

Summary of Results

External Quality Assessment of Water Microbiology

Recreational and Surface Water Scheme

Distribution Number: S109 Sample Numbers: S109A, S109B

Distribution Date:	January 2023
Results Due:	10 February 2023
Report Date:	21 February 2023
Samples prepared and quality control tested by:	Divya George Nafeesa Hussain Cansev Katar Margaret Njenga Zak Prior Jake Videlefsky
Data analysed by:	Joanna Donn Nita patel
Report compiled by:	Joanna Donn Nita Patel
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For further information on the scheme please refer to:

Scheme Guide: https://www.gov.uk/government/publications/food-and-water-proficiency-testing-schemes-scheme-guide

Guide to Scoring and Statistics:

https://www.gov.uk/government/publications/food-and-water-proficiency-testing-schemes-scoring-systems-and-statistics

General guidance for z-scores:

Participants' enumeration results are converted into z-scores using the following formula:

 x_i = participants' result expressed (expressed as a log 10 value)

 $Z = (x_i - X_{pt})$ X_{pt} = assigned value (participants' consensus median (expressed as a log 10 value) σ_{pt} = the fixed standard deviation for the examination (calculated by FEPTU)

The σ_{pt} -value expresses the acceptable difference between the individual participant's result and the participants' consensus median. The σ_{pt} -value used for calculating z-scores for all parameters in the Recreational and Surface Water Scheme is 0.35. A guide to interpreting z-scores follows, although laboratories must interpret their scores in the context of their own laboratory situation.

z = -1.99 to +1.99 satisfactory z = -2 to -2.99 or +2 to +2.99 questionable z = < -3.00 or > +3.00 unsatisfactory

It is usually recommended that z-scores exceeding +/-2 are investigated to establish the possible cause. As a general rule, UKHSA recommends that all questionable and unsatisfactory results are investigated.

FEPTU Quality Control: To demonstrate homogeneity of the sample, a minimum of 10 LENTICULE® discs, selected randomly from a batch, are tested in duplicate for parameters requiring enumeration.

To demonstrate stability of the sample, a minimum of six LENTICULE discs, selected randomly from a batch, are examined throughout the distribution period for enumeration parameters.

UKHSA uses methods stipulated in the Microbiology of Recreational and Environmental Waters (2000) and the DWI's series of documents: The Microbiology of Drinking Water (2002) - Methods for the Examination of Waters and Associated Materials.

The FEPTU results are used for guidance in the preliminary intended results notification, letters are posted on the website immediately after every distribution; electronic notification of their availability is sent to all participants.

Refer to section 17.0 of the Scheme Guide if you have experienced difficulties with any of the examinations .

https://www.gov.uk/government/publications/food-and-water-proficiency-testing-schemes-scheme-guide

Participants are reminded that reporting an incorrect or false negative results for water samples could have serious public health implications.

Please contact FEPTU staff for advice and information:

Repeat samples Carmen Gomes or Kermin Daruwalla Tel: +44 (0)20 8327 7119

Data Analysis Nita Patel Fax:

Microbiological advice Nita Patel or Zak Prior Email: foodeqa@ukhsa.gov.uk

General comments and complaints Nita Patel or Zak Prior FEPTU's website

Scheme consultants Stephen Bullock

Scheme Co-ordinator Nita Patel

Accreditation: UKHSA Water EQA Scheme for Recreational and Surface Water is accredited by the United Kingdom Accreditation Service (UKAS) to ISO/IEC 17043:2010.



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Sample: S109A

Swimming pool waters

Contents: Staphylococcus aureus (17) (wild strain), Enterobacter cloacae (12) (wild strain), Escherichia coli (10) (wild strain),

Enterococcus faecalis (52) (wild strain), Pseudomonas aeruginosa (26) (wild strain), Staphylococcus sciuri (29) (wild strain),

Micrococcus sp. (29 per mL) (wild strain) - all levels are per 100mL unless otherwise stated

Expected Results:

All counts are expressed as colony forming units (cfu) per 100mL except the colony count at 37°C/24h which is cfu per mL.

The fixed standard deviation value (*Opt* value) used for calculation of the z-scores is **0.35** for all parameters.

Parameter	Coagulase positive staphylococci	Coliform bacteria	Escherichia coli	Enterococci	Pseudomonas aeruginosa	Total staphylococci	Colony Count 37°C/24 h
FEPTU median	17	22	11	52	26	45	29
No. results returned	39	78	82	70	79	26	76
Assigned value (Participants median all	17	28	14	49	20	46	39
Uncertainty of assigned value*	0.04	0.02	0.02	0.01	0.02	0.03	0.02
Participants mean (all results)	17	27	14	48	20	45	38
Expected Range	5 - 54	9 - 87	4 - 44	15 - 155	6 - 63	15 - 145	12 - 123
Standard deviation**	0.25	0.15	0.18	0.09	0.16	0.12	0.11
No of outlying counts	2	1	2	0	6	2	3
False positives	N/A	N/A	N/A	N/A	N/A	N/A	N/A
False negatives	1	1	2	0	3	0	0
Your result							
Score for performance assessment							
Z-score							

^{*} U(Xpt) is based on results transformed to a log10 scale

^{**} Robust \mathcal{S}^* based on median absolute deviation about the participants' median (MADe)

Total sent samples	87
Not examined	2
Non returns	2
Late returns	0

Sample: S109B

Swimming pool waters

Contents: Escherichia coli (17) (wild strain), Enterococcus faecium (35) (wild strain), Pseudomonas aeruginosa (17) (wild strain),

Staphylococcus saprophyticus (18) (NCTC 7292), Leuconostoc mesenteroides (19 per mL) (wild strain) - all levels are per

100mL unless otherwise stated

Expected Results:

All counts are expressed as colony forming units (cfu) per 100mL except the colony count at 37°C/24h which is cfu per mL.

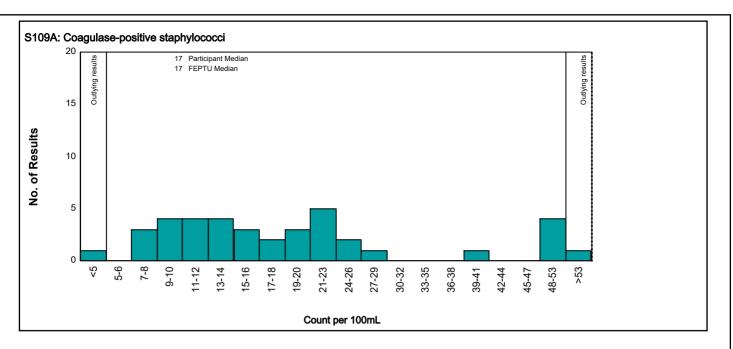
The fixed standard deviation value (*Opt* value) used for calculation of the z-scores is **0.35** for all parameters.

Parameter	Coagulase positive staphylococci	Coliform bacteria	Escherichia coli	Enterococci	Pseudomonas aeruginosa	Total staphylococci	Colony Count 37°C/24 h
FEPTU median	0	17	17	35	17	18	19
No. results returned	38	78	82	70	80	27	76
Assigned value (Participants median all	0	29	28	32	19	21	40
Uncertainty of assigned value*	N/A	0.03	0.03	0.01	0.02	0.05	0.03
Participants mean (all results)	0	29	28	32	19	21	35
Expected Range	N/A	9 - 92	9 - 89	10 - 100	6 - 60	1 - 66	1 - 126
Standard deviation**	N/A	0.17	0.17	0.08	0.17	0.22	0.25
No of outlying counts	N/A	3	2	2	4	0	6
False positives	2	N/A	N/A	N/A	N/A	N/A	N/A
False negatives	N/A	1	0	1	0	6	6
Your result							
Score for performance assessment							
Z-score							

^{*} $U(X_{pt})$ is based on results transformed to a log_{10} scale

^{**} Robust \mathcal{S}^{\star} based on median absolute deviation about the participants' median (MADe)

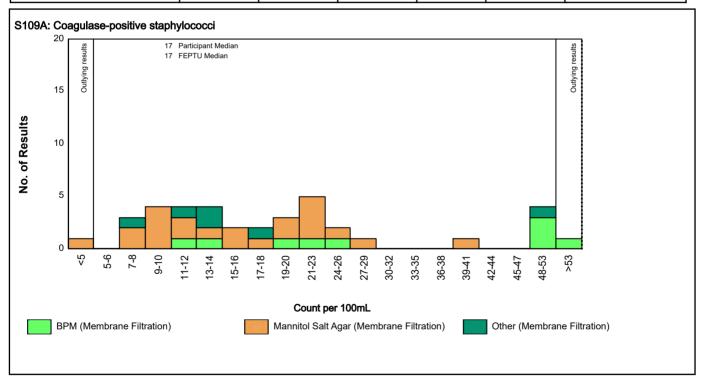
Total sent samples	87
Not examined	2
Non returns	2
Late returns	0

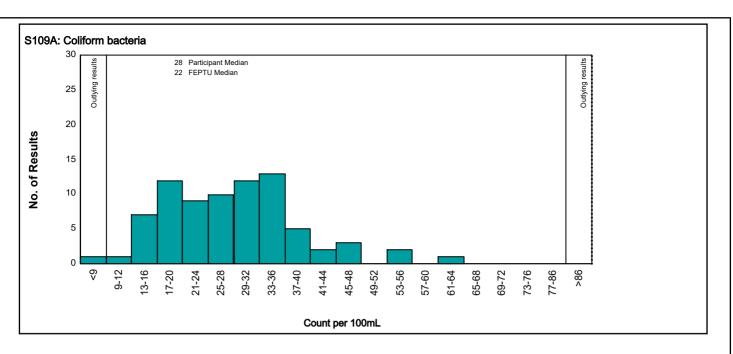


S109A: Coagulase-positive staphylococci

FEPTU Method: BPM

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reporte	ŧd
ВРМ	10	0	26	37	0.32	11 - 9	1
Mannitol Salt Agar	22	0	57	15	0.21	0 - 4	0
Other (Membrane filtration)	6	0	15			-	

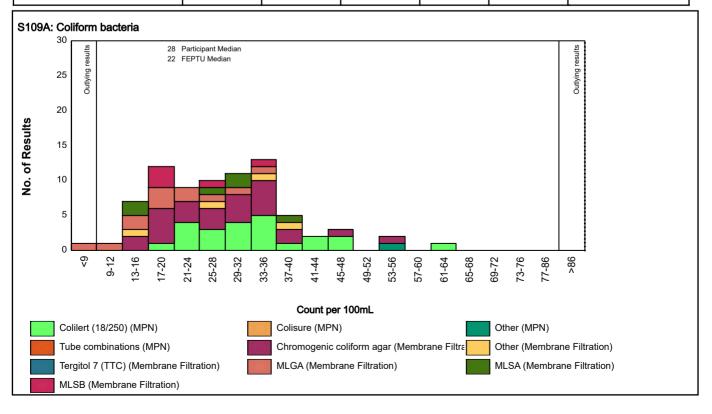


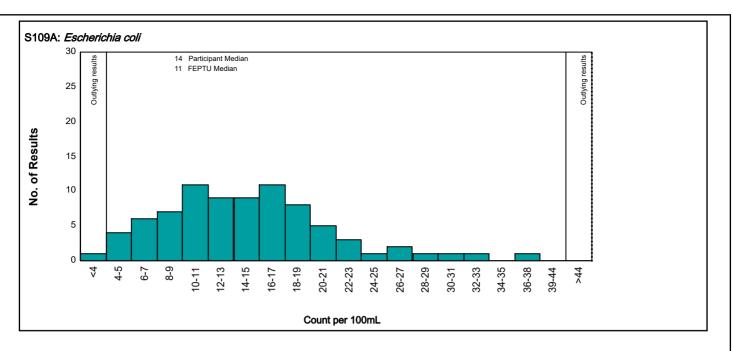


S109A: Coliform bacteria

FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reporte
Colilert (18/250)	23	0	29	32	0.12	20 - 62
Colisure	0	0	0			-
Other (MPN)	1	0	1			-
Tube combinations	0	0	0			-
Chromogenic coliform agar	26	0	33	28	0.15	13 - 54
Other (Membrane filtration)	4	0	5			-
Tergitol 7 (TTC)	0	0	0			-
MLGA	12	0	15	18	0.18	0 - 33
MLSA	6	0	7			-
MLSB	5	0	6			-

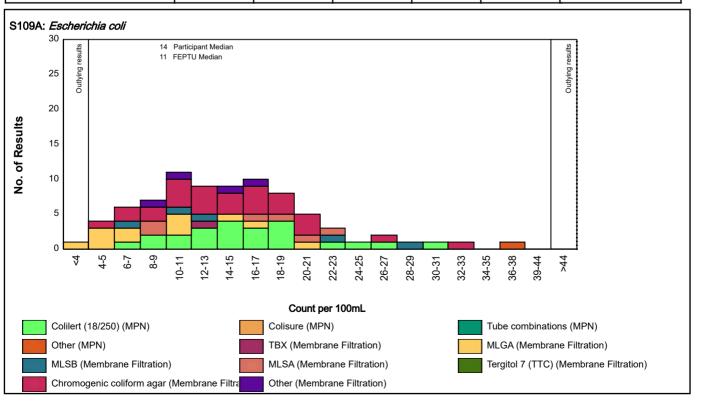


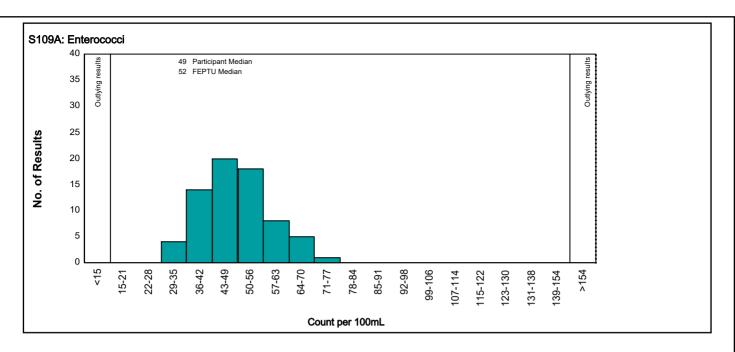


S109A: Escherichia coli

FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Repo	orted
Colilert (18/250)	23	0	28	15	0.15	7 -	31
Colisure	0	0	0			-	
Tube combinations	0	0	0			-	
Other (MPN)	1	0	1			-	
TBX	1	0	1			-	
MLGA	12	1	15	8	0.26	0 -	20
MLSB	5	0	6			-	
MLSA	6	0	7			-	
Tergitol 7 (TTC)	0	0	0			-	
Chromogenic coliform agar	28	0	35	14	0.17	4 -	33
Other (Membrane filtration)	4	0	5			-	

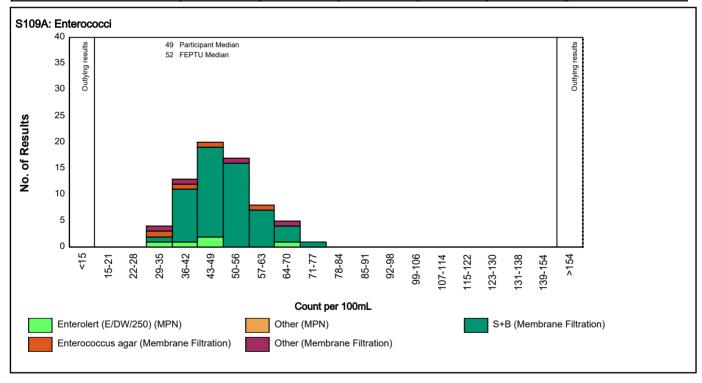


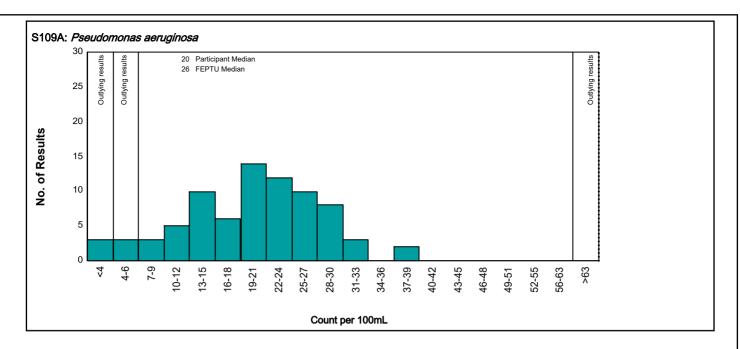


S109A: Enterococci

FEPTU Method: S+B

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
Enterolert (E/DW/250)	5	0	7			-
Other (MPN)	0	0	0			-
S+B	55	1	80	49	0.08	34 - 71
Enterococcus agar	4	0	5			-
Other (Membrane filtration)	4	0	5			-

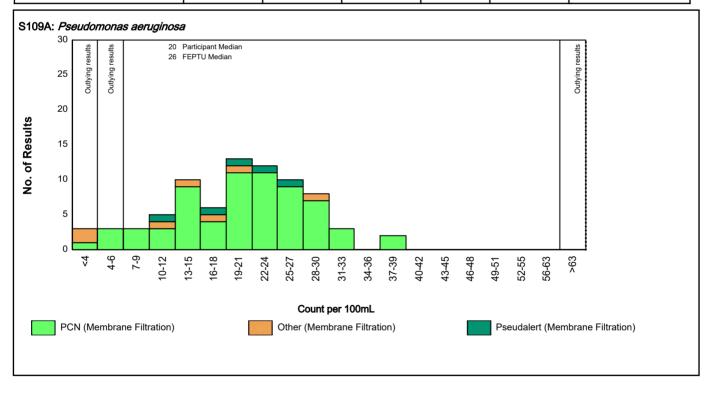


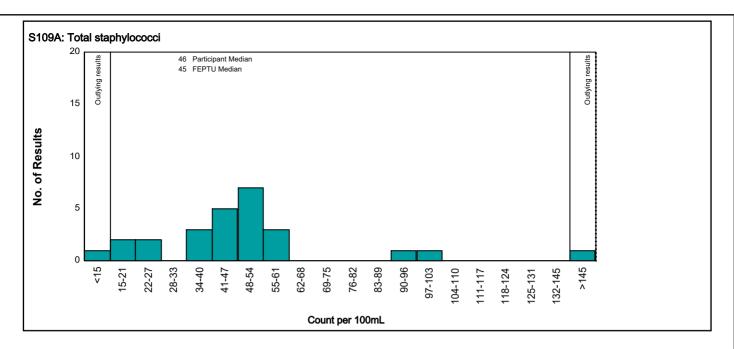


S109A: Pseudomonas aeruginosa

FEPTU Method: PCN

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
PCN	66	0	84	21	0.16	0 - 38
Other (Membrane filtration)	7	0	8			-
Pseudalert	5	0	6			-

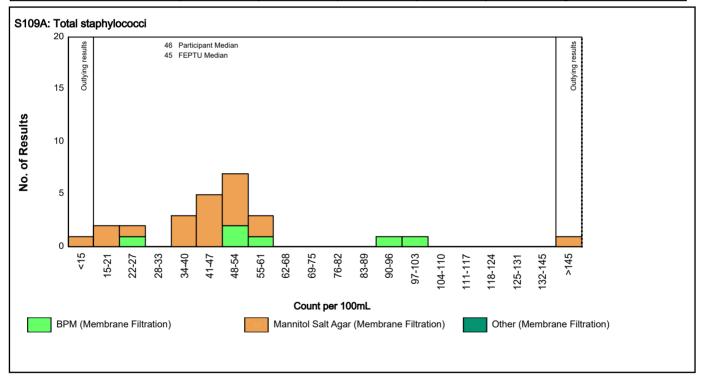


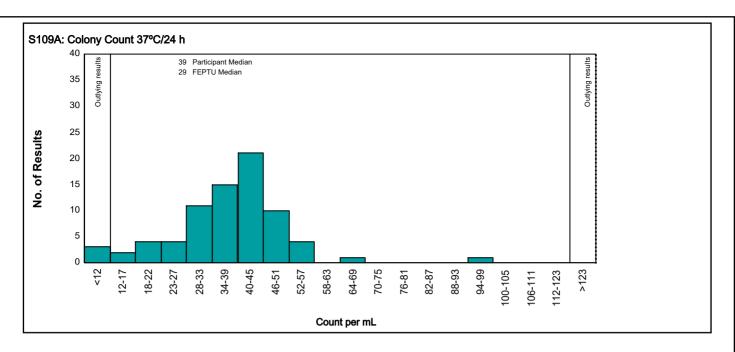


S109A: Total staphylococci

FEPTU Method: BPM

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
BPM	6	0	23			-
Mannitol Salt Agar	20	0	76	42	0.12	8 - 146
Other (Membrane filtration)	0	0	0			-

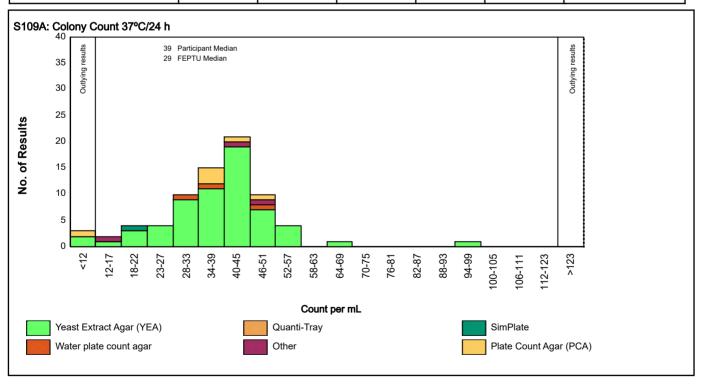




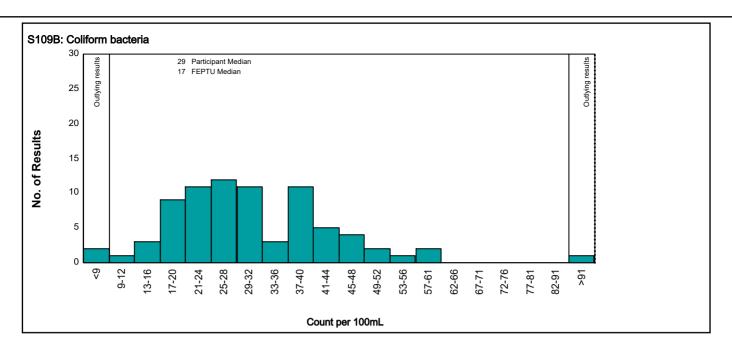
S109A: Colony Count 37°C/24 h

FEPTU Method: Yeast Extract Agar (YEA)

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
Yeast Extract Agar (YEA)	62	0	82	40	0.10	4 - 99
Quanti-Tray	0	0	0			-
SimPlate	1	0	1			-
Water plate count agar	3	0	4			-
Other	3	0	4			-
Plate Count Agar (PCA)	6	0	8			-



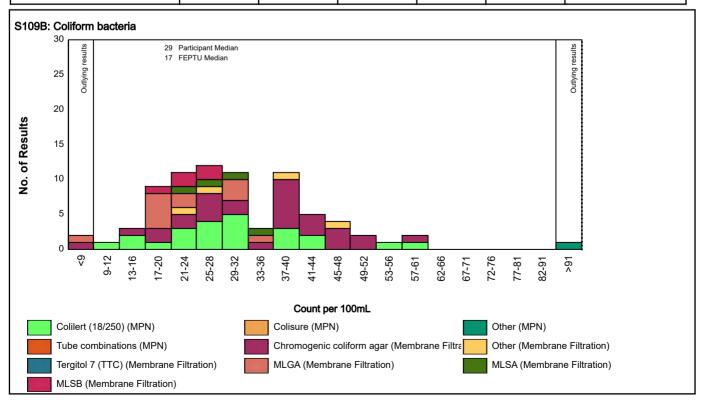
	rlococci							
		No data	a for graph					
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Method based presentation S109B: Coagulase-positive staphylococci FEPTU Method: BPM								
Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range	e Rep	orted
BPM	10	0	27	0	0.00	0	-	62
Mannitol Salt Agar	22	0	59	0	0.00	0	-	0
Other (Membrane filtration)	5	1	13				-	
109B: Coagulase-positive staph	•							
S109B: Coagulase-positive staph		No dat	a for graph					

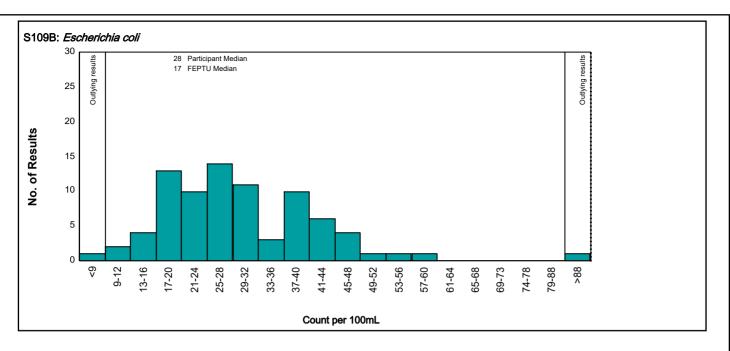


S109B: Coliform bacteria

FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Repor	ted
Colilert (18/250)	23	0	29	29	0.17	12 -	59
Colisure	0	0	0			-	
Other (MPN)	1	0	1			-	
Tube combinations	0	0	0			-	
Chromogenic coliform agar	29	0	37	37	0.14	0 -	61
Other (Membrane filtration)	4	0	5			-	
Tergitol 7 (TTC)	0	0	0			-	
MLGA	12	0	15	21	0.12	8 -	33
MLSA	4	0	5			-	
MLSB	5	0	6			-	



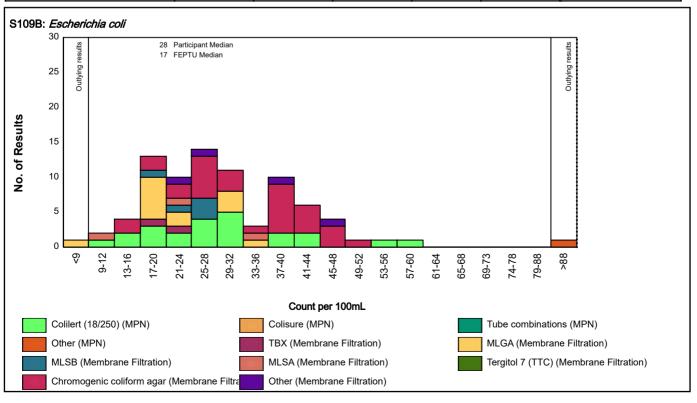


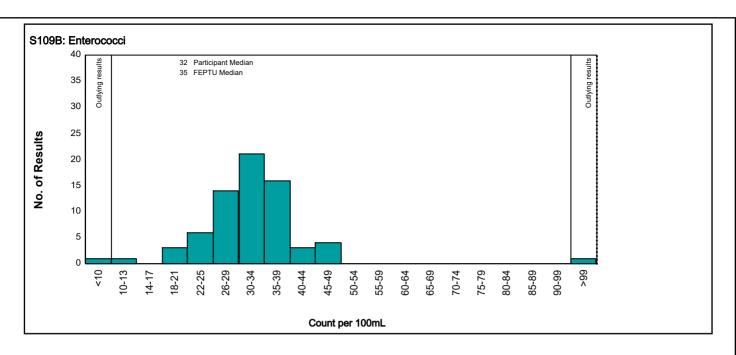
S109B: Escherichia coli

FEPTU Method: Chromogenic coliform

agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Repor	rted
Colilert (18/250)	23	0	28	28	0.17	12 -	59
Colisure	0	0	0			-	
Tube combinations	0	0	0			-	
Other (MPN)	1	0	1			-	
TBX	2	0	2			-	
MLGA	13	0	15	20	0.08	8 -	33
MLSB	5	0	6			-	
MLSA	3	0	3			-	
Tergitol 7 (TTC)	0	0	0			-	
Chromogenic coliform agar	31	0	37	34	0.14	14 -	52
Other (Membrane filtration)	4	0	4			-	

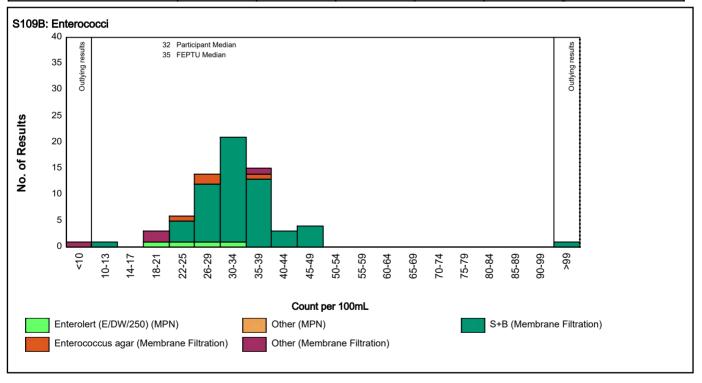


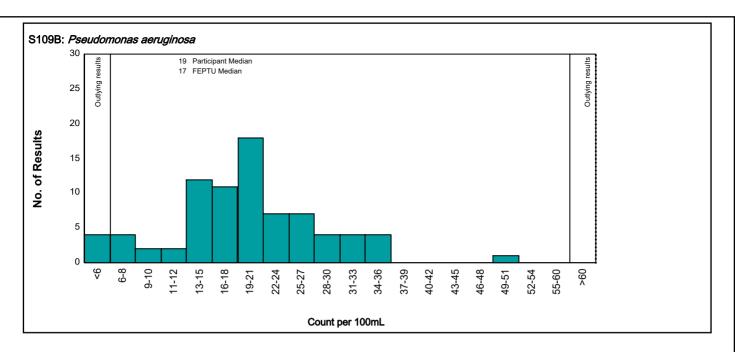


S109B : Enterococci

FEPTU Method: S+B

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
Enterolert (E/DW/250)	4	0	5			-
Other (MPN)	0	0	0			-
S+B	57	1	82	32	0.07	12 - 169
Enterococcus agar	4	0	5			-
Other (Membrane filtration)	4	0	5			-

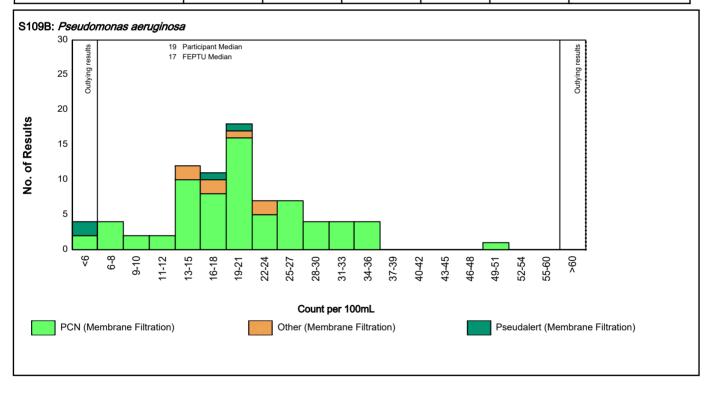


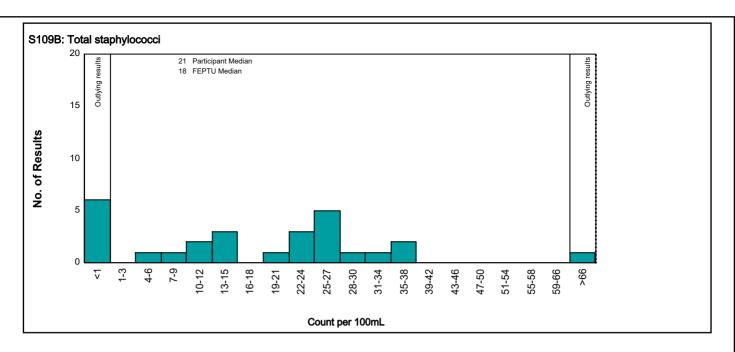


S109B: Pseudomonas aeruginosa

FEPTU Method: PCN

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
PCN	69	0	86	20	0.17	3 - 50
Other (Membrane filtration)	7	0	8			-
Pseudalert	4	0	5			-

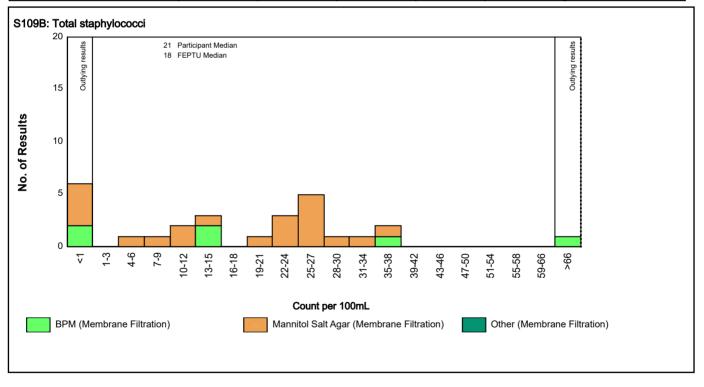


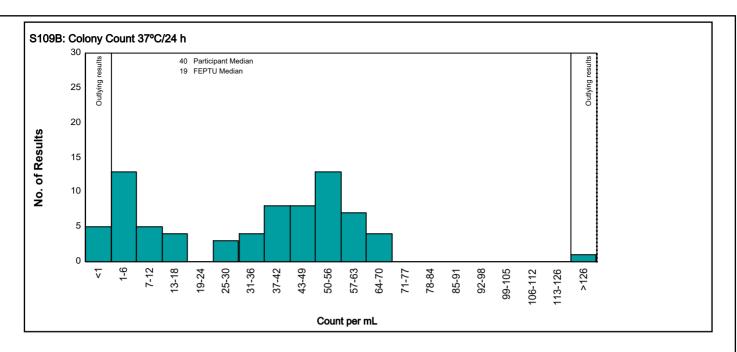


S109B: Total staphylococci

FEPTU Method: BPM

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
BPM	6	0	22			-
Mannitol Salt Agar	21	0	77	22	0.13	0 - 35
Other (Membrane filtration)	0	0	0			-

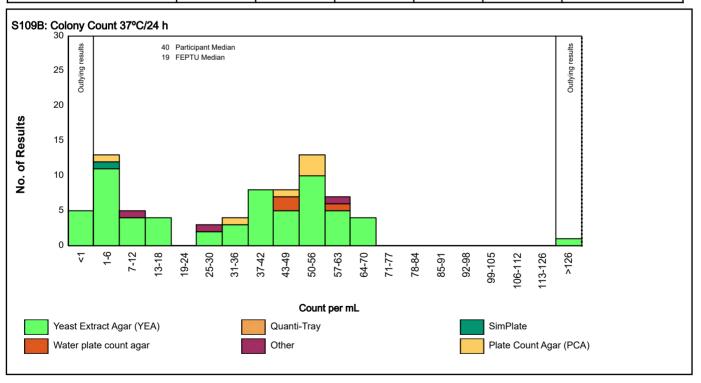




S109B: Colony Count 37°C/24 h

FEPTU Method: Yeast Extract Agar (YEA)

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log ₁₀)	Range Reported
Yeast Extract Agar (YEA)	62	1	82	40	0.28	0 - 2410
Quanti-Tray	0	0	0			-
SimPlate	1	0	1			-
Water plate count agar	3	0	4			-
Other	3	0	4			-
Plate Count Agar (PCA)	6	0	8			-



Sample specific comment

S109B: Total staphylococci

6(27) (22%) of the laboratories reported a false negative result for this examination. This sample contained a *Staphylococcus saprophyticus* and the participants' median was 21 colony forming units per 100mL.

In the FEPTU laboratory the following growth patterns was observed following incubation at 37°C for 48 hours:

Media	Colony description	Comment
Baird Parker media (BPM)	Pinprick round black colonies	Counts observed were lower compared to MSA and RPF media
Mannitol Salt agar (MSA)	1mm round yellow colonies	
Rabbit plasma fibrinogen (RPF)	1mm round grey colonies (no halo)	

A breakdown of the results by media used is shown in the table below:

Media	Range of counts reported per 100mL (number of laboratories)
ВРМ	0 (2) 14 - 100 (4)
MSA	0 (4) 4 – 35 (17)

This examination has not been scored due to the low performance achieved by laboratories. Laboratories reporting an incorrect result are encouraged to request a repeat sample from FEPTU for their own internal investigation.

S109B: Colony count 37°C/24 h

A Kolmogorov–Smirnov (KS) test showed that the data was not evenly distributed for this examination. Therefore, those laboratories reporting a count outside the low end of the expected range have been awarded a score of 2.

General comments

Method based presentation of enumeration results:

Participants are advised if less than 10 laboratories report a result for a method, no data is shown for the Median, Robust SD and the Range Reported in the 'Method based presentation' tables.

Numbers shown in the 'Excluded Results' column are laboratories that reported a censored value.

If you do not return a result for a distribution, you will not be able to view all the participants' results data in your individualised report. Please contact us if you require this information on footeqa@ukhsa.gov.uk.

End of report.

