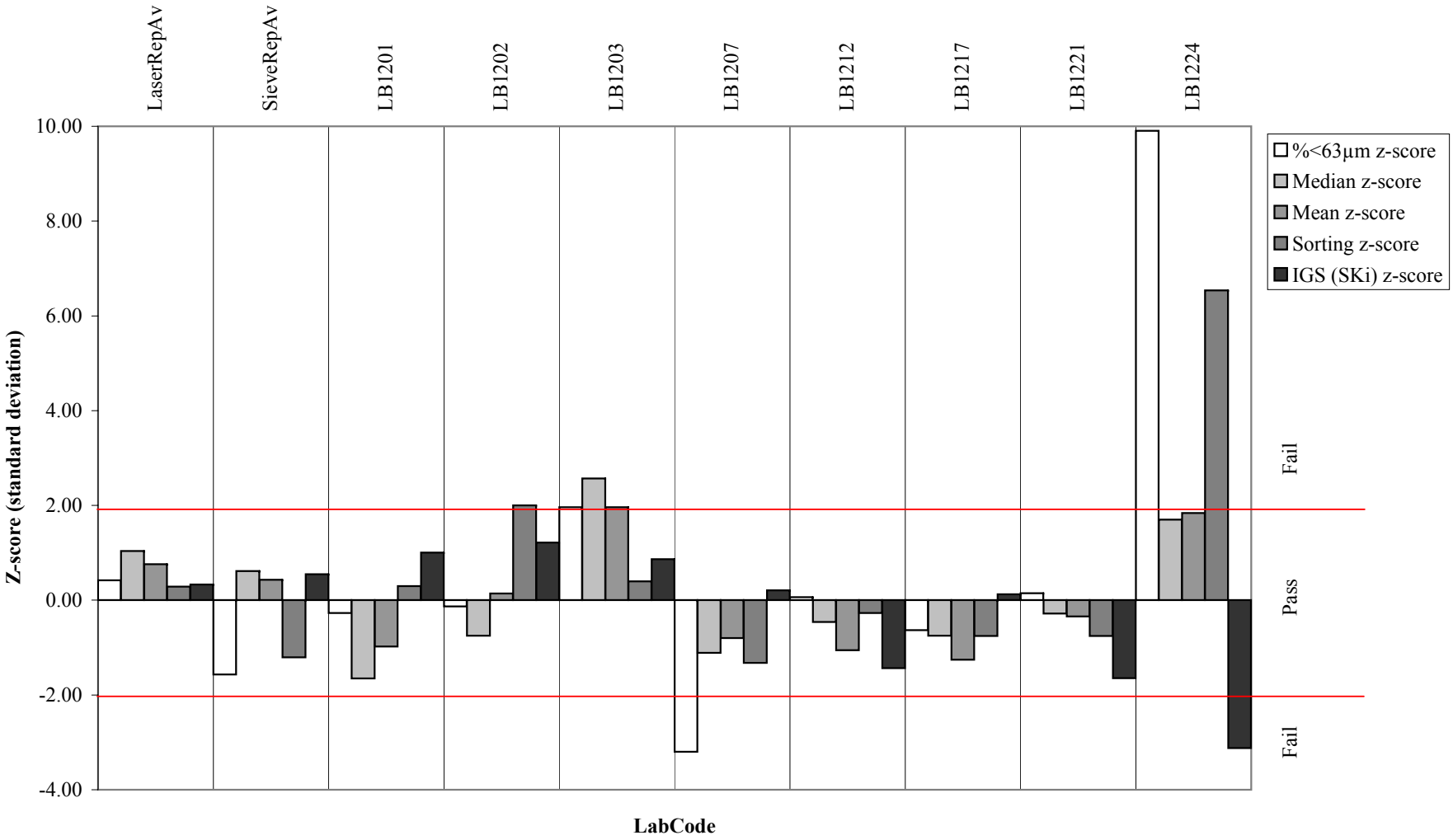


Figure 6. Z-scores for PS27 derived statistics (replicated data not displayed).

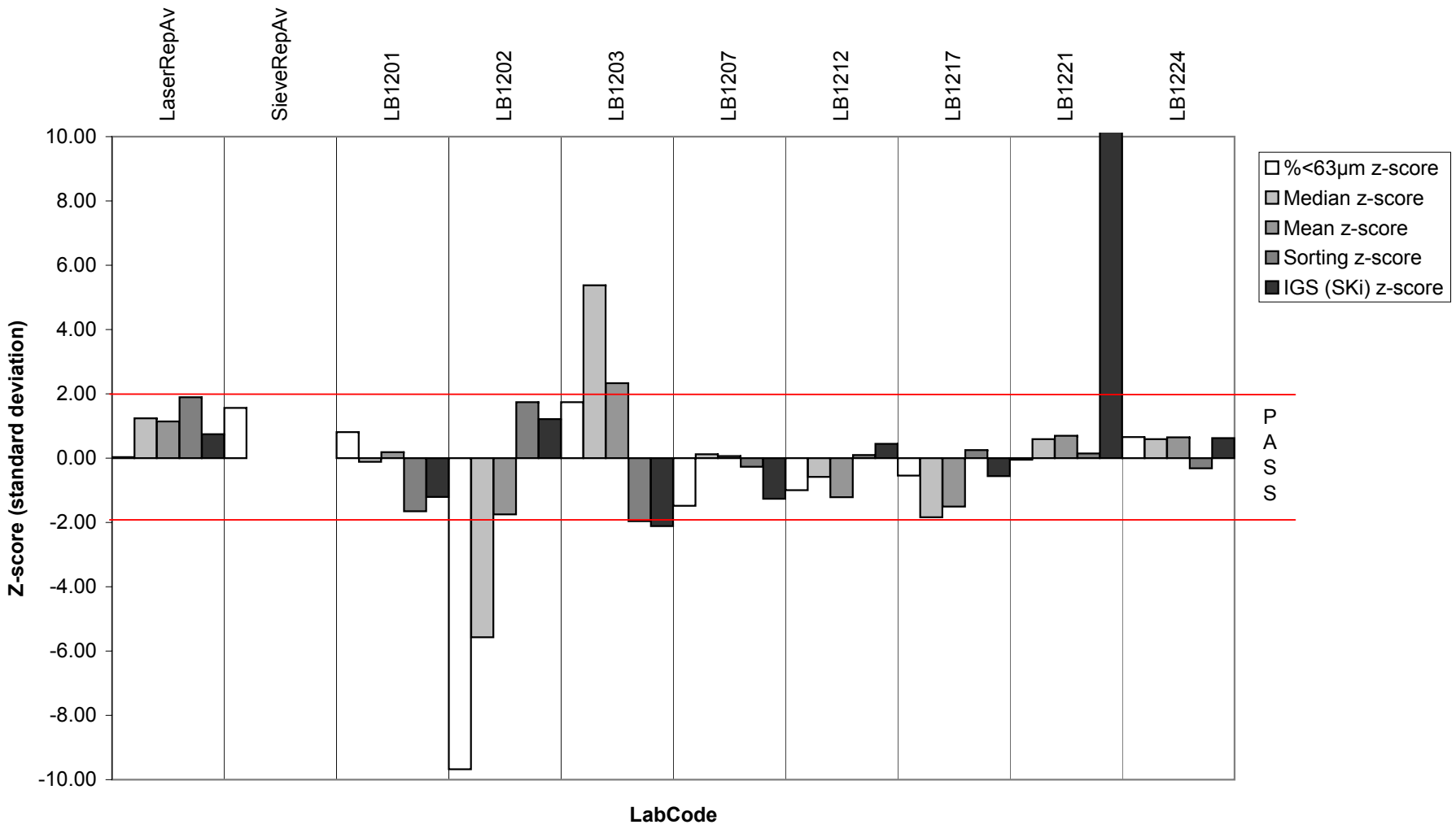


Figure 7. The number of differences from the AQC identification of specimens distributed in RT26 for each of the participating laboratories. Arranged in order of increasing number of differences.

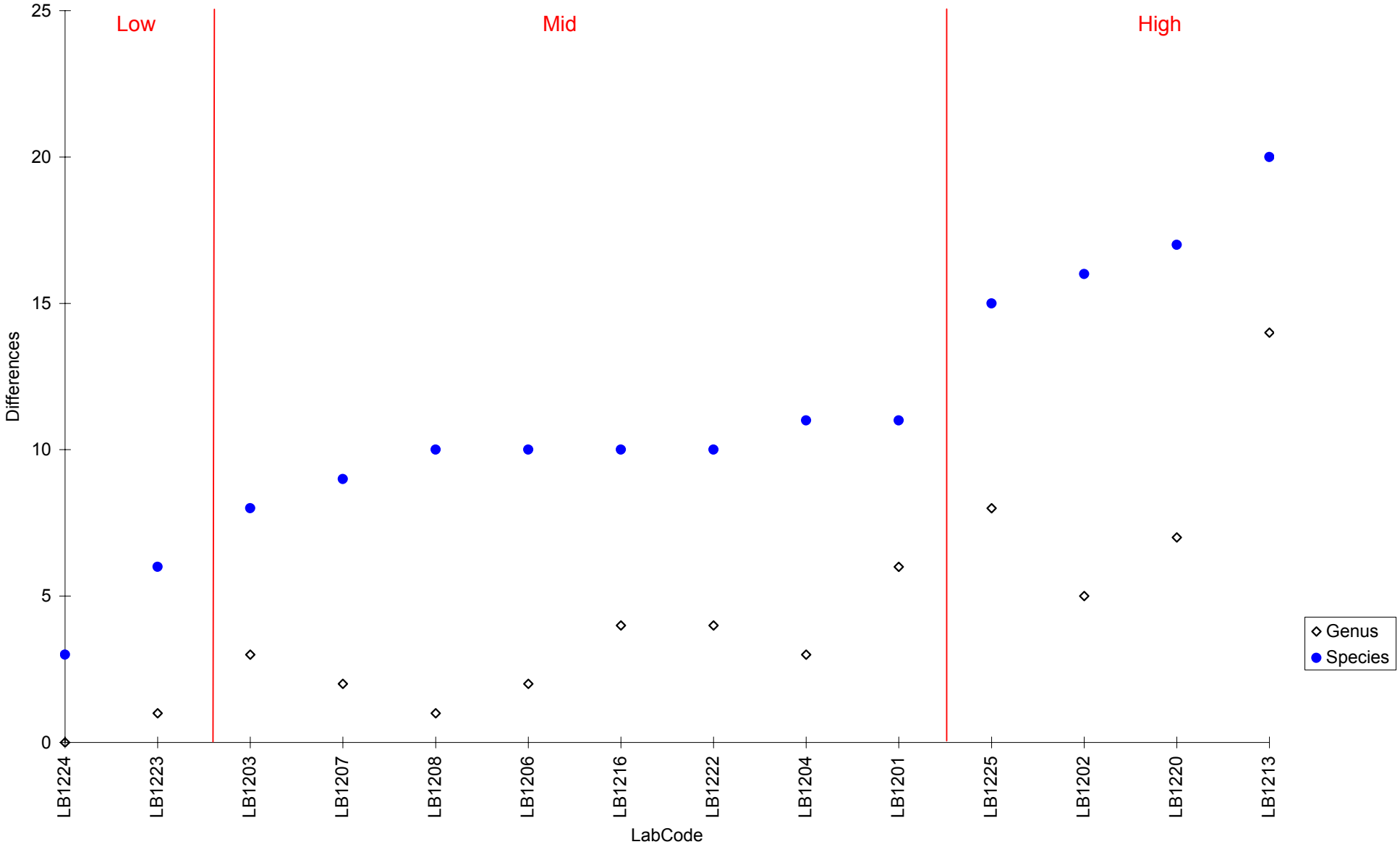


Figure 8. The number of differences from the AQC identification of specimens distributed in RT27 for each of the participating laboratories. Arranged in order of increasing number of differences.

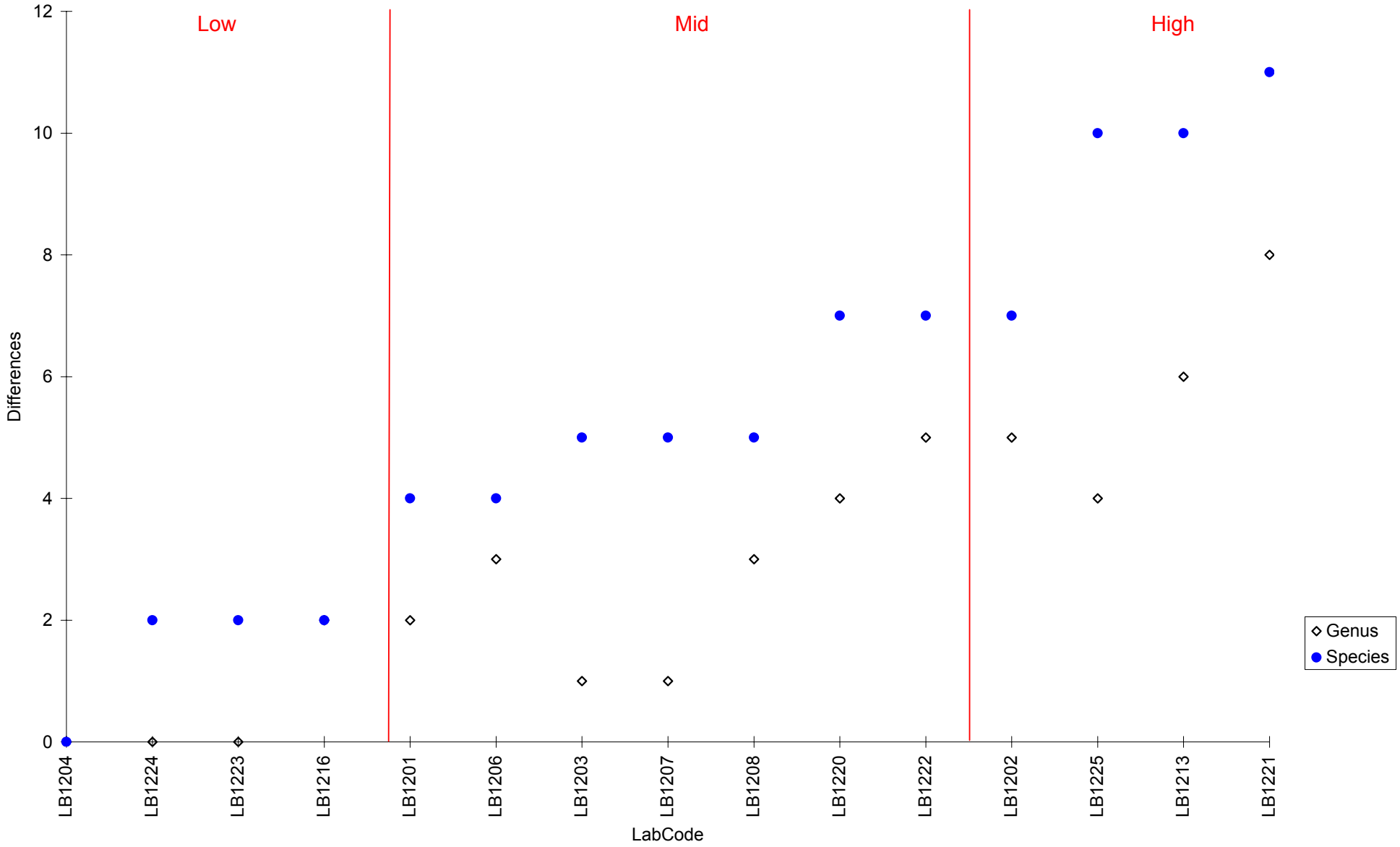
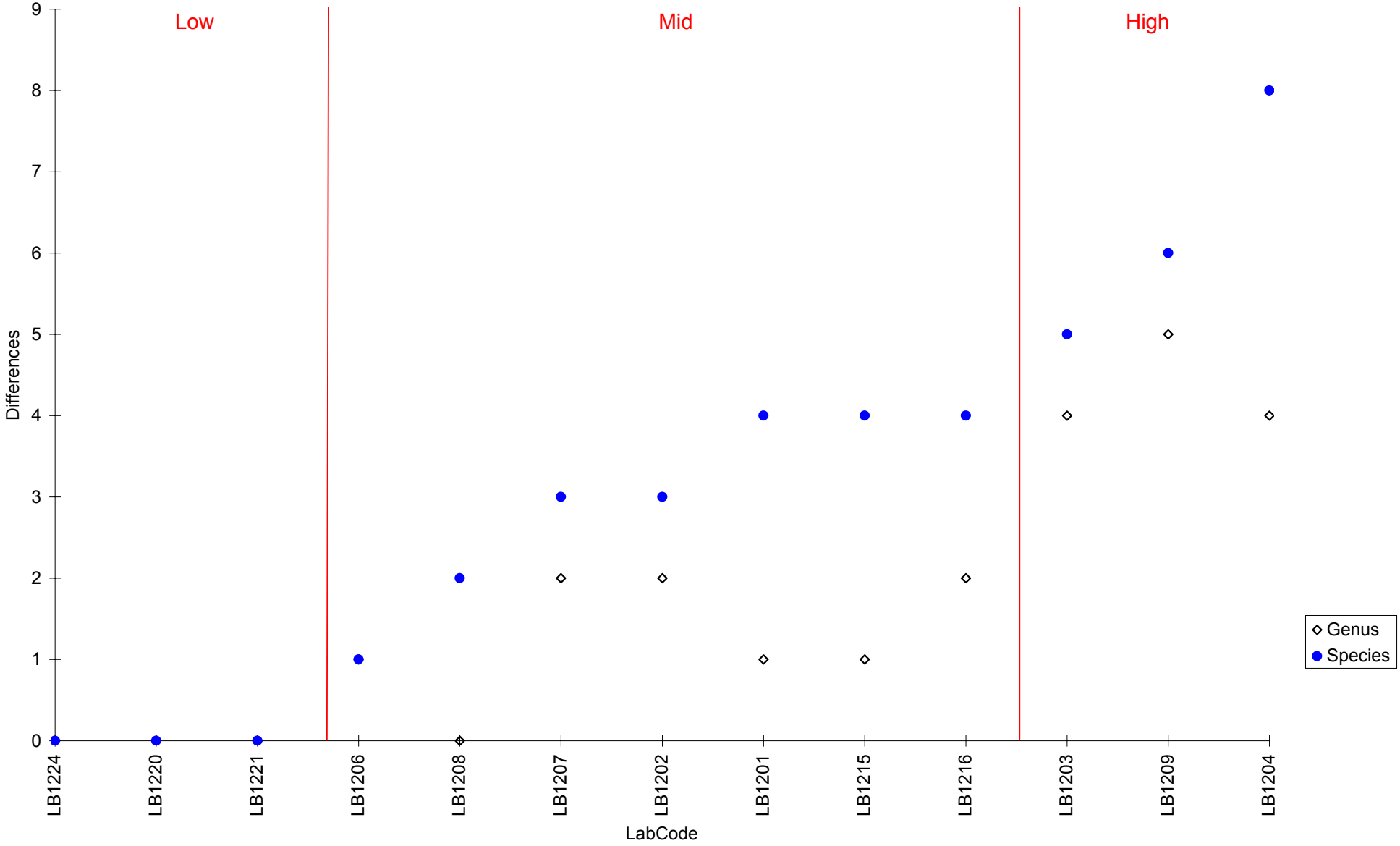


Figure 9. The number of differences from the AQC identification of specimens distributed in RT28 for each of the participating laboratories. Arranged in order of increasing number of differences.



Appendices

Appendix 1.

Participant Laboratory Reference Collection exercise (LR)

Objective:

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

LR10 is a special **'identification amnesty'** version of the previous exercises – all of the submitted specimens can be deemed unidentifiable or of uncertain identity by the participant laboratory (*i.e.* problem taxa). Submission of problem taxa is optional and laboratories can use this exercise for the verification of normal reference specimens as in previous LR exercises. If unidentified specimens are provided please give as much habitat data as possible to assist identification.

Protocol:

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

Preparation:

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

Timescale:

Please send specimens to Unicomarine Ltd. by 4th November 2005. 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

Version 1.1 Remedial Action Protocol August 2002

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

1.2 Particle Size Standards

1.2.1 Derived Statistics targets

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

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

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

Section C – Supplementary Report on the Phytoplankton Component from the Marine Institute of Ireland (PHY-ICN-05-MI3).

PHY-ICN-05-MI3 VR3.0

Biological Effects Quality Assurance in Monitoring Programmes (BEQUALM): Phytoplankton Enumeration and Identification Proficiency Test

Table of Contents

1. Summary

The Marine Institute, Galway, Ireland, has conducted an NMBAQC Phytoplankton Enumeration and Identification ring trial, under the auspices of BEQUALM.

The purpose of this is to compare the performance of laboratories engaged in national official or non-official phytoplankton monitoring programmes throughout Ireland and the UK. The Marine Institute is accredited to ISO 17025 for phytoplankton identification and enumeration, and recognises that regular Quality Control assessments are crucial to ensure a high standard of data.

In September 2005 an invitation to laboratories involved in phytoplankton analysis was issued. All labs expressing an interest were then sent further details and a query relating to the optimal time frame of availability for individual analysts.

Samples, instructions and results sheets were sent to all interested analysts according to their individual availability.

Analysts were given seven days to return results to the MI once samples were received.

The inter-comparison has results from twenty-one analysts in ten labs throughout Ireland, Northern Ireland, Scotland and England.

2. Introduction

Biological effects measurements are increasingly being incorporated into national and international environmental monitoring programmes to supplement chemical measurements. The Biological Effects Quality Assurance in Monitoring Programmes (BEQUALM) project, funded by the European Union through the Standards, Measurements and Testing programme of the European Commission, was initiated in 1998. This was in direct response to the requirements of OSPAR to establish a European infrastructure for biological effects QA/QC, in order that laboratories contributing to national and international marine monitoring programmes can attain defined quality standards.

3. Participants

In total, twenty-one analysts from ten laboratories participated in PHY-ICN-05-MI3. These laboratories were located in Ireland, Northern Ireland, Scotland, England and Wales. A complete list of the participating laboratories is given in Appendix I.

4. Materials and Methodology

4.1 Phytoplankton samples and micrographs

The inter-comparison exercise is comprised of two parts:

(a) **enumeration of cells** - cultured stock was used for enumeration, using the Utermöhl method. The cultures used were *Lingulodinium polyedrum*, initially obtained from the Culture Collection of the Instituto Espanol de Oceanografia, in Vigo Spain. These cultures have been maintained in the Phytoplankton Laboratory in the Marine Institute, Galway since August '03. In August '05 part of this culture was sub-sampled for this Inter-comparison exercise.

A set of two sample bottles was prepared for each analyst. Cells were fixed with Lugols iodine and individually isolated into each bottle, until one held a predetermined higher number (17,000 cells/l), and the other a lower number (7000 cells/l). The bottle contained sterile seawater and Lugols iodine. When the count was completed, the volume was then brought up to 25mls using sterile seawater. Bottles were labeled A and B along with the analyst's individual code. Those labeled A had a random distribution of higher (17,000 cells/l) or lower (7000 cells/l) number of cells, with corresponding opposite levels in those labeled B for each analyst.

The true value for the lower count was obtained from 3 replicate counts of 10 samples chosen randomly from a pool of 25 set samples. The same method was used for the higher count true value. These samples were produced in the same manner as the exercise samples.

NOTE: It should be noted that for the purposes of this report all lower count results are called 'sample A' and all higher count results are called 'sample B'.

Once prepared, each set of samples was couriered to the analyst.

(b) **identification of species** - a sheet of field micrographs was given to each participating analyst for identification purposes. Micrographs were chosen from the collection established by Marine Institute phytoplankton personnel during the routine national monitoring programme.

4.2 Instructions for counting and identification

Detailed instructions had to be followed for PHY-ICN-05-MI3. These instructions are attached in Appendix II. Samples had to be settled and cells counted and calculated according to these instructions. Fourteen micrograph's had to be identified to an appropriate level.

All required results had to be returned in the official results sheets.

4.3 Statistical analysis

The original number of cells which were counted into the sample containers and converted to cells/litre, were taken as reference values for the calculation of percentage error.

The mean and standard deviation of analyst's results were used in the calculation of 95% confidence intervals and Z-scores.

All of these methods are used as a measure of lab performance.

5. Results and Discussion

As all participants were given detailed instructions in the setting up and analysis of the samples, the variance between the results should mainly be due to individual factors – such as counting/transferring of cells into the sample bottles, and preparation, sample set-up and counting bias in the analysis of the samples.

5.1 Phytoplankton Counts (cell concentrations)

All enumeration results were collated and three aspects were examined statistically for each count level. These were:

(a) percentage error of the original count.

(b) 95% confidence interval taken as twice standard deviation.

(c) Z-scores

Details of the statistical results are contained in Appendix III.

(a) percentage error of the original count:

The percentage error of the original count is the difference between the analyst's count and the original number counted into the sample bottle, and is expressed as a percentage of the original value.

For sample A, (the lower cell count), this ranged between –40% and 37.14%.

When put into groups of 10 percentage points (Fig 1.) the spread is very even for sample A results. The 0%-10%, 11%-20% and 21%-30% groups of percentage error of the original count, each contain 26.3% of the analysts results, with the 31%-40% group containing 21% of results.

For sample B, (the higher cell count), the range is between -45.41% and 6.82%. When grouped the 0%-10% and 11%-20% each hold 31.6% of the results. The 21%-30% group contains 15.8% of analyst's results, with the 31%-40% group containing 5.3% of results. However 15.8% of results were between 41% and 46% away from the 'true' value.

From the above analysis it can be surmised that the samples containing the higher number of cells were more widely undercounted.

	% Range	Analysts results as percentage of total no of analysts
Sample A (lower counts)	0 to 10	26.3%
	11 to 20	26.3%
	21 to 30	26.3%
	31 to 40	21%
Sample B (higher counts)	0 to 10	31.6%
	11 to 20	31.6%
	21 to 30	15.8%
	31 to 40	5.3%
	41 to 50	15.8%

Fig 1. Results of percentage error of the original count, grouped into 10 percentile ranges.

(b) 95% confidence interval as twice standard deviation.

For the purposes of this proficiency test, the 95% confidence interval is obtained by the equation:

2(standard deviation)+/- mean.

Where the mean and standard deviations are calculated from the analysts results.

In sample A all results except one was within the 95% limits. In sample B all results were within the limits

(c) z -scores:

z-scores are transformed data that change any set of scores to a new set with a mean of 0 and a standard deviation of 1. In this case each returned count is compared against the mean of all counts. All results falling within a −2 to +2 standard deviation range are deemed acceptable.

For results of sample A, 94.7% of analysts were within the acceptable range. This can be further broken down to 73.7% of results being within the −1 to +1 range, and 21% being within the −2 to +2 range. 5.2% of results were greater than 3 standard deviations - an unacceptable result. The overall absolute average for all these results is 0.712

For results of sample B, all analysts were within the acceptable range. Again this can be further broken down to 73.7% of results being within the 1 standard deviation range, and the remainder, 26.3%, within 2 standard deviations. The overall absolute average for all these results is 0.733.

5.2 Phytoplankton species identification

All micrographs results were tabulated and scores given for correct identification.

Marks were awarded as follows:

- 5 for correct genus, 5 for correct species.
- Some photos could not be identified to species level due to incomplete detail in the photo. In these cases, the correct species result is 'sp.'. If the cell was identified to species level by the analyst, then the mark for species was 0.
- If the photo was identifiable to species level and the analyst marked it as 'sp.', then 2.5 marks were given in the species section.

- If an old synonym was used in either the genus or species section then 4 marks were given.

Results were presented as overall percentage correct, percentage error of the maximum result (100% correct), and z-scores of the mean of results. Details of the identification results are contained in Appendix IV.

5.3 Performance evaluation

Out of twenty analysts taking part in the identification section, 25% of analysts were within 5% of the maximum score level. A further 35% of analysts were within 10% of the maximum score level.
20% of analysts were between 10% and 20% of the maximum score.
15% of analysts were between 20% and 30% of the maximum score and 5% of analysts were just outside 30% of the maximum score.

It is worth noting that 85% of analysts had scores of over 90% in the genus section with 55% of analysts getting the maximum score.
In the species section 30% of analysts had scores of over 90%, with 35% of analysts scoring between 80% and 90%, 15% of analysts scoring between 70% and 80% and the remainder (22% of analysts), scoring between 40% and 70%.

6. Conclusions and Recommendations

Overall, this proficiency test proved very successful both in terms of interest from labs involved in phytoplankton analysis and overall results.
Some changes may be recommended for future tests, particularly in the type of sample preparation used – especially if incorporating it with identification of cells. Also statistical methods should be decided on for biological tests of this nature.
In March 2006 a workshop is being conducted to which all participating analysts are invited. It is proposed that the overall test results will be examined, and the above points discussed.

Appendix I: Participating laboratories

Table showing participating laboratories in the proficiency test PHY-ICN-05-MI3.

Please note that some labs submitted multiple data sets.

Laboratory	Country	No. Of Participants
Marine Institute, Galway	Ireland	4
Marine Institute, Bantry	Ireland	1
Environmental Protection Agency, Dublin	Ireland	1
Environment & Heritage Service, Lisburn	N. Ireland	1
DARD, Aquatic Systems, Belfast	N. Ireland	2
FRS Marine Laboratory, Aberdeen	Scotland	4
SEPA, East Kilbride	Scotland	2
SEPA, Riccarton	Scotland	1
CEFAS Laboratory, Lowestoft	England	4
Marine Biological & Chemical Consultants	Wales	1

Appendix II: Instructions

Instructions for Sample Preparation, Counting, Calculations and Identification

Please note that these instructions are designed strictly for use in this intercomparison.

1. Introduction

This 3rd Phytoplankton Ring Test is being conducted to determine any inter-laboratory variations for enumeration and identification between labs in Ireland and the United Kingdom. Please adhere to the following instructions strictly. Please note that these instructions are specific for this ring test.

2. Preliminary Check and Time Restrictions

Upon receipt of the samples please make sure that you have received everything listed in the Return Slip form (Form 1). Complete the form and send it by Fax to the Marine Institute, Galway. Fax No. 00353 91 730470. A receipt of Fax is necessary for the Marine Institute to validate the test process for your lab.

Analysts have **seven days** to return results to the Marine Institute, in the pre-addressed envelope provided. Results received after this will be void.

3. Equipment

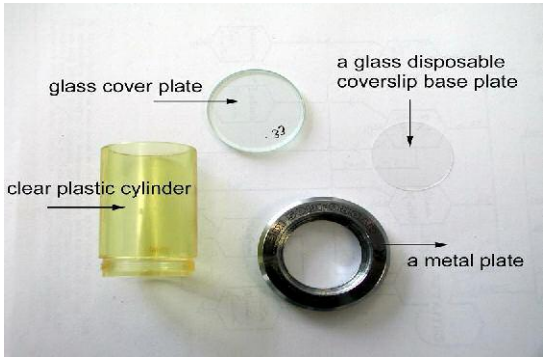
- Two Utermöhl counting chambers. Ideally 25ml vol., as each sample contains 25ml. However where laboratories are set up to use 10ml chambers, a sample reduction step may be carried out.

- Base plates and glass covers.

- Inverted Microscope.

4. Sample Preparation

Sedimentation counting chambers consist of a clear plastic cylinder, a metal plate, a glass disposable coverslip base plate and a glass cover plate. Two sets will be required.



4.1 Place a disposable glass base plate on a cleaned metal plate.

4.2 Screw the plastic cylinder into the metal plate. Extra care should be taken when setting up chambers. Glass base plates are fragile and break easily causing cuts and grazes. Careless handling can easily damage metal plates, and render them unusable.

4.3 For this intercomparison, once the chamber is set up, test for the possibility of leaks by filling the completed chamber with water and allowing to rest for a few minutes. If no leakage occurs, pour out the water and proceed with the next step. Make sure all the water is emptied.

4.3 To set up a sample for analyses invert the sample tube gently at least three times to ensure that the phytoplankton are evenly distributed throughout the sample. Do not shake the tube to avoid air bubbles and damaged cells. Pour the sample into the 25ml counting chamber and cover with a glass cover plate. In the event of the sample not filling the chamber, top up with sterile seawater, to complete the vacuum and avoid air pockets. Give the chamber a label corresponding to the label of the sample in question.

4.4 Use a horizontal surface to place chambers protected from vibration and strong sunlight.

4.5 Allow the sample to settle for a minimum of twelve hours.

4.6 Use the 20X objective to count the phytoplankton.

The cells in the samples are from a uni-algal culture of Lingulodinium polyedrum. Due to the nature of the species some cells may be encysted. For this intercomparison it is required to count **all viable cells**, including those that appear cyst-like. Do not count empty theca.

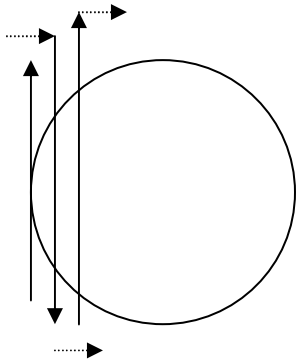
4.7 Enumeration results for each sample are to be entered on the Results Sheet (Form 2 Section A)

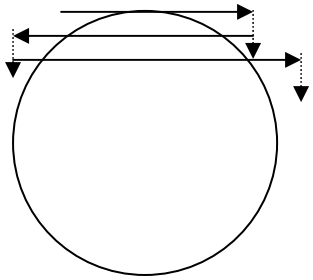
5. Counting Strategy

For this test a whole base plate count will be conducted.

The whole base plate of the chamber is counted by enumerating all viable cells within a continuous motion of field of view for the entire area of the base plate.

This can be done by going from left to right or top to bottom, in a continuous series of sinuous movements in such a manner that the whole base plate is observed. Make sure the field of view does not exclude any uncounted area or overlap any area already counted.





6. Conversion Calculations of Cell Counts

The number of cells found is converted to cells.L^{-1} . Please show calculation step in Form 2, section A.

7. Identification

Photographs of cells found in samples from the field are on the Identification Sheet. Each photo also has the dimensions of the cell listed. Please identify and include your results on the Results Sheet (Form 2 Section B).

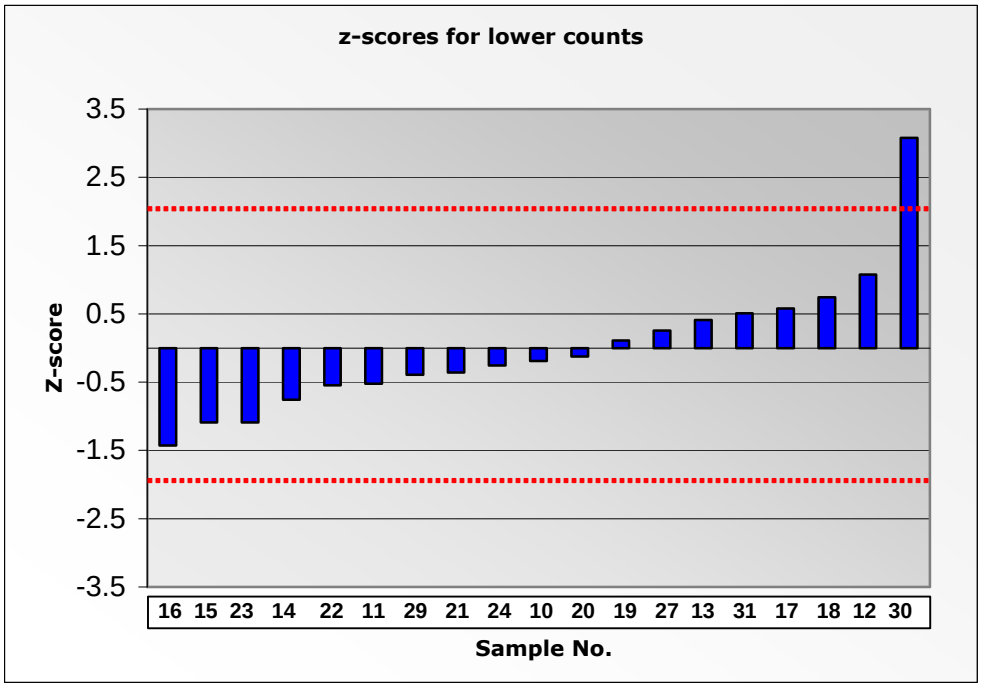
Appendix II: Detailed results of the enumeration test

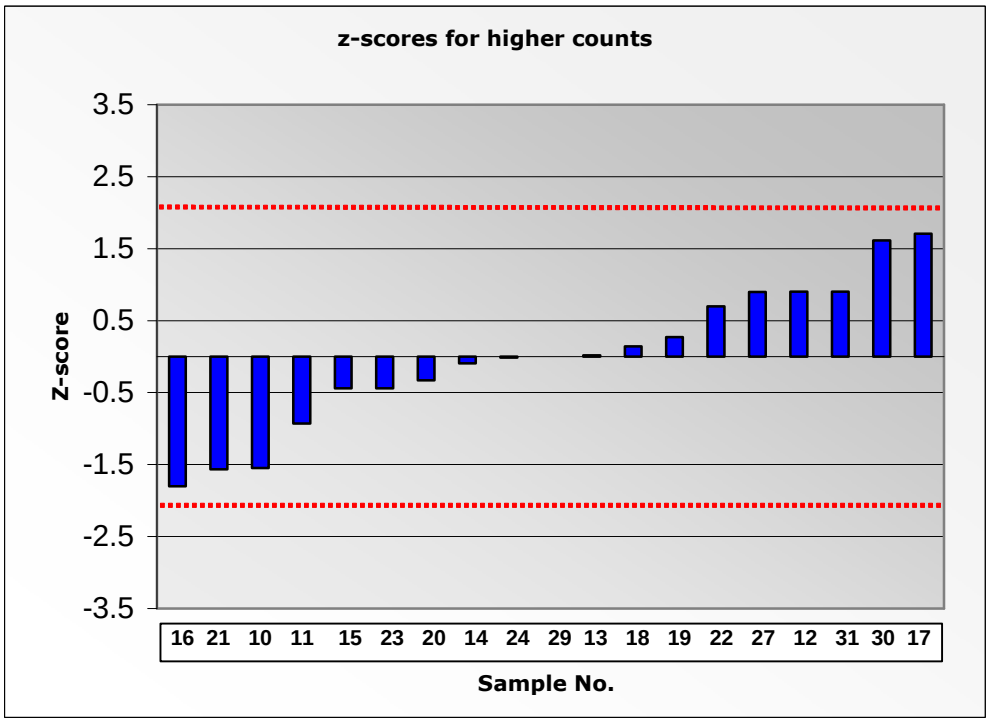
Statistical analysis: Cell counts showing percentage error of the original count ('true' value) and 95% confidence intervals of the counted results.

	Smaller counts				Larger counts			
Sample No	**Count**	**True Value**	**Error**	**% Error**	**Count**	**True Value**	**Error**	**% Error**
10	**5680**	7000	-1320	-18.86	**9920**	17000	-7080	-41.65
11	**5280**	7000	-1720	-24.57	**11480**	17000	-5520	-32.47
12	**7200**	7000	200	2.86	**16120**	17000	-880	-5.18
13	**6400**	7000	-600	-8.57	**13880**	17000	-3120	-18.35
14	**5000**	7000	-2000	-28.57	**13600**	17000	-3400	-20.00
15	**4600**	7000	-2400	-34.29	**12720**	17000	-4280	-25.18
16	**4200**	7000	-2800	-40.00	**9280**	17000	-7720	-45.41
17	**6600**	7000	-400	-5.71	**18160**	17000	1160	6.82
18	**6800**	7000	-200	-2.86	**14200**	17000	-2800	-16.47
19	**6040**	7000	-960	-13.71	**14520**	17000	-2480	-14.59
20	**5760**	7000	-1240	-17.71	**13000**	17000	-4000	-23.53
21	**5480**	7000	-1520	-21.71	**9880**	17000	-7120	-41.88
22	**5252**	7000	-1748	-24.97	**15598**	17000	-1402	-8.25
23	**4600**	7000	-2400	-34.29	**12720**	17000	-4280	-25.18
24	**5600**	7000	-1400	-20.00	**13800**	17000	-3200	-18.82
27	**6214**	7000	-786	-11.23	**16111**	17000	-889	-5.23
29	**5440**	7000	-1560	-22.29	**13840**	17000	-3160	-18.59
30	**9600**	7000	2600	37.14	**17920**	17000	920	5.41
31	**6520**	7000	-480	-6.86	**16120**	17000	-880	-5.18

Mean	5908.7368				13835.211			
SD	1198.6439				2530.1687			
2SD	2397.2878				5060.3375			
			95% Confidence Intervals				95% Confidence Intervals	
			Lower	Upper			Lower	Upper
			3511.45	**8306.0246**			**8774.87**	**18895.548**

Barcharts ranking of analysts according to z-scores





Appendix IV: Detailed results of the identification test

Section B Identification Results: **Photo's A - G**

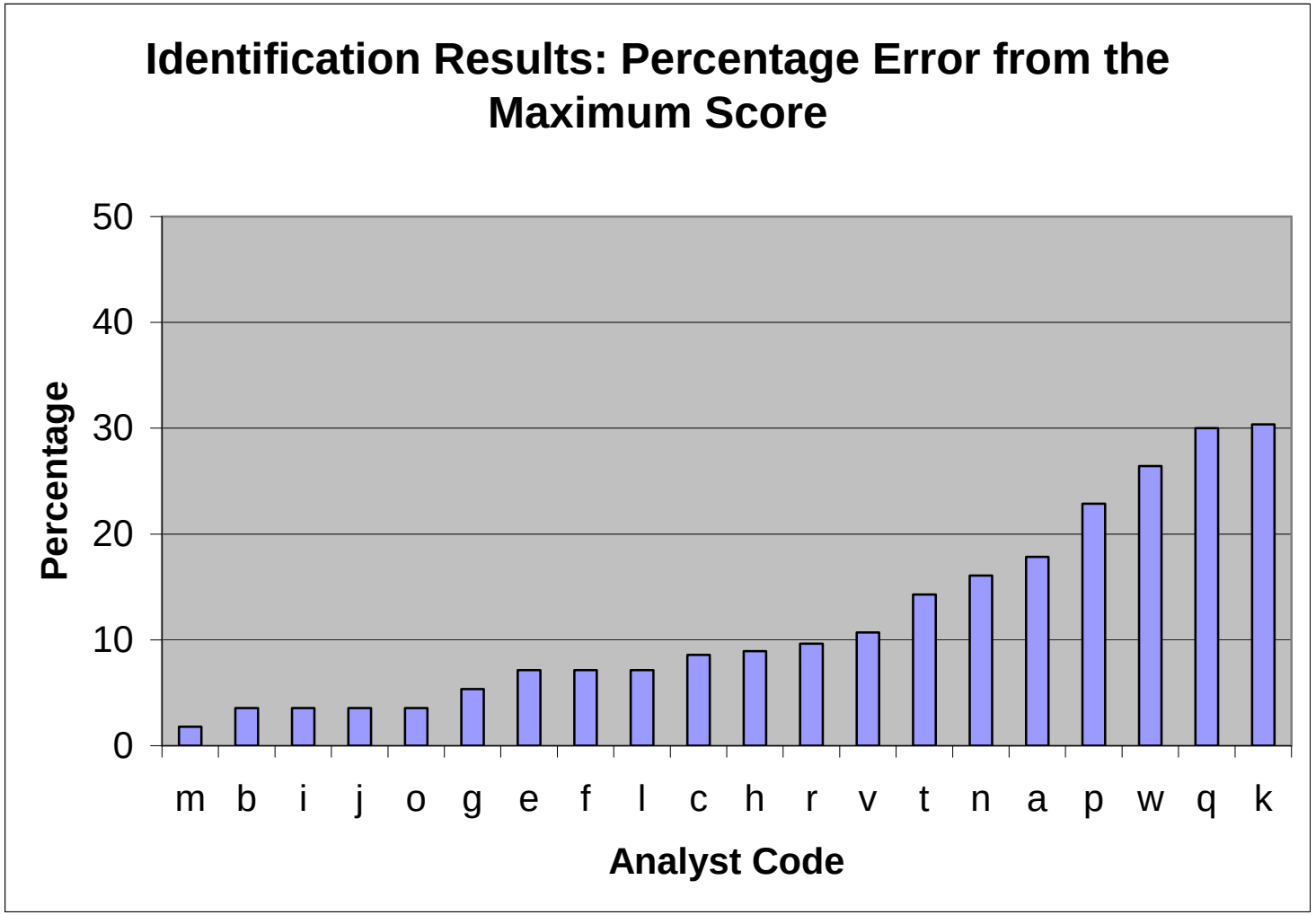
Analyst		**Results**						
IRE2005-INT-		**A**	**B**	**C**	**D**	**E**	**F**	**G**
		Heterocapsa	*Karinia*	*Protoperidinium*	*Alexandrium*	*Dinophysis*	*Protoperidinium*	*Chaetoceros*
		sp.	*mikimotoi*	*ovatum*	*sp.*	*acuta*	*stenii*	*sp.*
a		*H. niel*	*K. mikimotoi*	*P. ovatum*	*A. tamarense*	*D. acuta*	*P. stenii*	*C. laciniosus*
b		*Heterocapsa sp.*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
c		*Gymnodiniaceae*	*Gyrodinium aureulum*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
e		*Heterocapsa sp.*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*C. subtilis*
f		*Heterocapsa*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetocerus sp.*
g		*Heterocapsa sp.*	*K. mikimotoi*	*Protoperidinium sp.*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
h		*Heterocapsa sp.*	*K. mikimotoi*	*Protoperidinium sp.*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*C. subtilis*
i		*Heterocapsa sp.*	*K. mikimotoi*	*Protoperidinium sp.*	*Alexandrium sp.*	*D. sp. (acuta)*	*P. sp (stenii)*	*Chaetoceros sp.*
j		*Heterocapsa sp.*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
k				*P. ovatum*	*A. tamarense*	*D. acuta*	*P. stenii*	*C. affinis*
l		*H. triquetra*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
m		*Heterocapsa sp.*	*K. mikimotoi*	*Protoperidinium sp.*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
n		*Gymnodinium ?*	*K. mikimotoi*	*Protoperidinium ?*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*C. affinis*
o		*H. sp (poss niei)*	*K. mikimotoi*	*P. ovatum*	*A. sp. (tamarense)*	*D. acuta*	*P. stenii*	*C. sp (poss laciniosis)*
p		*G. conicum ?*	*Gyrodinium aureulum*	*P. ovatum*	*Gonyaulax. tamareusis*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
q		*H. triquetra*	*Gymno. mikimotoi*	*P. pellucidium*	*A. tamarense*	*D. norvegica*	*P. stenii*	*Chaetoceros*
r		*Gym.(poss wulffii/ proticum)*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*C. (affinis)*
t		*Gymnodinium sp*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*C. affinis*
v		*Unid sp. Naked dino*	*K. mikimotoi*	*P. ovatum*	*Alexandrium sp.*	*D. acuta*	*P. stenii*	*Chaetoceros sp.*
w		*Gym. veneficum*	*Gymno. aureolum*	*P. ovatum*	*Peridiniella danicum*	*D. acuta*	*P. stenii*	*C. lacinosum*

Section B Identification Results: **Photo's H - N**

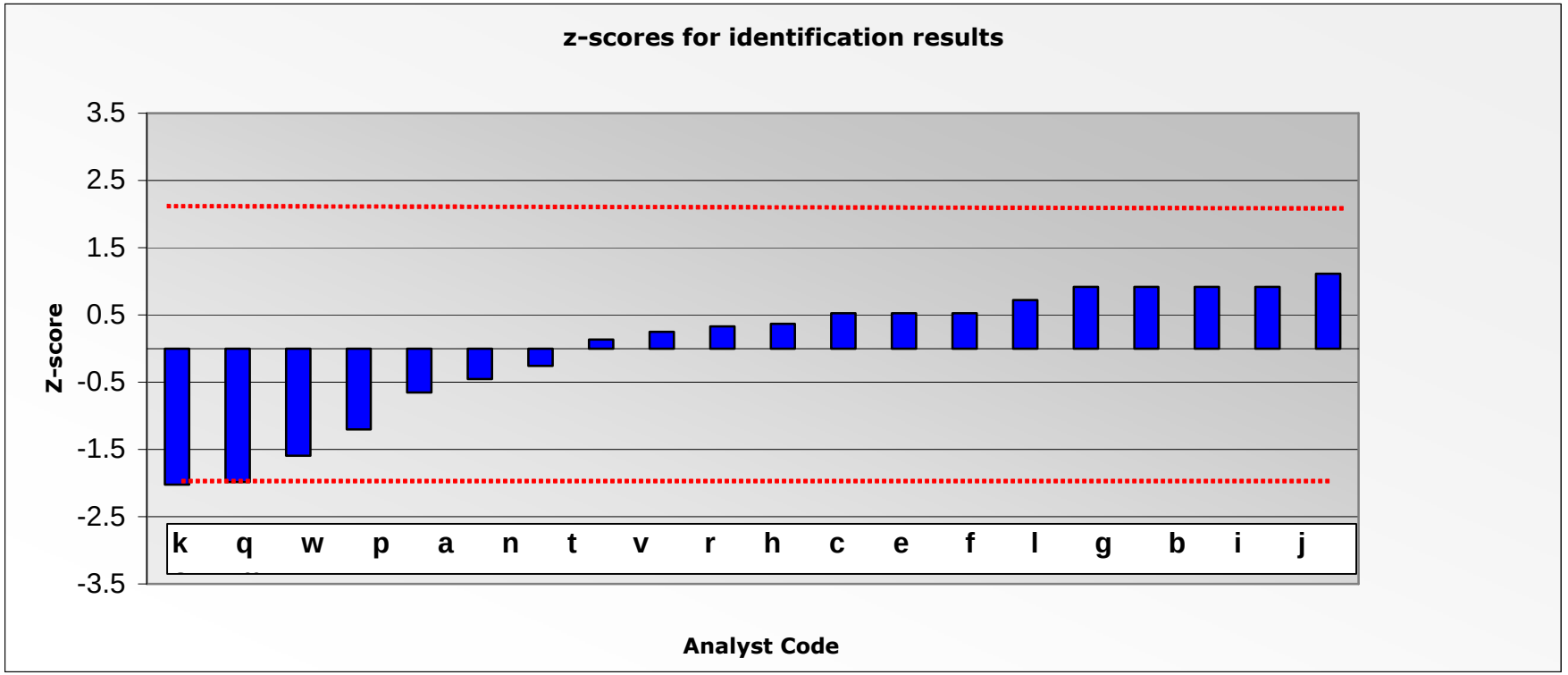
Analyst		**Results**						
IRE2005-INT-		***H***	***I***	***J***	***K***	***L***	***M***	***N***
		Ceratium	*Prorocentrum*	*Dinophysis*	*Noctiluca*	*Pseudo-nitzschia*	*Dinophysis*	*Dinophysis*
		tripos	*lima*	*acuminata*	*scintillans*	*seriata group*	*rotundata*	*hastata*
a		*C. tripos*	*P. scuttellum*	*D. acuminata*	*N. scintillans*	*Ps. delicatissima*	*D. rotundata*	*D. odiosa*
b		*Ceratium sp.*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
c		*C. tripos*	*P. cf lima*	*D. acuminata*	*N. scintillans*	*Ps. seriata gp*	*D. nasutum*	*D. hastata*
e		*Ceratium spp.*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
f		*C. tripos*	*Prorocentrum sp*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
g		*C. tripos*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. seriata*	*D. rotundatum*	*D. hastata*
h		*Ceratium sp.*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
i		*Ceratium sp.(tripos)*	*P. lima*	*D. sp. (acuminata)*	*N. sp. (scintillans)*	*Ps. sp. (seriata)*	*D. sp. (rotundatum)*	*D. sp. (hastate)*
j		*Ceratium sp.*	*P. sp. (lima)*	*D. acuminata*	*Noctiluca sp.*	*Ps.sp. (seriata type gp)*	*D. rotundata*	*D. odiosa*
k		*C. horridum*	*P. lima*	*D. punctata*	*N. scintillans*	*Ps. sp*	*D. nasutum*	*D. odiosa*
l		*C. tripos*	*Prorocentrum sp*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
m		*C. tripos*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. seriata gp*	*Phalachroma sp / D. rotundatum*	*D. hastata*
n		*C. tripos*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
o		*C. sp (tripos?)*	*P. sp (saitellum?)*	*D. acuminata*	*N. scintillans*	*Ps. sp*	*D. rotundata*	*D. odiosa*
p		*C. tripos*	*P. lima*	*D. punctata*	*N. scintillans*	*Ps. multiseries*	*D. nasutum*	*D. odiosa*
q		*C. longipes*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps. seriata*	*D. rotundata*	*D. acuta*
r		*C. tripos*	*P. concavum / lima*	*D. acuminata*	*N. scintillans*	*Ps. seriata gp*	*P. rotundatum*	*D. odiosa*
t		*C. tripos*	*P. lima*	*D. acuminata*	*N. scintillans*	*Ps fraudulenta*	*P./D. rotundata*	*D. odiosa*
v		*Ceratium sp. (tripos?)*	*Prorocentrum s*	*D. acuminata*	*N. scintillans*	*Ps sp.*	*D. rotundatum / nasutum*	*D. hastata*
w		*C. tripos*	*P. lima*	*D. recurva*	*N. scintillans*	*Ps. seriata*	*D. nasuta*	*D. hastata*

Table showing scores for identification results:

	A		B		C		D		E		F		G		H		I		J		K		L		M		N			
	Heterocapsa	*sp*	*Karinia*	*mikimotoi*	*Protoperidinium*	*ovatum*	*Alexandrium*	*sp*	*Dinophysis*	*acuta*	*Protoperidinium*	*stenii*	*Chaetocerous*	*sp*	*Ceratium*	*tripos*	*Prorocentrum*	*lima*	*Dinophysis*	*acuminata*	*Noctiluca*	*scintillans*	*Pseudo-nitzschia*	*seriata group*	*Dinophysis*	*rotundatum*	*Dinophysis*	*hastata*	**Total**	**%**
a	5	0	5	5	5	5	5	0	5	5	5	5	5	0	5	5	5	0	5	5	5	5	5	0	5	5	5	5	115	82.1
b	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	5	5	2.5	5	5	5	5	135	96.4
c	0		4	4	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	128	91.4
e	5	5	5	5	5	5	5	5	5	5	5	5	5	0	5	2.5	5	5	5	5	5	5	5	2.5	5	5	5	5	130	92.9
f	5		5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	2.5	5	5	5	5	130	92.9
g	5	5	5	5	5	2.5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	0	5	5	5	5	132.5	94.6
h	5	5	5	5	5	2.5	5	5	5	5	5	5	5	0	5	2.5	5	5	5	5	5	5	5	2.5	5	5	5	5	127.5	91.1
i	5	5	5	5	5	2.5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	135	96.4
j	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	2.5	5	5	5	5	5	5	135	96.4
k					5	5	5	0	5	5	5	5	5	0	5	0	5	5	5	0	5	5	5	2.5	5	5	5	5	97.5	69.6
l	5	0	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	2.5	5	5	5	5	130	92.9
m	5	5	5	5	5	2.5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	137.5	98.2
n	0		5	5	5		5	5	5	5	5	5	5	0	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	117.5	83.9
o	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	2.5	5	5	5	5	135	96.4
p	0	0	4	4	5	5	0	0	5	5	5	5	5	5	5	5	5	5	5	0	5	5	5	0	5	5	5	5	108	77.1
q	5	0	4	4	5	0	5	0	5	0	5	5	5		5	0	5	5	5	5	5	5	5	0	5	5	5	0	98	70
r	0	0	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	5	5	5	5	5	4	5	5	5	126.5	90.4
t	0	0	5	5	5	5	5	5	5	5	5	5	5	0	5	5	5	5	5	5	5	5	5	0	5	5	5	5	120	85.7
v	0	0	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	2.5	5	5	5	5	5	2.5	5	5	5	5	125	89.3
w	0	0	4	4	5	5	0	0	5	5	5	5	5	0	5	5	5	5	5	0	5	5	5	0	5	5	5	5	103	73.6



Anayst Code	% Error
m	1.8
b	3.6
i	3.6
j	3.6
o	3.6
g	5.4
e	7.1
f	7.1
l	7.1
c	8.6
h	8.9
r	9.6
v	10.7
t	14.3
n	16.1
a	17.9
p	22.9
w	26.4
q	30.0
k	30.4



Analyst	z-score	Analyst	z-score	Analyst	z-score	Analyst	z-score
k	-2.024	**n**	-0.455	**c**	0.369	**b**	0.918
q	-1.985	**t**	-0.259	**e**	0.526	**i**	0.918
w	-1.593	**v**	0.133	**f**	0.526	**j**	0.918
p	-1.200	**r**	0.251	**l**	0.526	**o**	0.918
a	-0.651	**h**	0.330	**g**	0.722	**m**	1.114