Public Health England

Protecting and improving the nation's health

Summary of Results

External Quality Assessment of Water Microbiology

Recreational and Surface Water Scheme

Distribution Number: S87   **Sample Numbers: S87A, S87B**

Distribution Date:	**November 2018**
Results Due:	**07 December 2018**
Report Date:	**18 December 2018**
Samples prepared and quality control tested by:	**Angela Appea** **Richard Borrill** **Thomas Harper** **Margaret Njenga** **Zak Prior** **Lili Tsegaye** **Vanessa Waite**
Data analysed by:	**Joanna Donn** **Manchari Rajkumar**
Report compiled by:	**Joanna Donn** **Manchari Rajkumar**
Authorised by:	**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:

$$Z = \frac{(x_i - X_{pt})}{\sigma_{pt}}$$

x_i = participants' result expressed (expressed as a log $_{10}$ value)

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, PHE 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.

PHE 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	Manchari Rajkumar or Nita Patel	**Fax:**	**+44 (0)20 8200 8264**
Microbiological advice	Nita Patel or Zak Prior	**Email:**	**foodeqa@phe.gov.uk**
General comments and complaints	Nita Patel or Zak Prior	FEPTU's website	
Scheme consultants	Julie E. Russell		
Scheme Co-ordinator	Nita Patel		

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

UKAS
PROFICIENCY TESTING

0006

Sample: S87A

Water sample from river, lake and stream

Contents: *Klebsiella pneumoniae* (wild strain), *Enterococcus faecalis* (wild strain), *Clostridium perfringens* (wild strain), *Salmonella* Derby 1,4,[5],12:f,g:[1,2] (wild strain), *Serratia liquefaciens* (wild strain)

Expected Results:

All counts are expressed as colony forming units (cfu) per 100mL.

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

Parameter	Coliform bacteria	*Escherichia coli*	Enterococci	Faecal coliforms	*Clostridium perfringens*	*Salmonella* spp.
FEPTU median	1.22×10^2 (2.09 $\log_{10}$)	0	56	140	1.09×10^2 (2.04 $\log_{10}$)	Detected in 1L
No. results returned	76	83	79	42	57	49
Assigned value (Participants median all results)	2.08×10^2 (2.32 $\log_{10}$)	0	54	74	1.20×10^2 (2.08 $\log_{10}$)	N/A
Uncertainty of assigned value*	0.03	N/A	0.01	0.05	0.03	N/A
Participants mean (all results)	1.96×10^2 (2.29 $\log_{10}$)	0	53	78	1.13×10^2 (2.05 $\log_{10}$)	N/A
Expected Range	$66 - 6.56 \times 10^2$	N/A	17 - 171	23 - 232	$38 - 3.?0 \times 10^2$	N/A
Standard deviation**	0.22	N/A	0.08		0.2	N/A
No of outlying counts	3	N/A	1	7	2	N/A
False positives	N/A	3	N/A	N/A	N/A	N/A
False negatives	1	N/A	0	4	0	0
Your result						
Score for performance assessment						
Z-score						

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

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

Total sent samples	91
Not examined	4
Non returns	1
Late returns	0

Sample: S87B

Water sample from river, lake and stream

Contents: *Escherichia coli* (wild strain), *Klebsiella pneumoniae* (wild strain), *Enterococcus gallinarum* (NCTC 11428), *Clostridium perfringens* (wild strain), *Leifsonia aquatica* (NCIMB 9460)

Expected Results:

All counts are expressed as colony forming units (cfu) per 100mL.

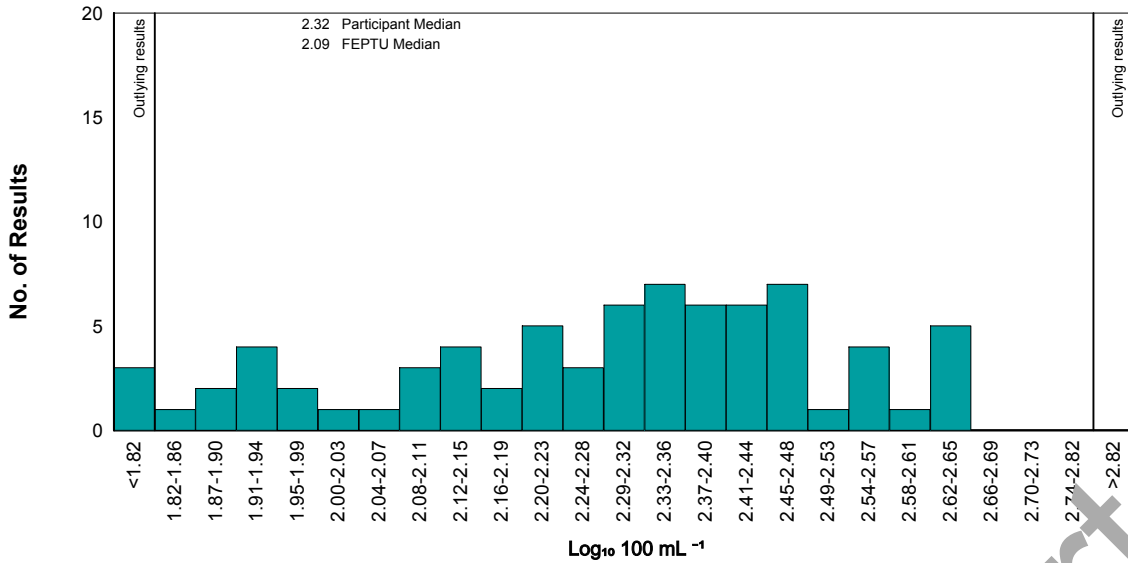The fixed standard deviation value (σpt value) used for calculation of the z-scores is **0.35** for all parameters.

Parameter	Coliform bacteria	*Escherichia coli*	Enterococci	Faecal coliforms	*Clostridium perfringens*	*Salmonella* spp.
FEPTU median	71 (1.85 $\log_{10}$)	47	37	65	90 (1.95 $\log_{10}$)	Not Detected in 1L
No. results returned	75	82	77	41	58	48
Assigned value (Participants median all results)	81 (1.91 $\log_{10}$)	53	42	55	1.02×10^2 (2.01 $\log_{10}$)	N/A
Uncertainty of assigned value*	0.03	0.03	0.03	0.04	0.02	N/A
Participants mean (all results)	83 (1.92 $\log_{10}$)	52	46	55	1.04×10^2 (2.02 $\log$)	N/A
Expected Range	$26 - 2.56 \times 10^2$	17 - 168	1 - 133	17 - 174	$32 - 3.?\times10^2$	N/A
Standard deviation**	0.2	0.19	0.15		0.15	N/A
No of outlying counts	4	7	0	4	2	N/A
False positives	N/A	N/A	N/A	N/A	N/A	0
False negatives	0	0	24	0	2	N/A
Your result						
Score for performance assessment						
Z-score						

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

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

Total sent samples	91
Not examined	5
Non returns	1
Late returns	0

S87A: Coliform bacteria

Histogram: No. of Results vs Log$_{10}$ 100 mL^{-1}

2.32 Participant Median
2.09 FEPTU Median

Outlying results (left and right)

X-axis categories: <1.82, 1.82-1.86, 1.87-1.90, 1.91-1.94, 1.95-1.99, 2.00-2.03, 2.04-2.07, 2.08-2.11, 2.12-2.15, 2.16-2.19, 2.20-2.23, 2.24-2.28, 2.29-2.32, 2.33-2.36, 2.37-2.40, 2.41-2.44, 2.45-2.48, 2.49-2.53, 2.54-2.57, 2.58-2.61, 2.62-2.65, 2.66-2.69, 2.70-2.73, 2.74-2.82, >2.82
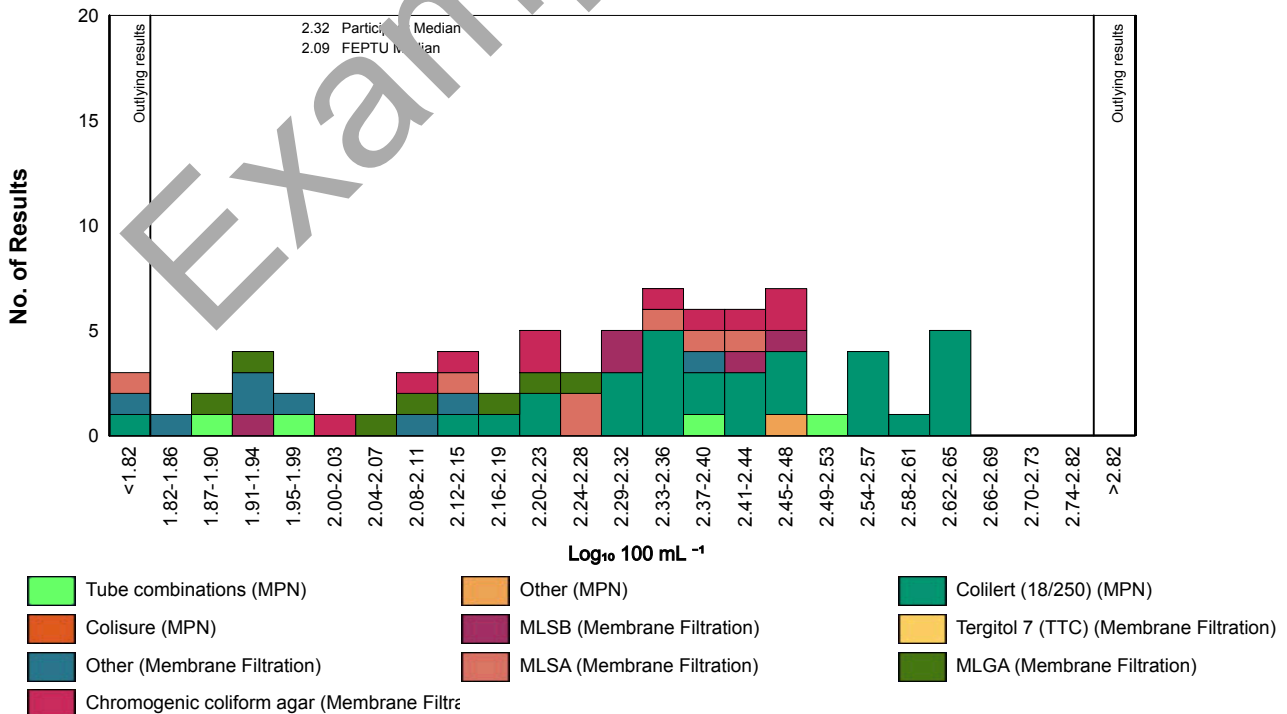
Method based presentation

S87A : Coliform bacteria   FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S^* (Log$_{10}$)	Range Reported	
Tube combinations	4	0	5			-	
Other (MPN)	1	0				-	
Colilert (18/250)	31	1	42	276	0.17	25	- 440
Colisure	0	0				-	
MLSB	5	0	6			-	
Tergitol 7 (TTC)	0	0	0			-	
Other (Membrane filtration)	8	0	10			-	
MLSA	7	0	9			-	
MLGA	7		9			-	
Chromogenic coliform agar	10	1	13	194	0.19	102	- 300

S87A: Coliform bacteria

Stacked histogram: No. of Results vs Log$_{10}$ 100 mL^{-1}

2.32 Participant Median
2.09 FEPTU Median

Outlying results (left and right)

Legend:
- Tube combinations (MPN)
- Other (MPN)
- Colilert (18/250) (MPN)
- Colisure (MPN)
- MLSB (Membrane Filtration)
- Tergitol 7 (TTC) (Membrane Filtration)
- Other (Membrane Filtration)
- MLSA (Membrane Filtration)
- MLGA (Membrane Filtration)
- Chromogenic coliform agar (Membrane Filtra...

S87A: *Escherichia coli*

No data for graph

Method based presentation

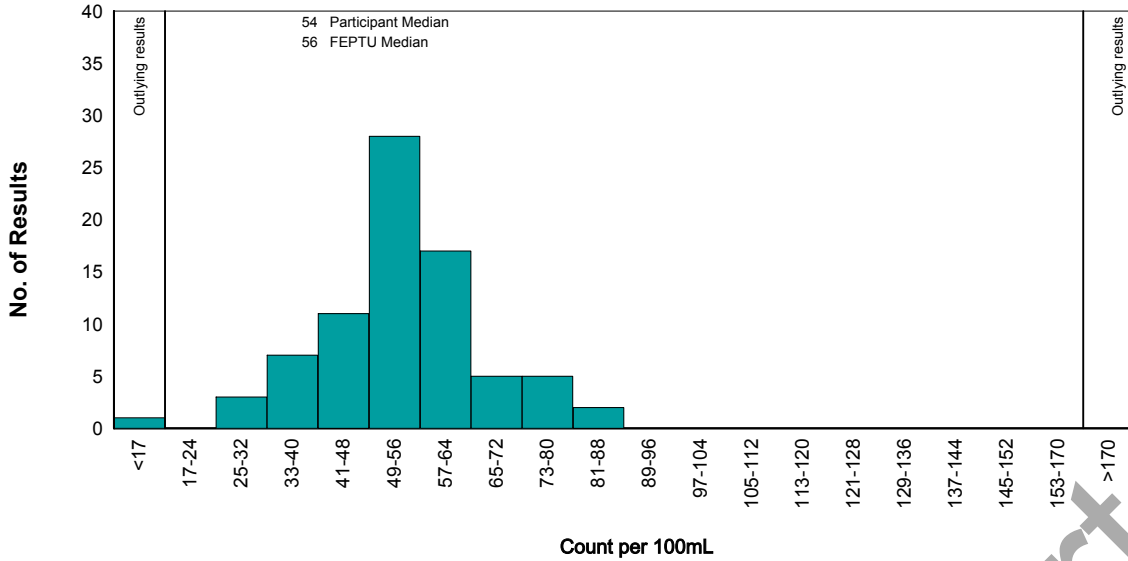S87A : *Escherichia coli*　　　　　　　　　　　　　　　　　FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log₁₀)	Range Reported		
Colilert (18/250)	30	4	43		0.00	0	-	0
Colisure	0	0	0				-	
Tube combinations	2	2	2				-	
Other (MPN)	1	3					-	
TBX	4	0	5				-	
MLGA	7	1	10				-	
MLSB	5	1	7				-	
MLSA	7		10				-	
Tergitol 7 (TTC)	0		0				-	
Chromogenic coliform agar	9	1	13				-	
Other (Membrane filtration)	4		5				-	

S87A: *Escherichia coli*

No data for graph

S87A: Enterococci

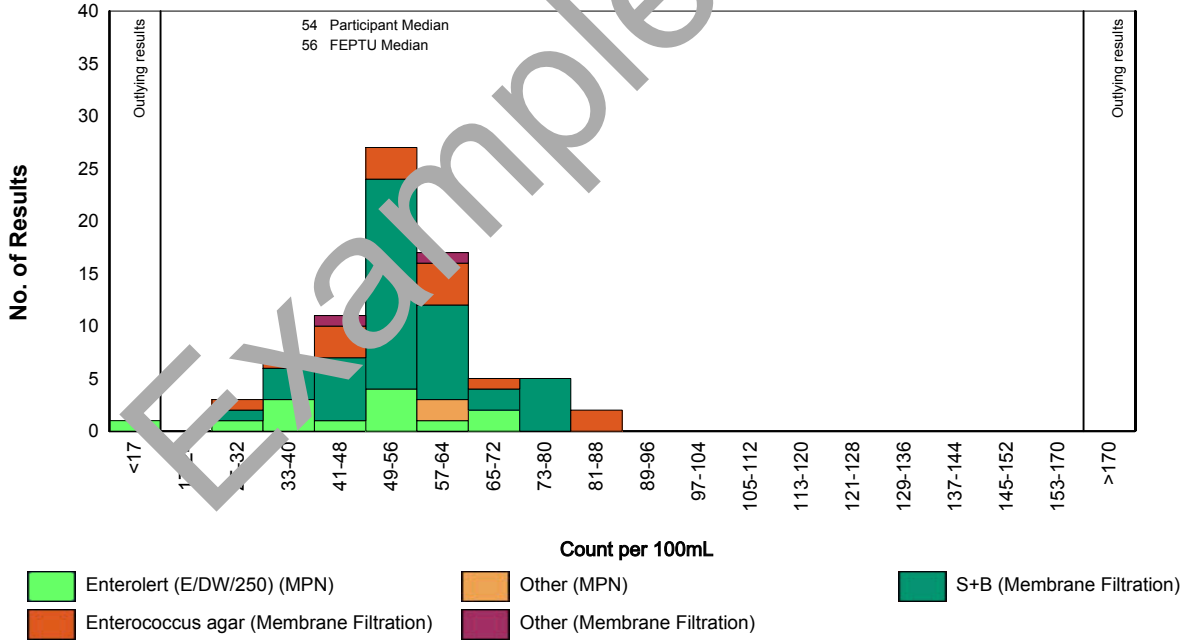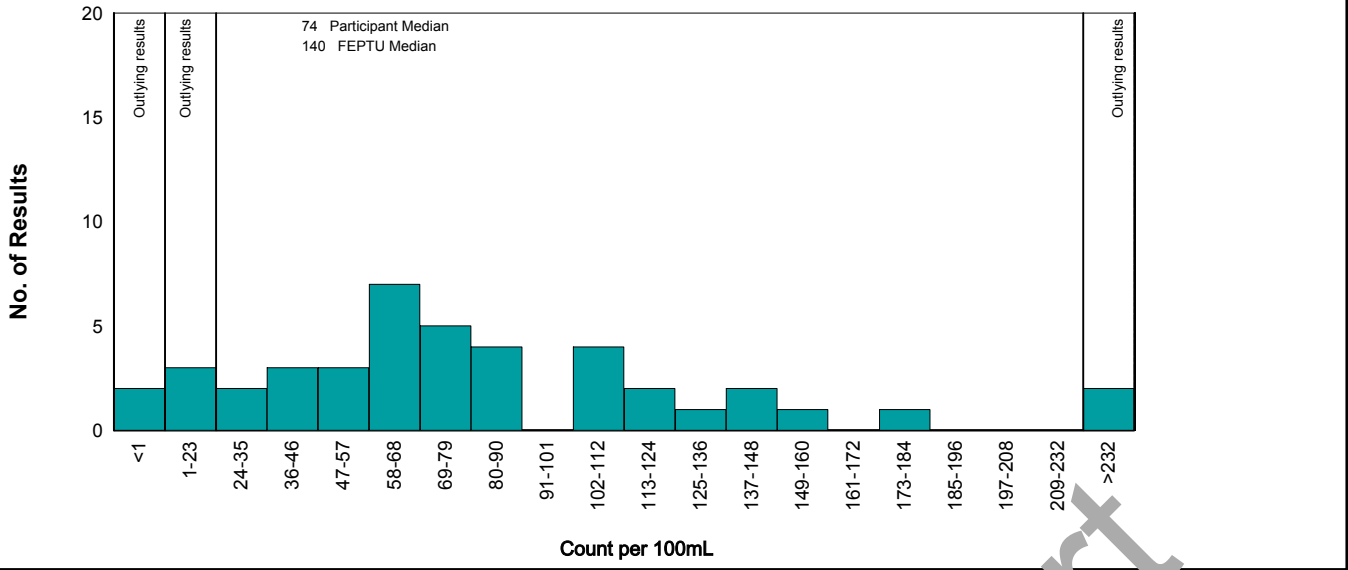## Method based presentation

S87A : Enterococci   FEPTU Method: S+B

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log₁₀)	Range Reported		
Enterolert (E/DW/250)	13	0	16	4	0.15	5	-	72
Other (MPN)	2	0					-	
S+B	46	0	58	54	0.06	30	-	80
Enterococcus agar	15	0		54	0.11	26	-	88
Other (Membrane filtration)	2	0	2				-	

S87A: Enterococci

Enterolert (E/DW/250) (MPN)   Other (MPN)   S+B (Membrane Filtration)

Enterococcus agar (Membrane Filtration)   Other (Membrane Filtration)

S87A: Faecal coliforms
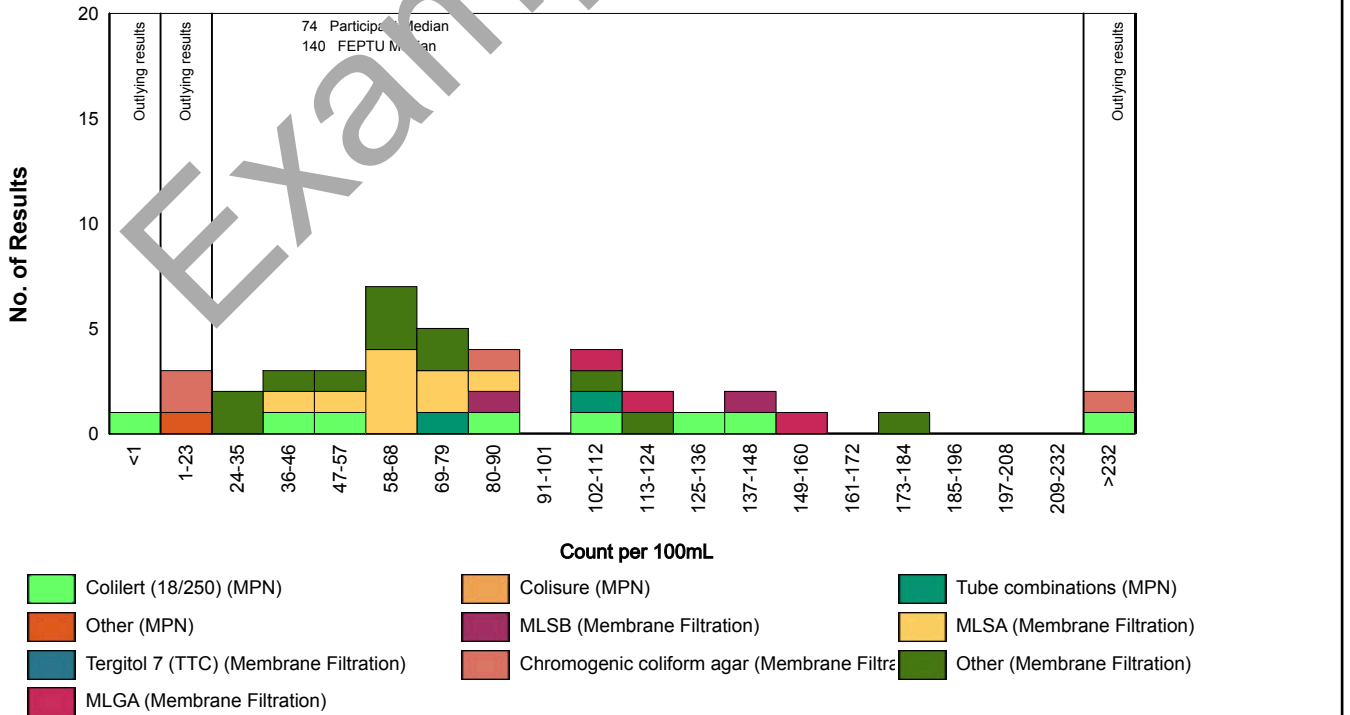

Method based presentation

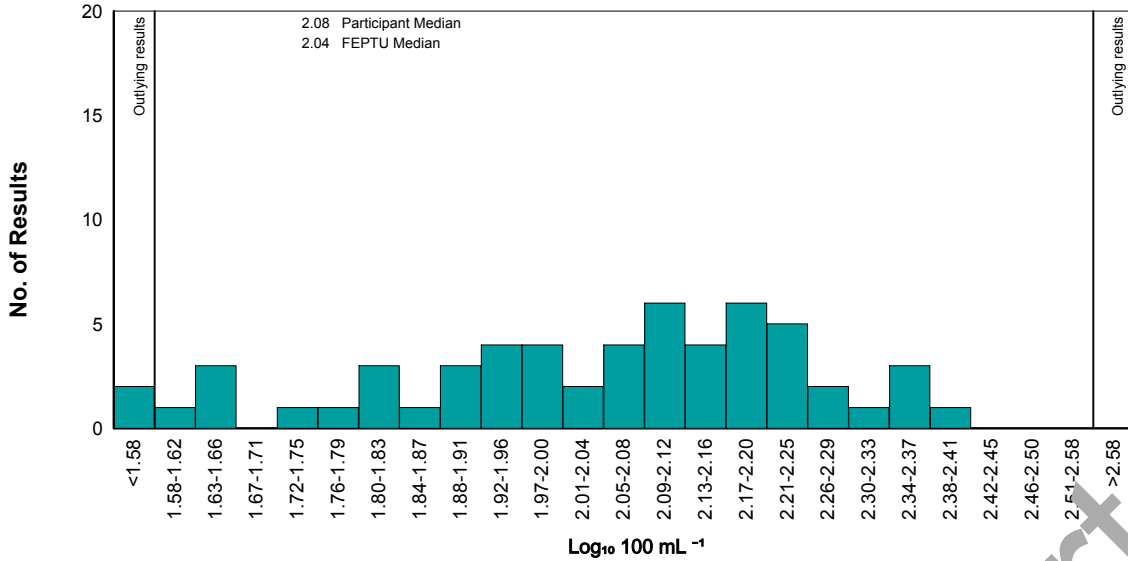S87A : Faecal coliforms   FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log₁₀)	Range Reported		
Colilert (18/250)	8	0	20				-	
Colisure	0	0	0				-	
Tube combinations	2	0	5				-	
Other (MPN)	0	1					-	
MLSB	2	0	5				-	
MLSA	9	0	23				-	
Tergitol 7 (TTC)	0	0	0				-	
Chromogenic coliform agar	3		7				-	
Other (Membrane filtration)	12		30	67	0.27	26	-	180
MLGA	3	0	7				-	

Legend:
- Colilert (18/250) (MPN)
- Colisure (MPN)
- Tube combinations (MPN)
- Other (MPN)
- MLSB (Membrane Filtration)
- MLSA (Membrane Filtration)
- Tergitol 7 (TTC) (Membrane Filtration)
- Chromogenic coliform agar (Membrane Filtra...)
- Other (Membrane Filtration)
- MLGA (Membrane Filtration)

S87A: *Clostridium perfringens*
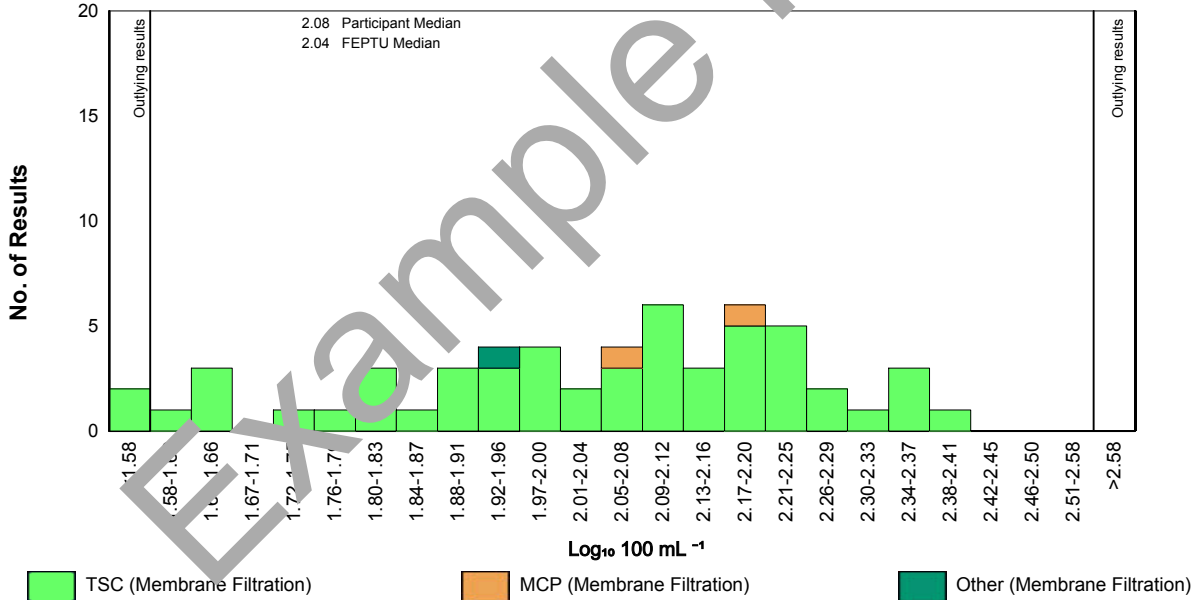

Method based presentation

S87A : *Clostridium perfringens*   FEPTU Method: TSC

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust *S** (Log₁₀)	Range Reported		
TSC	53	1	94	120	0.22	22	-	250
MCP	2	0					-	
Other (Membrane filtration)	1	0	1				-	

S87A: *Clostridium perfringens*

TSC (Membrane Filtration)   MCP (Membrane Filtration)   Other (Membrane Filtration)

Method based presentation

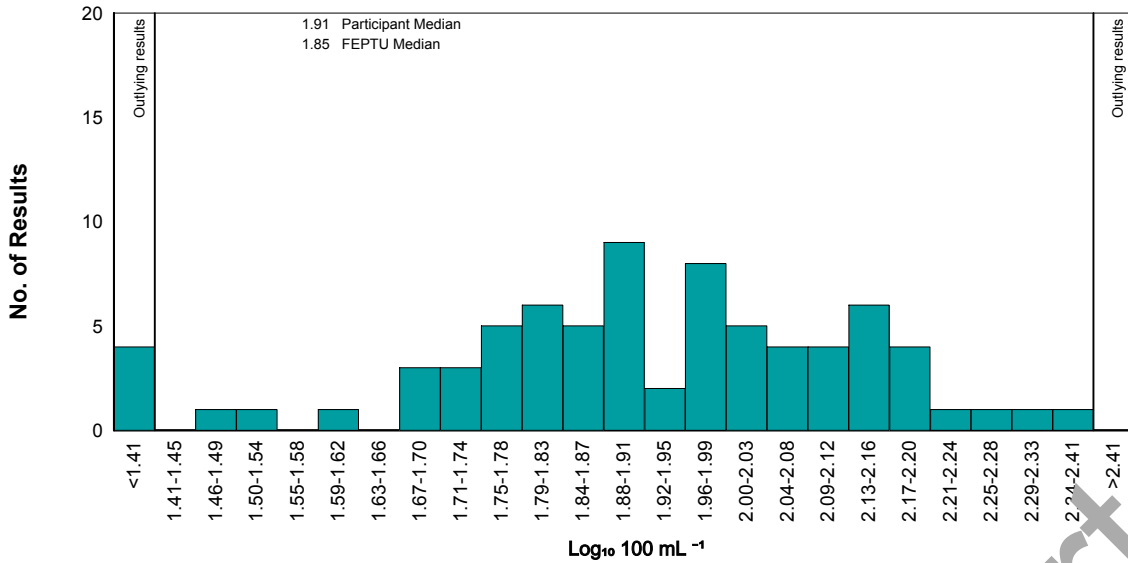S87A : *Salmonella* spp.   FEPTU Method: ISO 19250

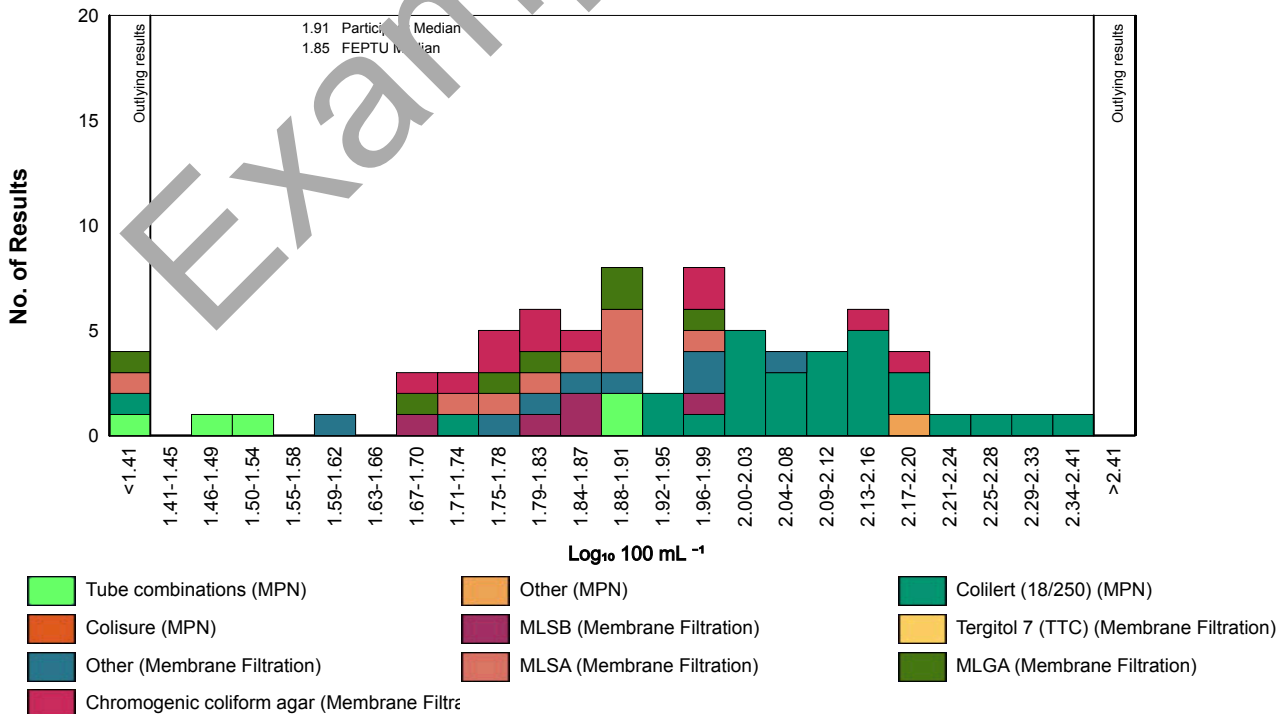| Method	No. Participants Detected	No. Participants Not Detected
VIDAS	0	0
PCR	2	0
Other	0	0
Enrichment XLD	14	0
ISO 19250	25	0
Enrichment BGA	1	0
Other (Membrane filtration)	5	0

S87B: Coliform bacteria
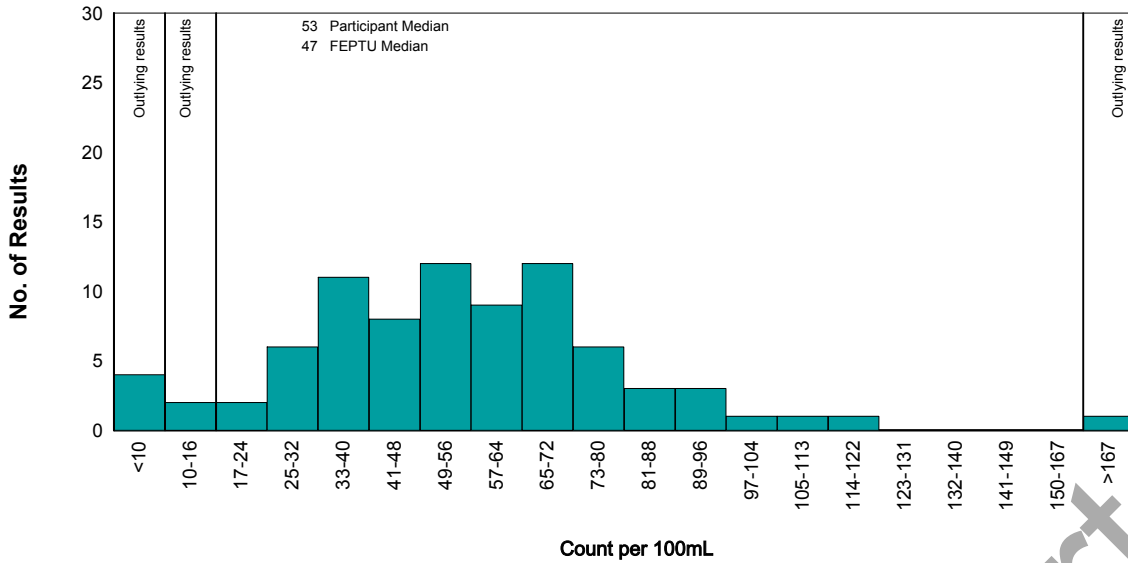
Method based presentation

S87B : Coliform bacteria

FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S^* (Log$_{10}$)	Range Reported		
Colilert (18/250)	28	1	37	130	0.11	10	-	219
Colisure	0	0	0				-	
Tube combinations	5	0	6				-	
Other (MPN)	1	0					-	
Tergitol 7 (TTC)	0	0	0				-	
Other (Membrane filtration)	8	0	10				-	
MLSA	9	0	12				-	
MLGA	7	0	9				-	
Chromogenic coliform agar	11	0	14	67	0.17	46	-	150
MLSB	5	0	6				-	

S87B: Coliform bacteria

- Tube combinations (MPN)
- Other (MPN)
- Colilert (18/250) (MPN)
- Colisure (MPN)
- MLSB (Membrane Filtration)
- Tergitol 7 (TTC) (Membrane Filtration)
- Other (Membrane Filtration)
- MLSA (Membrane Filtration)
- MLGA (Membrane Filtration)
- Chromogenic coliform agar (Membrane Filtra...

S87B: *Escherichia coli*
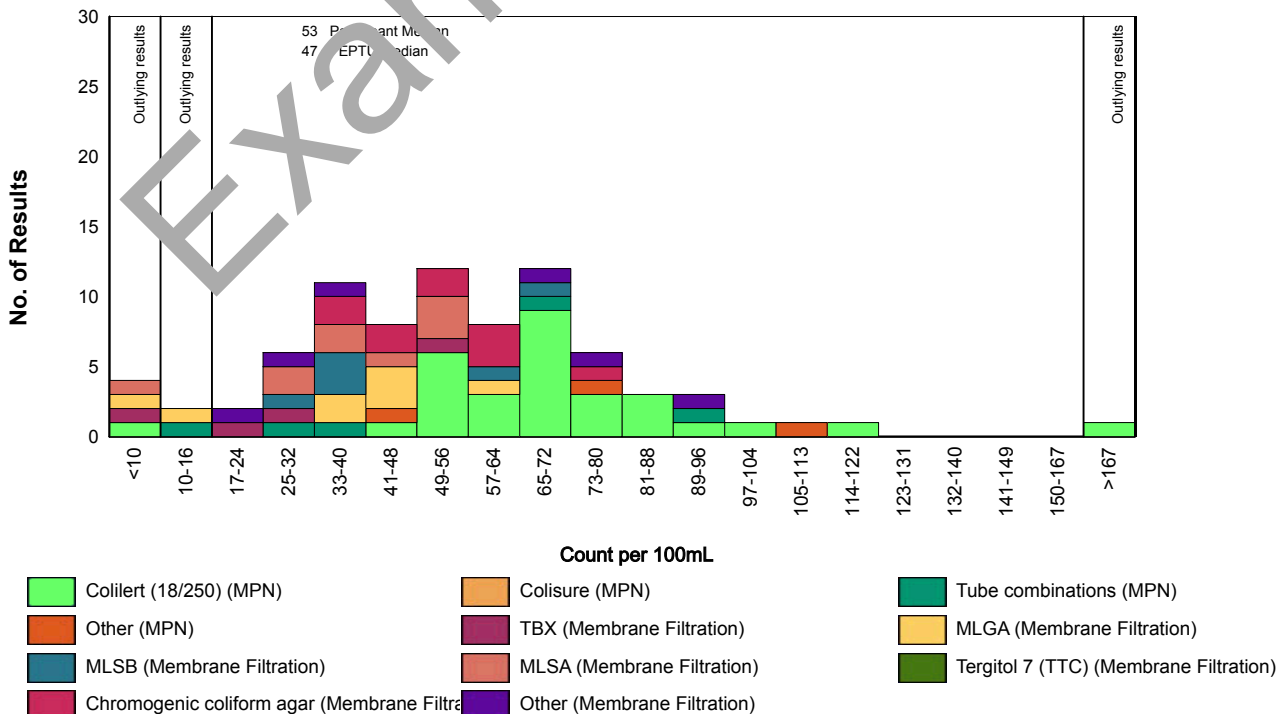

Method based presentation

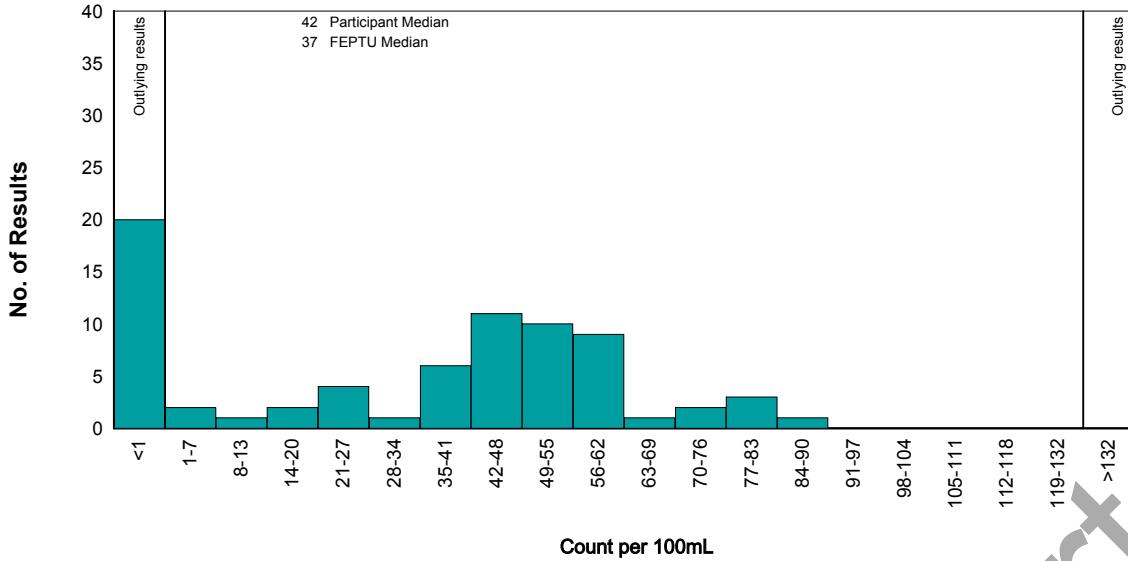S87B : *Escherichia coli*   FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust *S** (Log₁₀)	Range Reported		
Colilert (18/250)	30	1	37	6	0.11	4	-	195
Colisure	0	0	0				-	
Tube combinations	5	0	6				-	
Other (MPN)	3	0					-	
TBX	4	0	4				-	
MLGA	8	0	9				-	
MLSB	6	0	7				-	
MLSA	9	0	11				-	
Tergitol 7 (TTC)	0		0				-	
Chromogenic coliform agar	10	0	12	54	0.10	37	-	80
Other (Membrane filtration)	6		7				-	

S87B: *Escherichia coli*

- Colilert (18/250) (MPN)
- Colisure (MPN)
- Tube combinations (MPN)
- Other (MPN)
- TBX (Membrane Filtration)
- MLGA (Membrane Filtration)
- MLSB (Membrane Filtration)
- MLSA (Membrane Filtration)
- Tergitol 7 (TTC) (Membrane Filtration)
- Chromogenic coliform agar (Membrane Filtra
- Other (Membrane Filtration)

S87B: Enterococci

No. of Results (y-axis, 0–40)
Count per 100mL (x-axis: <1, 1-7, 8-13, 14-20, 21-27, 28-34, 35-41, 42-48, 49-55, 56-62, 63-69, 70-76, 77-83, 84-90, 91-97, 98-104, 105-111, 112-118, 119-132, >132)

42 Participant Median
37 FEPTU Median

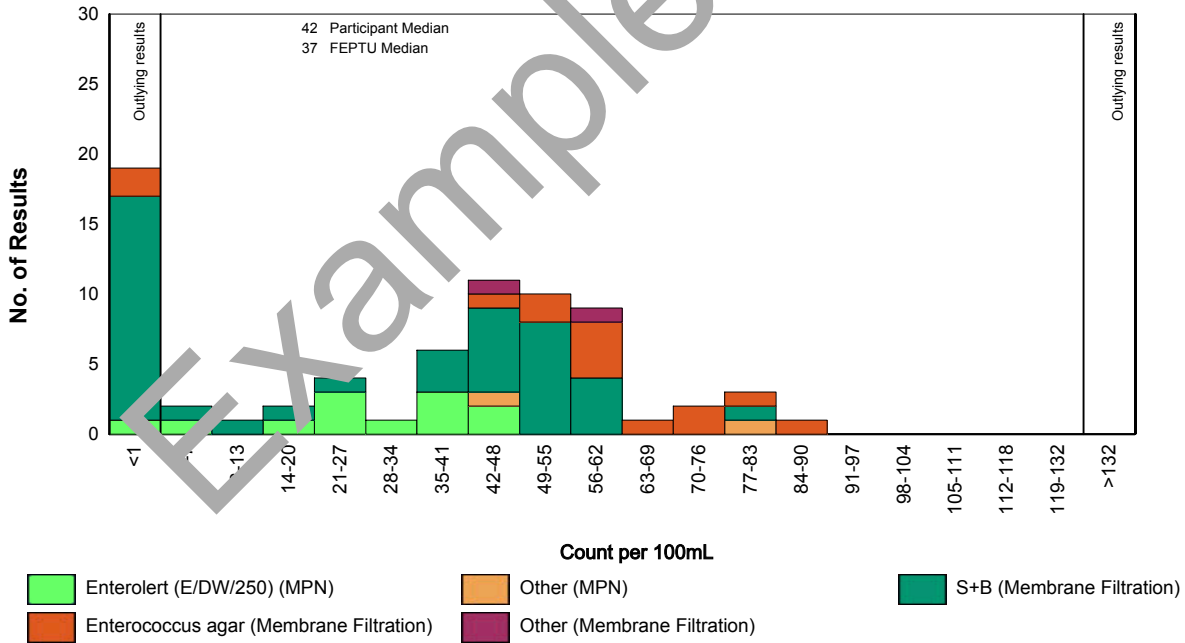Outlying results

Method based presentation

S87B : Enterococci   FEPTU Method: S+B
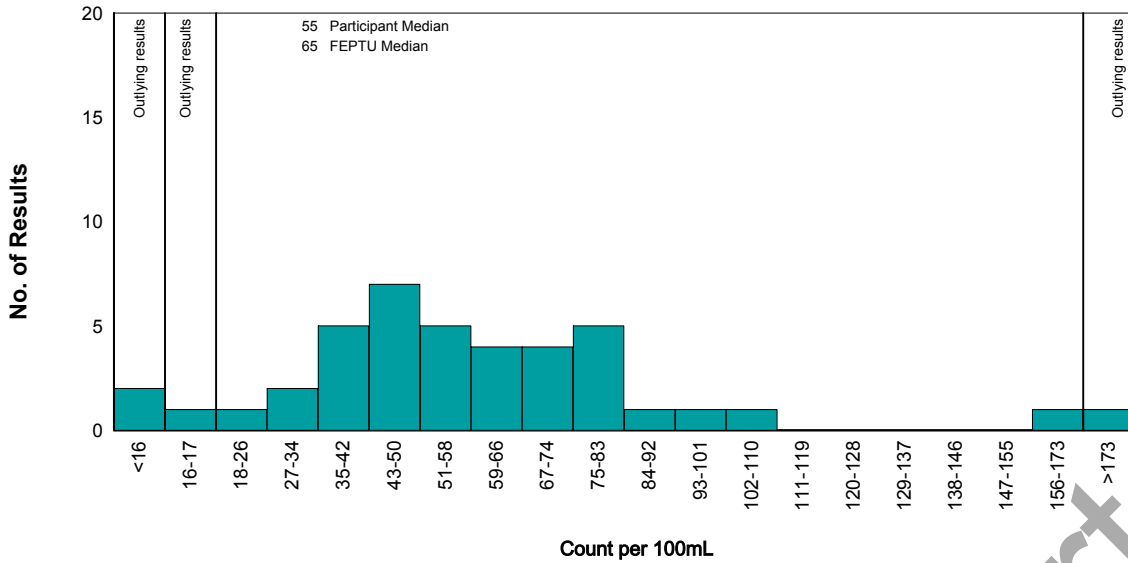
Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust S* (Log₁₀)	Range Reported		
Enterolert (E/DW/250)	12	1	16	2.	0.20	0	-	46
Other (MPN)	2	1					-	
S+B	42	3	58	38	0.10	0	-	79
Enterococcus agar	14	1		59	0.09	0	-	90
Other (Membrane filtration)	2	0	2				-	

S87B: Enterococci

No. of Results (y-axis, 0–30)
Count per 100mL (x-axis: <1, ...13, 14-20, 21-27, 28-34, 35-41, 42-48, 49-55, 56-62, 63-69, 70-76, 77-83, 84-90, 91-97, 98-104, 105-111, 112-118, 119-132, >132)

42 Participant Median
37 FEPTU Median

Outlying results

Legend:
- Enterolert (E/DW/250) (MPN)
- Other (MPN)
- S+B (Membrane Filtration)
- Enterococcus agar (Membrane Filtration)
- Other (Membrane Filtration)

S87B: Faecal coliforms

Histogram: No. of Results vs Count per 100mL. 55 Participant Median, 65 FEPTU Median. Outlying results markers at left (two) and right.
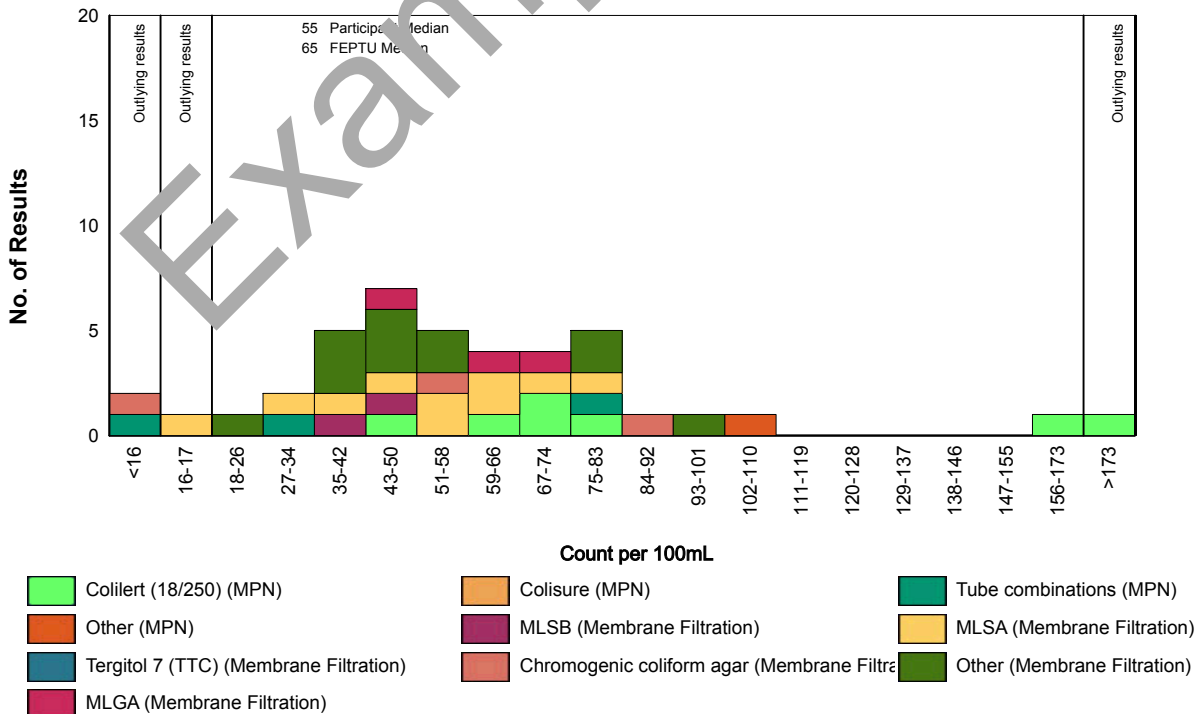
Method based presentation

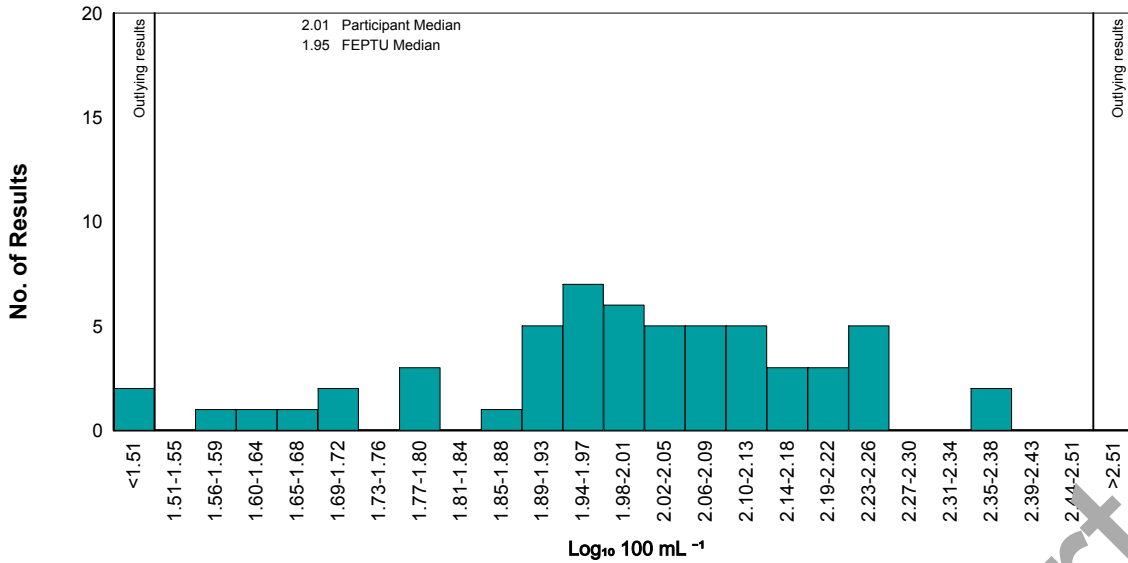S87B : Faecal coliforms   FEPTU Method: Chromogenic coliform agar

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust *S** (Log₁₀)	Range Reported	
Colilert (18/250)	7	0	17			-	
Colisure	0	0	0			-	
Tube combinations	3	0	7			-	
Other (MPN)	1	0				-	
MLSB	2	0	4			-	
MLSA	10	0	24	58	0.13	16	-	82
Tergitol 7 (TTC)	0	0	0			-	
Chromogenic coliform agar	3	0	7			-	
Other (Membrane filtration)	12		29	47	0.12	20	-	95
MLGA	3	0	7			-	

S87B: Faecal coliforms

Stacked histogram: No. of Results vs Count per 100mL. 55 Participant Median, 65 FEPTU Median.

Legend:
- Colilert (18/250) (MPN)
- Colisure (MPN)
- Tube combinations (MPN)
- Other (MPN)
- MLSB (Membrane Filtration)
- MLSA (Membrane Filtration)
- Tergitol 7 (TTC) (Membrane Filtration)
- Chromogenic coliform agar (Membrane Filtration)
- Other (Membrane Filtration)
- MLGA (Membrane Filtration)

S87B: *Clostridium perfringens*

2.01 Participant Median
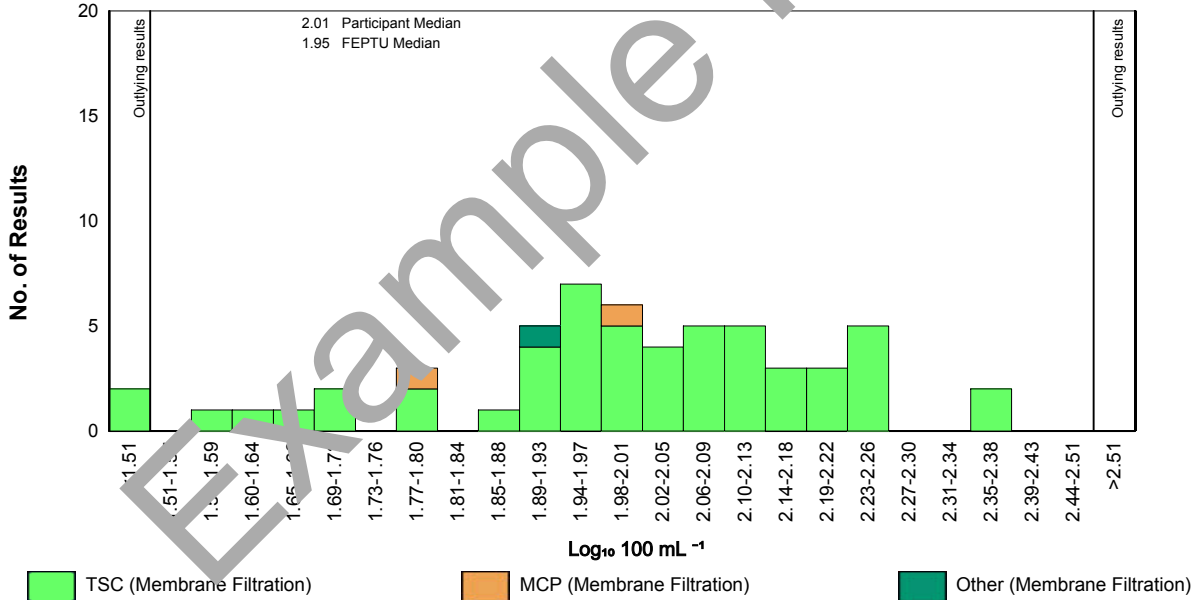1.95 FEPTU Median

Method based presentation

S87B : *Clostridium perfringens*　　　　　　　　　　　　　FEPTU Method: TSC

Method	Number of Results	Excluded Results	Percentage of the total	Median	Robust *S** (Log₁₀)	Range Reported		
TSC	53	1	94		0.16	0	-	220
MCP	2	0					-	
Other (Membrane filtration)	1	0	1				-	

S87B: *Clostridium perfringens*

2.01 Participant Median
1.95 FEPTU Median

TSC (Membrane Filtration)　　　MCP (Membrane Filtration)　　　Other (Membrane Filtration)

Method based presentation

Method	No. Participants Detected	No. Participants Not Detected
VIDAS	0	0
PCR	0	2
Other	0	0
Enrichment XLD	0	14
ISO 19250	0	25
Enrichment BGA	0	1
Other (Membrane filtration)	0	4

Sample specific comment

S87B – Enterococcus

24/77 (31%) of the participants reported a false negative results for this examination. The sample contained an *Enterococcus gallinarum* (approximately 37 colony forming units per 100 mL) which grew as pin-prick, maroon colonies on Slanetz and Bartley (S+B) agar after 48 hours incubation. It is recommended that membranes are examined, with a hand lens in a good light, and all red or maroon colonies counted as potential enterococci.

This examination has not been scored due to the higher than expected failure rate; however those laboratories reporting a false negative result should request a repeat sample from FEPTU for their own internal investigation.

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.

General comment:

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. Therefore, we will post generic reports on the website, which will be available for 12 months after the distribution has closed, so you can access the missing data.

End of report.

Example Report