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Proficiency Testing

Microbiology – Food

January 2018

Accred. no. 1457
Proficiency testing
ISO/IEC 17043

Quantitative analyses

- Aerobic microorganisms, 30 °C
- Enterobacteriaceae
- Thermotolerant *Campylobacter*
- *Listeria monocytogenes*

Qualitative analyses

- Thermotolerant *Campylobacter*
- *Listeria monocytogenes*
- *Salmonella*
- *Escherichia coli* O157
- Pathogenic *Vibrio* spp.
- *Yersinia enterocolitica*

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Abbreviations

Media

ALOA	Agar for *Listeria* according to Ottaviani & Agosti
APW 2%	Alcaline peptone water, 2 % NaCl
BGA	Brilliant Green Agar
BPW	Buffered Peptone Water
BS	Bromthymol blue Saccharose agar
CIN	Cefsulodin Irgasan Novobiocin agar
CT-SMAC	Cefixime Tellurite Sorbitol MacConkey agar
ITC	Irgasan Ticarcillin potassium Chlorate broth
LMBA	*Listeria monocytogenes* Blood Agar
mCCDA	Modified Charcoal Cephoperazone Deoxycholate Agar
MKTTn	Muller-Kauffmann Tetrathionate/novobiocin broth
MPCA	Milk Plate Count Agar
MRB	Modified Rappaport Broth
MSRV	Modified Semi-solid Rappaport-Vassiliadis enrichment media
mTSB	Modified Tryptone Soya Broth
OCLA	Oxoid Brilliance™ Listeria agar
PSB	Peptone Sorbitol Bile salts broth
PCA	Plate Count Agar
RVS	Rappaport-Vassiliadis Soy peptone broth
SMAC	Sorbitol MacConkey agar
SP	Salt Polymyxin broth
SSDC	*Salmonella/Shigella* Sodium Deoxycholate Calcium chloride agar
TCBS	Thiosulphate Citrate Bile salts Sucrose agar
TGE	Tryptone Glucose Extract agar
TSA	Tryptic Soya Agar
TSBY	Tryptone Soya Broth with Yeast extract
XLD	Xylose Lysine Deoxycholate agar
VRBG	Violet Red Bile Glucose agar

Organisations

AOAC	AOAC International
AFNOR	French National Standardisation Association
ISO	International Organization for Standardization
NMKL	Nordic Committee for Food Analyses
SLV/NFA	Livsmedelsverket/National Food Agency, Sweden

Contents

General information on results evaluation

Statistical evaluation of the results

Highly deviating values that did not belong to a strictly normal distribution after $\log_{10}$ transformation were identified as statistical outliers (Grubbs' test modified by Kelly (1)). In some cases, subjective adjustments were made to set limits based on knowledge of the mixture's contents. Outliers and false results were not included in the calculations of means and standard deviations. Results reported as "> value" were excluded from the evaluation. Results reported as "< value" were interpreted as being zero (negative result). All reported results are presented in Annex 1.

According to EN ISO/IEC 17043, for which the proficiency testing programme is accredited, it is mandatory for the participating laboratories to report method information for all their analyses. Method information is sometimes difficult to interpret, since many laboratories report a medium that that is not included in the standard method they refer to. Results from laboratories that report contradictory data on methods/media have either been excluded from the method analysis, or been added to the group of "Others", together with results from methods and media that are only used by 1-2 laboratories.

Mean values and standard deviations are normally provided for the different analyses. When the total number of reported results for an analysis is fewer than 20, the median is provided instead of the mean value. For method groups with fewer than 5 results, only the number of false results and outliers are provided.

Uncertainty of measurement for the assigned values

The uncertainty of measurement for an assigned value is calculated as the standard deviation divided by the square root of the number of correct results ("standard error"). The assigned value of evaluated parameters is the mean value of the participants results.

Table and figure legends

Tables

N	number of laboratories that performed the analysis
n	number of laboratories with satisfactory result
m	mean value in $\log_{10}$ cfu ml^{-1} (false results and outliers excluded)
s	standard deviation (false results and outliers excluded)
F	number of false positive or false negative results
<	number of low outliers
>	number of high outliers
	global results for the analysis
	values discussed in the text

Figures

Histograms of the analytical results for each mixture are presented. The mean value of the results is indicated in each histogram.

▨	values within the interval of acceptance (Annex 1)
■	outliers
□	false negative results
*	values outside of the x-axis scale

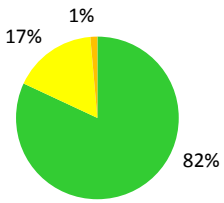
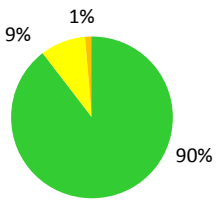
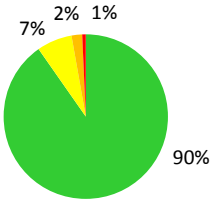
Results of the PT round January 2018

General outcome

Samples were sent to 154 laboratories, 32 in Sweden, 106 in other European countries, and 16 outside Europe. Of the 144 laboratories that reported results, 44 (31 %) provided at least one result that received an annotation. In the previous round with similar analyses (January 2017), the proportion was 44 %.

Individual results for each analysis of the PT round are listed in Annex 1 and are also available on the website after logging in: www2.slv.se/absint.

Table 1 *Microorganisms in each mixture and % of deviating results (N: number of reported results, F%: false positive or false negative, X%: outliers).*

		Mixture A				Mixture B				Mixture C			
% participants with 0 annotation 1 annotation annotation >2 annotations													
Microroganisms		*Campylobacter jejuni* *Proteus mirabilis* *Salmonella* Enteritidis *Vibrio parahaemolyticus*				*Escherichia coli* *Kocuria rhizophila* *Salmonella* Stockholm *Yersinia enterocolitica*				*Escherichia coli* O157 *Hafnia alvei* *Listeria monocytogenes* *Staphylococcus saprophyticus* *Vibrio cholerae* *Yersinia intermedia*			
Analysis		**Target organism**	**N**	**F%**	**X%**	**Target organism**	**N**	**F%**	**X%**	**Target organism**	**N**	**F%**	**X%**
Aerobic micro-organisms 30 °C		All	120	0	3	All	120	0	1	All	120	0	2
Enterobacteriaceae		*P. mirabilis*	104	6	9	*E. coli*	105	0	4	*H. alvei*	105	1	1
Thermo-tolerant *Campylo-bacter*	Quant.	*C. jejuni*	16	6	0	*(E. coli)*	17	6	0	-	17	0	0
	Qual.		25	0	-		25	8	-		25	0	-
L. mono-cytogenes	Quant.	-	67	1	0	-	67	0	0	*L. mono-cytogenes*	67	3	3
	Qual.		98	1	-		98	0	-		98	3	-
Salmonella		*S.* Enteritidis	114	3	-	*S.* Stockholm	114	4	-	-	114	4	-
E. coli O157		-	24	0	-	-	24	13	-	*E. coli O157*	24	13	-
Pathogenic *Vibrio* spp.		*V. para-haemolyticus*	19	11	-	-	19	0	-	*V. cholerae*	19	5	-
Y. enterocolitica		-	14	0	-	*Y. enterocolitica*	14	7	-	*(Y. intermedia)*	14	7	-

- no target organism or no value; (*microorganism*) false positive before confirmation
* the results are not evaluated

Aerobic microorganisms, 30 °C

Mixture A
The strain of *Proteus mirabilis* was present in the highest concentration and was main target organism for the analysis. The results were distributed around a distinct peak, and two low and two high outliers were reported. Three laboratories reported swarming of the strain on the plates; problems with counting colonies however does not appear to have been an overall issue for the laboratories.

Mixture B
The strains of *Escherichia coli* and *Kocuria rhizophila* were present in the highest concentrations and were the main target organisms for the analysis. The results were distributed around a distinct peak. One low outlier was reported.

Mixture C
The strains of *Hafnia alvei* and *Staphylococcus saprophyticus* were present in the highest concentrations and were the main target organisms for the analysis. The results were distributed around a distinct peak, and two low outliers were reported.

General remarks
As a whole, the analyses were unproblematic for the laboratories. The mean values for the different methods and media were similar. Outliers could not be attributed to the use of a specific method or medium.

The majority of the laboratories followed either NMKL 86:2013 (33 %), ISO 4833-1:2013 (22 %) or used 3M™ Petrifilm™ Aerobic Count (19 %). Compared to previous PT rounds, only a small number of laboratories followed the older versions NMKL 86:2003 or ISO 4833:2003. Four laboratories (3 %) used TEMPO® AC (bioMérieux® SA, Marcy l`Etoile, France), which is based on MPN (Most Probable Number). The sample is here incubated in a card that contains small wells with different volumes. A substrate in the card emits fluorescence when hydrolysed by the microorganisms, and the concentration is determined by the emitted fluorescence. The remaining 10 % of the laboratories followed national or laboratory/company-specific methods.

Both the NMKL and ISO methods prescribe incubation on Plate Count Agar (PCA) at 30 °C for 72 h. For Petrifilm AC there is however a variation, depending on which method that is followed. For example, AOAC® 990.12 prescribes incubation at 35 °C for 48 h while AFNOR 3M 01/1-09/89 prescribes 30 °C for 72 h.

In addition to PCA and Petrifilm AC, Milk Plate Count Agar (MPCA), Tryptic Soya Agar (TSA) and Tryptone Glucose Extract agar (TGE) were used.

Note: After the publication of the preliminary results, a few laboratories have noted that some of their results were incorrectly reported. E.g. the two low outliers for mixture A are (according to the laboratories themselves) incorrectly reported, and the correct results are within the accepted intervals for the analysis. The same has been noted for one of the low outliers for mixture C. Corrections of the reported results are however not possible to make after the publication of the preliminary results. The first reported values have therefore been used in the statistical evaluation, and they also remain in tables and figures in this report.

Results from analysis of aerobic microorganisms

Medium	N	Mixture A						Mixture B						Mixture C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	120	116	4.230	0.134	0	2	2	119	4.529	0.235	0	1	0	118	4.814	0.152	0	2	0
PCA	67	66	4.199	0.127	0	1	0	66	4.551	0.234	0	0	0	65	4.809	0.155	0	1	0
Petrifilm AC	23	22	4.271	0.126	0	1	0	23	4.473	0.262	0	0	0	22	4.827	0.147	0	1	0
MPCA	9	8	4.282	0.210	0	0	1	8	4.539	0.272	0	1	0	9	4.826	0.135	0	0	0
TSA	8	8	4.290	0.101	0	0	0	9	4.586	0.240	0	0	0	9	4.810	0.202	0	0	0
TGE	4	4	-	-	0	0	0	4	-	-	0	0	0	4	-	-	0	0	0
TEMPO AC	4	4	-	-	0	0	0	4	-	-	0	0	0	4	-	-	0	0	0
Other*	5	4	4.266	0.177	0	0	1	5	4.385	0.152	0	0	0	5	4.799	0.085	0	0	0

* The group Other includes e.g. nutrient agar (NA) and Compact Dry™ TC.

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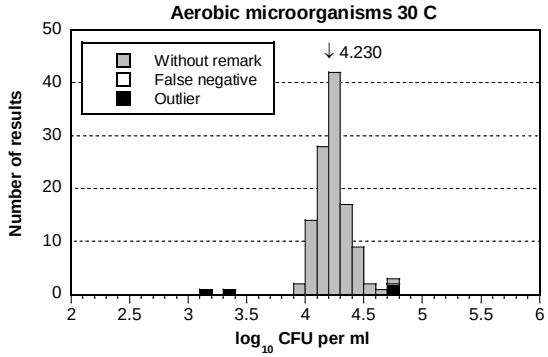

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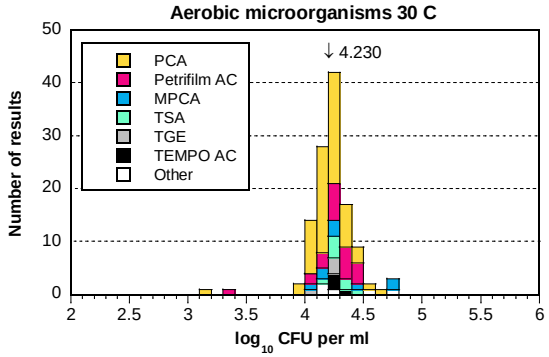

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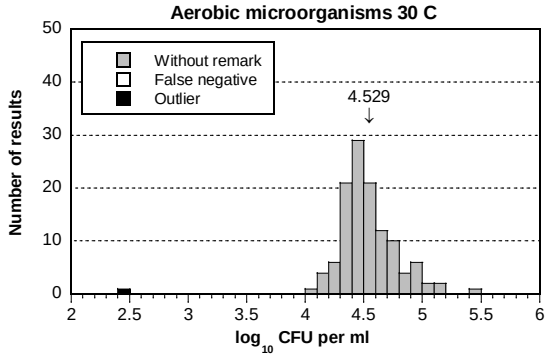

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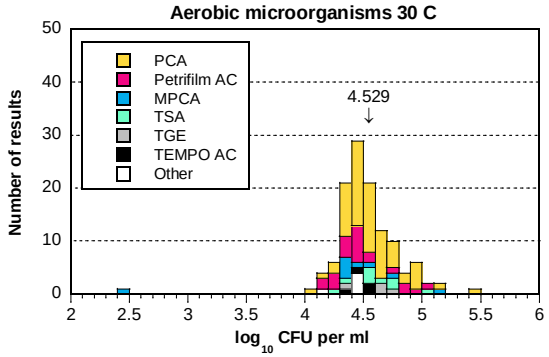

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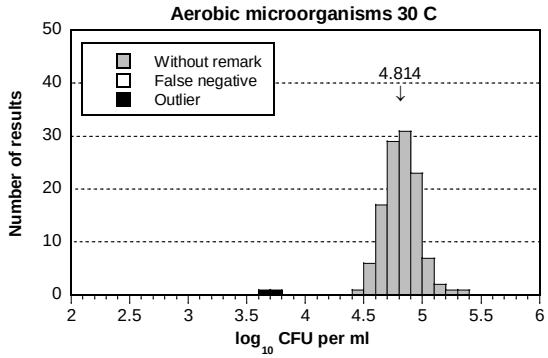

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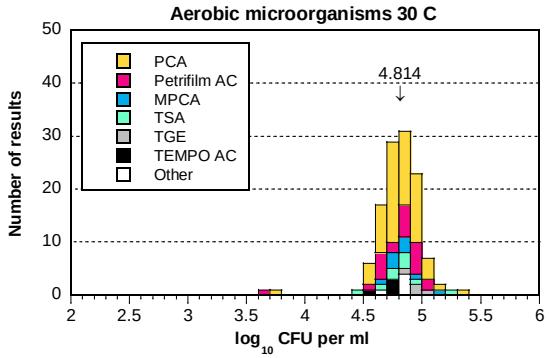

Enterobacteriaceae

Mixture A
The strain of *Proteus mirabilis* was target organism for the analysis. The majority of the results were distributed around a distinct peak. However nine low outliers were reported, as well as six false negative results. The same mixture was used in the PT round January 2017 – and similar number of deviating results were reported at that time. Among users of 3M™ Petrifilm™ Enterobacteriaceae (Petrifilm EB) only one low outlier was reported, and it is possible that *P. mirabilis* was easier to distinguish due to the colour indicator present in this medium. Low outliers and false negative results in the mixture were otherwise reported almost exclusively by users of Violet Red Bile Glucose agar (VRBG), which however at the same time was the most common medium.

Mixture B
The strain of *Escherichia coli* was target organism for the analysis. The results were distributed around a distinct peak, and two low and two high outliers were reported.

Mixture C
The strain of *Hafnia alvei* was target organism. The results were distributed around a distinct peak, and one low outlier and one false negative result were reported.

General remarks
As a whole, the analyses were unproblematic for the laboratories. The exceptions were the low outliers and the false negative results for mixture A. The mean values for the different methods and media were however very similar, for all three mixtures.

As in previous PT rounds, most laboratories reported following either NMKL 144:2005 (47 %), Petrifilm EB (21 %) or ISO 21528-2:2004 (11 %). Six laboratories (6 %) stated that they followed ISO 21528-1:2004, which is a method based on MPN (Most Probable Number) for the analysis of Enterobacteriaceae. The two ISO methods were during 2017 replaced by ISO 21528-1:2017 (MPN) and ISO 21528-2:2017 (colony-count technique). The MPN method is recommended when the expected level of Enterobacteriaceae is lower than 100 cfu g^{-1}. The new ISO methods were however not implemented by more than a few laboratories. Three laboratories reported following ISO 21528-2:2017, whereas no laboratory reported following ISO 21528-1:2017. Still, the mean values were highly similar, irrespective of which ISO version that was used, for all three mixtures. As in the analysis of aerobic microorganisms, a few laboratories used fluorescence-based methods (TEMPO® Enterobacteriaceae).

Enterobacteriaceae are Gram-negative and oxidase-negative bacteria that ferment glucose with the production of acid by-products. On VRBG – which is used in both NMKL 144 and ISO 21528-2 – they form pink/red colonies, with our without a bile precipitation zone. The appearance is similar on Petrifilm EB, which also includes a colour indicator for the detection of acid by-products and a plastic film for detection of gas production. It is possible that these factors contributed to the low numbers of false negative results and low outliers for Petrifilm EB.

Presumptive colonies in VRBG shall according to NMKL 144:2005 be confirmed with an oxidase test. In comparison, ISO 21528-2:2004 states that presumptive colonies shall be confirmed with both an oxidase test and a glucose fermentation test. In the new revision ISO 21528-2:2017 this has been modified slightly and glucose agar has been replaced by glucose oxidation/fermentation (OF) medium. Oxidase-negative colonies that produce acid from glucose in the OF medium are confirmed as Enterobacteriaceae.

Results from analysis of Enterobacteriaceae

Medium	N	Mixture A						Mixture B						Mixture C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	105	89	4.085	0.224	6	9	0	101	4.193	0.175	0	2	2	103	4.345	0.232	1	1	0
VRBG	72	58	4.052	0.226	5	8	0	69	4.189	0.174	0	1	2	71	4.359	0.242	0	1	0
Petrifilm EB	22	21	4.149	0.242	0	1	0	22	4.216	0.197	0	0	0	21	4.356	0.201	1	0	0
TSA/VRB	3	3	-	-	0	0	0	3	-	-	0	0	0	3	-	-	0	0	0
TEMPO EB	3	3	-	-	0	0	0	3	-	-	0	0	0	3	-	-	0	0	0
Other*	5	4	4.064	0.096	1	0	0	4	4.150	0.156	0	1	0	5	4.258	0.203	0	0	0

* The group Other includes e.g. Compact Dry™ ETB.

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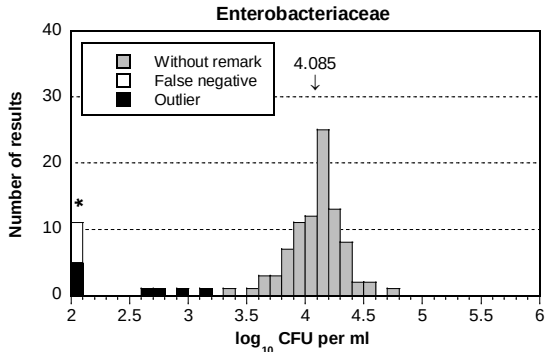

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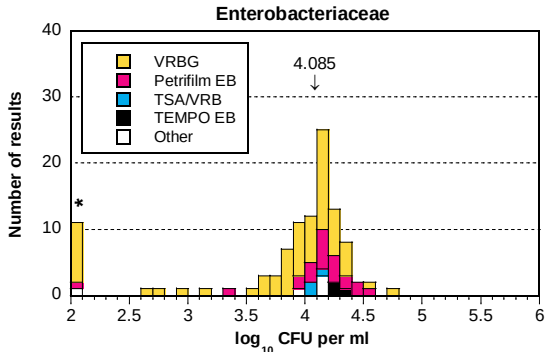

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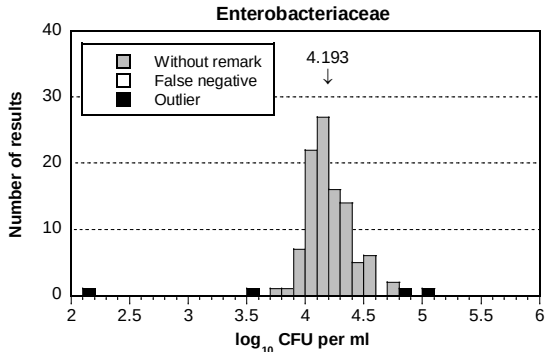

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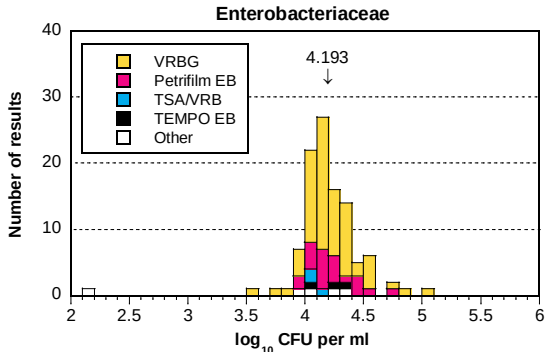

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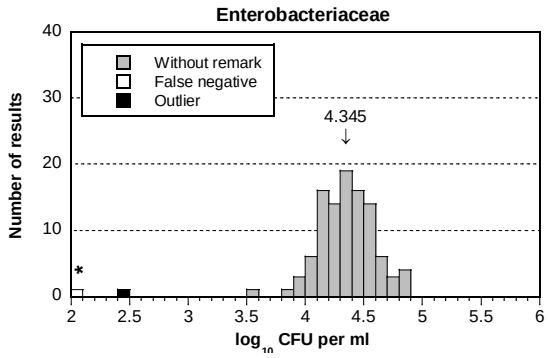

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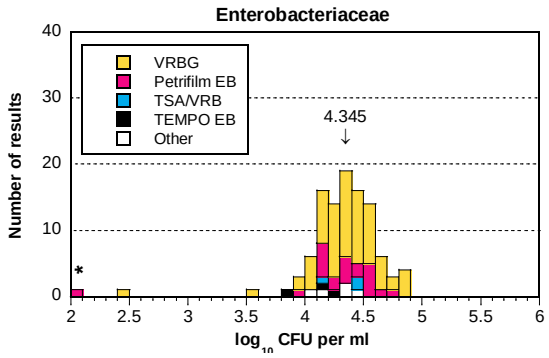

Thermotolerant *Campylobacter*

Mixture A
The strain of *Campylobacter jejuni* was target organism for the analysis. One laboratory reported a false negative result in the quantitative analysis.

Mixture B
No target organism was present in mixture B. Laboratories may however have identified *Escherichia coli*, which is false positive for the analysis. False positive results were reported by one laboratory in the quantitative analysis and by two laboratories in the qualitative analysis.

Mixture C
No target organism was present in the mixture. All laboratories reported correct results, in both the quantitative and in the qualitative analysis.

General remarks
Only 17 and 25 laboratories participated in the quantitative and qualitative analysis, respectively. The results are therefore difficult to evaluate statistically. However, the analyses appear to have been unproblematic for the majority of the laboratories.

NMKL 119 and ISO 10272 (different versions) were the most used methods in both the quantitative and the qualitative analysis. The majority of the laboratories had also started using the new ISO 10271-2:2017 and 10272-2:2017 instead of the older ISO 10272-1:2006 and 10272-2:2006. The three laboratories that followed the older ISO 10272-2:2006 in the quantitative analysis all reported lower results compared to the other methods, but it cannot be ruled out that it is simply due to chance. In the qualitative analysis, one laboratory stated that they followed ISO 17995, which is a method for detection of *Campylobacter* in water. Here, it can also be mentioned that NMKL 119:2007 being revised and the new version will likely be more similar to the new ISO 10272-2:2017 and 10272-1:2017.

The results in the quantitative analysis had a relatively large distribution, something that has been observed in several earlier PT rounds. *Campylobacter* spp. are sensitive to mechanical stress and to dehydration. Differences in the results might therefore be a consequence of a too harsh surface spreading. At the National Food Agency, *Campylobacter* spp. are carefully spread onto pre-warmed plates and the final drying of the bacterial suspension is done by leaving the lids of the plates slightly open (maximum five minutes).

The majority of the laboratories (76 %) in the qualitative analysis used Bolton broth for the enrichment step, but Preston broth was also used. In the selective step, most laboratories used modified charcoal cephoperazone deoxycholate agar (mCCDA) (84 %) but CampyFood Agar and CHROMagar™ were also used. In the quantitative analysis all laboratories except one reported using mCCDA.

All laboratories except one in each analysis reported performing some kind of confirmation. *Campylobacter* spp. are Gram-negative, oxidase-positive and catalase-positive – they can also be confirmed by their appearance in a microscope. The bacteria are normally spiral-shaped rods that display a characteristic darting/rotating movement. *C. jejuni*, *C. coli* and *C. lari* can further be separated by differences in their hydrolysis of hippurate and indoxyl acetate, and their sensitivity/resistance to nalidixic acid and cephalothin. A few laboratories in this PT also reported using Maldi-TOF or API® CAMPY for the confirmation.

Results from quantitative analysis of thermotolerant Campylobacter

Method	N	Mixture A						Mixture B						Mixture C					
		n	Med*	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	17	15	1.97	-	1	0	0	16	-	-	1	-	-	17	-	-	0	-	-
ISO 10272-2:2017	9	7	2.10	-	1	0	0	8	-	-	1	-	-	9	-	-	0	-	-
NMKL 119:2007	5	5	2.10	-	0	0	0	5	-	-	0	-	-	5	-	-	0	-	-
ISO 10272-2:2006	3	3	-	-	0	0	0	3	-	-	0	-	-	3	-	-	0	-	-
Other	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

* Med = median

Results from qualitative analysis of thermotolerant Campylobacter

Method	N	Mixture A			Mixture B			Mixture C		
		n	+/-	F	n	+/-	F	n	+/-	F
All results	25	25	Pos	0	23	Neg	2	25	Neg	0
NMKL 119:2007	13	13	Pos	0	11	Neg	2	13	Neg	0
ISO 10272-1:2017	6	6	Pos	0	6	Neg	0	6	Neg	0
ISO 10272-1:2006	3	3	Pos	0	3	Neg	0	3	Neg	0
Other*	3	3	Pos	0	3	Neg	0	3	Neg	0

* The group Other includes e.g. ISO 17995, VIDAS, and one PCR method.

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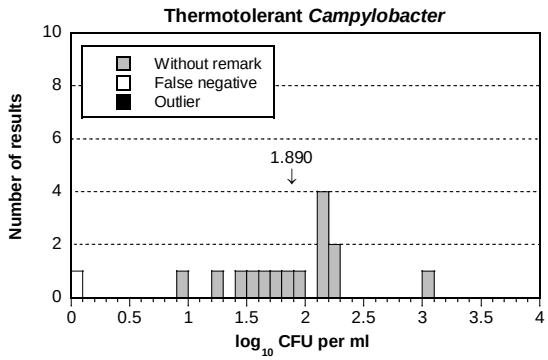

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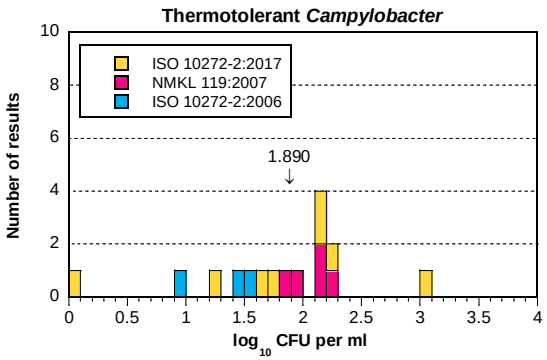


Listeria monocytogenes

Mixture A

No target organism for the analysis was present in the mixture. One laboratory in the quantitative analysis and one laboratory in the qualitative analysis reported a false positive result.

Mixture B

No target organism for the analysis was present in the mixture. All laboratories in both the quantitative and the qualitative analysis reported correct results.

Mixture C

The strain of *Listeria monocytogenes* was target organism. The results in the quantitative analysis were distributed around a distinct peak and two low outliers, as

well as two false negative results were reported. In the qualitative analysis, three false negative results were reported.

General remarks

As a whole, the analyses were without major problems for the laboratories. Outliers and false results could not be attributed to the use of a specific method or medium.

New versions of ISO 11290-1 (qualitative) and 11290-2 (quantitative) were published during 2017. The revised methods distinguish between detection/enumeration of *Listeria* spp. and *Listeria monocytogenes*, and changes have also been made e.g. in which confirmation tests that should be performed. The qualitative method ISO 11290-1:2017 is based on primary enrichment in half-Fraser broth, followed by secondary enrichment in Fraser broth. Aliquots from both enrichments are plated onto selective agar for *Listeria* according to Ottaviani & Agosti (ALOA) and onto another selective medium chosen by the laboratory. In the quantitative method ISO 11290-2:2017 the sample is first suspended in buffered peptone water (BPW) or in half-Fraser broth and material is then transferred from these to ALOA. The quantitative and qualitative methods used in NMKL 136:2010 are similar to the ones in the ISO methods.

Typical colonies of *L. monocytogenes* are on ALOA blue-green due to β-glucosidase activity, and are surrounded by an opaque halo due to hydrolysis of inositol in the medium. The halo is sometimes weak, or may not be present at all. *L. monocytogenes* can be confirmed by microscopy, catalase test, and by tests of β-haemolysis and carbohydrate utilazation (fermentation of rhamnose and xylose). *L. monocytogenes* is catalase-positive, displays β-haemolysis on blood agar, and ferments rhamnose but not xylose. Confirmation can also be done by the increased and decreased β-haemolysis displayed by *L. monocytogenes* in the presence of *Staphylococcus aureus* and *Rhodococcus equi* respectively (CAMP test).

ISO 11290-1 and ISO 11290-2 were the most commonly used methods in both the quantitative and the qualitative analysis (29 % and 45 % of the laboratories respectively). The majority of the laboratories however still followed the older versions of the respective methods. In addition to ISO 11290 and NMKL 136, many laboratories used RAPID'L.mono or VIDAS®. Listeria Precis™ was also used by a few laboratories in both analyses. RAPID'L.mono uses a chromogenic medium that identifies the enzyme phosphatidylinositol phospholipase C (PI-PLC) in *L. monocytogens*, and that also identifies both *Listeria* spp. and *L. monocytogens* by the fact that they do not metabolize xylose. The method in Listeria Precis™ in a similar way uses a chromogenic medium that detects *Listeria* spp. and *L. monocytogenes* β-glucosidase cleavage of X-glucoside in the medium Brilliance™ Listeria. In comparison, VIDAS® is based on detection of specific *L. monocytogenes* antigen, by a method based on ELFA (*Enzyme Linked Fluorescent Assay*). The alternative methods are all validated by AFNOR and/or NordVal.

As in previous proficiency testing rounds, ALOA and Oxoid Brilliance™ Listeria-agar (previously OCLA) were the most used media. However PALCAM, Listeria monocytogenes blood agar (LMBA), Oxford Listeria selective agar, and other types of chromogenic media were also used. Confirmation was carried out by most laboratories. In total, confirmation (in various forms) was carried out by 85 % and 88 % of the laboratories in the qualitative and quantitative analyses respectively.

Results from quantitative analysis of Listeria monocytogenes

Method	N	Mixture A						Mixture B						Mixture C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	67	66	-	-	1	-	-	67	-	-	0	-	-	63	2.418	0.114	2	2	0
ISO 11290-2:1998 /Amd 1:2004	16	16	-	-	0	-	-	16	-	-	0	-	-	15	2.405	0.069	0	1	0
NMKL 136:2010*	16	15	-	-	1	-	-	16	-	-	0	-	-	15	2.417	0.122	1	0	0
RAPID'L.mono	15	15	-	-	0	-	-	15	-	-	0	-	-	14	2.416	0.094	0	1	0
ISO 11290-2:2017	10	10	-	-	0	-	-	10	-	-	0	-	-	9	2.393	0.110	1	0	0
Listeria Precis	4	4	-	-	0	-	-	4	-	-	0	-	-	4	-	-	0	0	0
ISO 11290-2:1998	4	4	-	-	0	-	-	4	-	-	0	-	-	4	-	-	0	0	0
Other	2	2	-	-	0	-	-	2	-	-	0	-	-	2	-	-	0	0	0

* The group NMKL 136:2010 includes one laboratory that followed NMKL 136:2007.

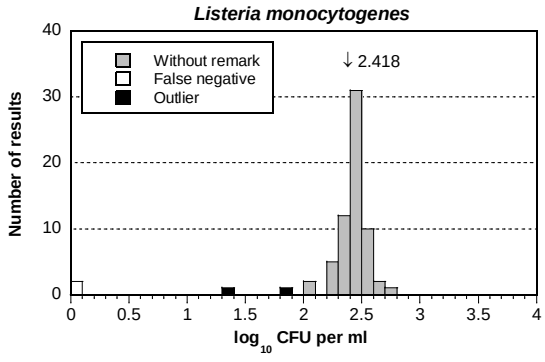
Results from qualitative analysis of Listeria monocytogenes

Method	N	Mixture A			Mixture B			Mixture C		
		n	+/-	F	n	+/-	F	n	+/-	F
All results	98	97	Neg	1	98	Neg	0	95	Pos	3
RAPID'L.mono	17	17	Neg	0	17	Neg	0	17	Pos	0
VIDAS	16	16	Neg	0	16	Neg	0	16	Pos	0
NMKL 136:2010*	14	13	Neg	1	14	Neg	0	14	Pos	1
ISO 11290-1:1996 /Amd 1:2004	14	14	Neg	0	14	Neg	0	14	Pos	0
ISO 11290-1:2017	12	12	Neg	0	12	Neg	0	12	Pos	1
PCR method	9	9	Neg	0	9	Neg	0	9	Pos	0
Listeria Precis	5	5	Neg	0	5	Neg	0	5	Pos	0
ISO 11290-1:1996	2	2	Neg	0	2	Neg	0	2	Pos	0
Other**	9	9	Neg	0	9	Neg	0	9	Pos	1

* The group NMKL 136:2010 includes one laboratory that followed NMKL 136:2007.

** The group Other includes IDF 143A:1995, SwabSure ListeriaP, as well as national and/or company-specific methods.

C



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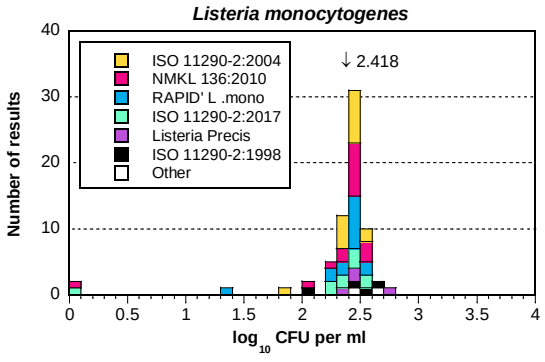


Salmonella

Mixture A
The strain of *Salmonella* Enteritidis was target organism for the analysis. Three laboratories reported a false negative result.

Mixture B
The strain of *Salmonella* Stockholm was target organism for the analysis. Five laboratories reported a false negative result. The concentration of the strain in the mixture was low, approximately 5 CFU ml^{-1} in the internal tests at the National Food Agency. With the reservation that all laboratories appear to have performed some type of enrichment step, the low concentration is however unlikely to be the reason for the false negative results, unless only a very small volume was inoculated into the enrichment medium.

Mixture C
No target organism for the analysis was present in the mixture. Four laboratories reported a false positive result.

General remarks
Most laboratories followed the traditional methods ISO 6579-1:2017 or NMKL 71:1999, which are highly similar. Both are based on pre-enrichment in buffered peptone water (BPW), followed by selective enrichment in Rappaport-Vassiliadis soy peptone broth (RVS) and subsequent inoculation onto selective xylose lysine deoxycholate agar (XLD) and another selective medium chosen by the laboratory. In contrast to NMKL 71:1999, ISO 6579-1:2017 also includes selective enrichment in Muller-Kauffmann tetrathionate/novobiocin broth (MKTTn). RVS can also be replaced by modified semi-solid Rappaport-Vassiliadis enrichment media (MSRV) for the analysis of motile *Salmonella*. Confirmation is by biochemical (e.g. mannitol and urea) and serological (e.g. *Salmonella* polyvalent O and H antisera) tests. Confirmation (in various forms) was in this proficiency testing carried out by the majority (95 %) of the laboratories.

The new ISO 6579-1:2017 was published in the beginning of 2017 and replaced previous ISO-methods for the detection of *Salmonella*. The majority of the 33 laboratories that analysed according to ISO however still followed the older versions 6579:2002 or ISO 6579:2002/Amd 1:2007. Among the changes in the new version from 2017 are that detection of β-galactosidase and indole is optional in the confirmation step, whereas positive results for agglutination against both O and H antigen is required for a strain to be considered as *Salmonella*.

Users of NMKL methods can in addition to NMKL 71:1999 also choose to follow NMKL 187:2016. The latter method is intended for detection of motile *Salmonella* and, similarly to ISO 6579-1:2017, uses MSRV instead of RVS during the selective enrichment step. Notably, all three laboratories that followed NMKL 187 stated that they followed the older version NMKL 187:2006. The new version from 2016 contains clarifications regarding the choice of the selective agar medium complementary to XLD, and the concentration of Novobiocin in MSRV. It also contains new paragraphs regarding pre-enrichment of samples from primary animal production, faecal samples and swab samples.

On XLD, which was used by the majority of the laboratories, typical *Salmonella* form transparent red colonies with a black center. As a complementary medium to

XLD, the laboratories mainly used chromogenic media such as Brilliance™ Salmonella, Rambach™ agar, and brilliant green agar (BGA).

Similar to the analysis of *Listeria monocytogenes*, several laboratories chose to analyse with VIDAS® or RAPID'Salmonella, instead of with the traditional ISO and NMKL methods. Regardless of the choice of method or medium, the analyses were without major problem for the laboratories. No obvious differences between results from the different methods and media could be identified. No false results were reported by the 5 % of the laboratories that did not perform a confirmation.

Results from qualitative analysis of Salmonella

Method	N	Mixture A			Mixture B			Mixture C		
		n	+/-	F	n	+/-	F	n	+/-	F
All results	114	111	Pos	3	109	Pos	5	110	Neg	4
NMKL 71:1999	31	30	Pos	1	30	Pos	1	31	Neg	0
ISO 6579-1:2017	15	15	Pos	0	15	Pos	0	13	Neg	2
VIDAS*	15	15	Pos	0	14	Pos	1	15	Neg	0
PCR method	14	14	Pos	0	14	Pos	0	13	Neg	1
ISO 6579:2002	10	10	Pos	0	9	Pos	1	9	Neg	1
ISO 6579:2002/Amd 1:2007	8	8	Pos	0	8	Pos	0	8	Neg	0
RAPID'Salmonella	6	5	Pos	1	6	Pos	0	6	Neg	0
NMKL 187:2007	3	3	Pos	0	3	Pos	0	3	Neg	0
Other**	12	11	Pos	1	10	Pos	2	12	Neg	0

* The group VIDAS includes two laboratories that analysed with MINI VIDAS®.

** The group Other includes Neogen® Reveal® 2.0 *Salmonella*, Oxoid Salmonella Precis™, as well as national and/or company-specific methods.

Escherichia coli O157

Mixture A

No target organism for the analysis was present in the mixture. All laboratories reported a correct negative result.

Mixture B

No target organism for the analysis was present in the mixture. Three laboratories reported a false positive result.

Mixture C

The strain of *Escherichia coli* O157 was target organism for the analysis. Three laboratories reported a false negative result. The concentration of the strain in the mixture was low, approximately 6 CFU ml^{-1} in the internal tests at the National Food Agency. With the reservation that all laboratories appear to have performed some type of enrichment step, the low concentration is however unlikely to be the reason for the false negative results, unless only a very small volume was inoculated into the enrichment medium.

General remarks

Only 24 laboratories performed the analysis, and the results are therefore difficult to evaluate statistically. However no obvious differences between the methods and media

can be identified. Confirmation test (in various forms) were performed by 20 of the laboratories (83 %) which is a similar number compared to the January PT round 2017.

Most laboratories followed either of the traditional methods NMKL 164:2005 or ISO 16654:2001. The methods in these are similar: enrichment in modified tryptone soya broth (mTSB), followed by immunomagnetic separation and isolation on cefixime tellurite sorbitol MacConkey agar (CT-SMAC) and another medium selected by the laboratory. Confirmation is by a test for indole production as well as agglutination with *E. coli* O157 antiserum. Here, it can also be mentioned that NMKL 164:2005 is undergoing revision – there is however no estimated date for when a new version will be available.

The majority of the laboratories (63 %) incubated on CT-SMAC, but sorbitol MacConkey agar (SMAC) and CHROMagar™ O157 were also used. On CT-SMAC and SMAC, bacteria that ferment sorbitol (most non-pathogenic *E. coli*) are distinguished from those that do not (most *E. coli* O157). The inclusion of cefimixin and tellurite in CT-SMAC makes it more selective compared to SMAC, and it inhibits growth of many *Proteus* spp. och *Aeromonas* spp., which often are sorbitol-negative. Sorbitol-negative *E. coli* O157 form transparent colonies on CT-SMAC and SMAC, approximately 1-2 mm in diameter and with a dark center. Sorbitol-positive *E. coli* instead form red colonies on these media. In comparison, on CHROMagar™ *E. coli* O157 form mauve (purple) colonies that can be distinguished from other colonies (blue or colourless) that may grow on this medium.

Results from qualitative analysis of E. coli *O157*

Method	N	Mixture A			Mixture B			Mixture C		
		n	+/-	F	n	+/-	F	n	+/-	F
All results	24	24	Neg	0	21	Neg	3	21	Pos	3
ISO 16654:2001*	6	6	Neg	0	5	Neg	1	4	Pos	2
NMKL 164:2005	4	4	Neg	0	4	Neg	0	4	Pos	0
PCR method	4	4	Neg	0	4	Neg	0	4	Pos	0
VIDAS	3	3	Neg	0	3	Neg	0	3	Pos	0
Other**	7	7	Neg	0	5	Neg	2	6	Pos	1

* The group ISO 16654:2001 includes one laboratory that used a modified version of the standard.
** The group Other includes national and/or company-specific methods.

Pathogenic *Vibrio* spp.

Mixture A

The strain of *Vibrio parahaemolyticus* was target organism for the analysis. Two laboratories reported a false negative result.

Mixture B

No target organism for the analysis was present in the mixture. All laboratories reported a correct negative result.

Mixture C

The strain of *Vibrio cholerae* was target organism for the analysis. One laboratory reported a false negative result.

General remarks

Only 19 laboratories performed the analysis, and most used similar methods and media. The results are therefore difficult to evaluate statistically. The majority of the laboratories however reported correct results, and the small number of false negative results could not be attributed to the use of a specific method or medium. All laboratories except one also stated that they performed some kind of confirmation.

A new version of the ISO method, ISO 21872-1:2017, was published during 2017. It replaces the previous ISO/TS 21872-1:2007, as well as ISO/TS 21872-2:2007. The new method contains several changes, including the performance of confirmation with biochemical and/or PCR methods.

The majority of the laboratories followed either NMKL 156:1997 or ISO/TS 21872-1:2007. Only one laboratory stated that they followed the new ISO 21872-1:2017. The new ISO method follows roughly the same principle as the previous version. Primary and secondary enrichment is in alkaline peptone water with 2 % NaCl (APW 2 %) and is followed by inoculation onto selective thiosulphate citrate bile salts sucrose agar (TCBS). Another medium, chosen by the laboratory, is inoculated in parallel to TCBS. Subcultured colonies are subsequently confirmed by biochemical tests, PCR and/or real-time PCR. The procedure in NMKL 156:1997 is similar to ISO 21872-1:2017, but also includes enrichment in salt polymyxin broth (SP). The NMKL method only includes biochemical confirmation tests.

All laboratories stated that colonies were isolated on TCBS. One laboratory reported parallel isolation on CHROMagar™ Vibrio. Bile salts in TCBS inhibit the growth of Gram-positive microorganisms, whereas a high pH promotes the growth of *V. cholerae*. On this medium, *Vibrio* spp. form either green of yellow colonies, depending on if they ferment sucrose or not. *V. parahaemolyticus* and *V. vulnificus* (sucrose-negative) normally form blue-green colonies, 2-3 mm in diameter, whereas *V. cholerae* (sucrose-positive) normally form yellow colonies, 1-2 mm in diameter.

At the National Food Agency, the strain of *V. parahaemolyticus* in mixture A formed typical colonies on TCBS, regardless of whether the enrichment was carried out in APW 2 % or in SP. Similarly, the strain of *V. cholerae* in mixture C formed characteristic yellow colonies on TCBS. On a few plates, for unknown reasons, some colonies of *V. cholerae* were however smaller than the rest. Still, during the confirmation both of these colony morphologies were oxidase-positive and sensitive to vibriostaticum O129. During an initial test of mixture A, *P. mirabilis* formed small, atypical and light green colonies on TCBS. These colonies were however oxidase-negative and could therefore be distinguished from *V. parahaemolyticus* during the confirmation.

Results from qualitative analysis of pathogenic Vibrio *spp.*

Method	N	Mixture A			Mixture B			Mixture C		
		n	+/-	F	n	+/-	F	n	+/-	F
All results	19	17	Pos	2	19	Neg	0	18	Pos	1
NMKL 156:1997	9	8	Pos	1	9	Neg	0	9	Pos	0
ISO/TS 21872-1:2007	7	6	Pos	1	7	Neg	0	7	Pos	0
ISO/TS 21872-1:2007/Cor 1:2008	1	1	Pos	0	1	Neg	0	0	Pos	1
ISO 21872-1:2017	1	1	Pos	0	1	Neg	0	1	Pos	0
Other*	1	1	Pos	0	1	Neg	0	1	Pos	0

* The group Other includes national and/or company-specific methods.

Yersinia enterocolitica

Mixture A
No target organism for the analysis was present in the mixture. All laboratories reported a correct negative result.

Mixture B
The strain of *Yersinia enterocolitica* was target organism for the analysis. One laboratory reported a false negative result.

Mixture C
No target organism for the analysis was present. The mixture did however contain a strain of *Yersinia intermedia*, which is false positive for the analysis. At the National Food Agency, the strain was oxidase-negative and did not display agglutination against neither O:3 nor O:9 antisera. It was however difficult to identify as *Y. intermedia* with API 20E. One laboratory reported a false positive result.

The concentration of *Y. intermedia* in the mixture was low, approximately 5 CFU ml^{-1} in the internal tests at the National Food Agency. With the reservation that all laboratories appear to have performed some type of enrichment step, it is unlikely that any of the (correct) negative results are due to *Y. intermedia* not being detected at all.

General remarks
Only 14 laboratories performed the analysis, and the results are therefore difficult to evaluate statistically. The low number of false results that were reported could not be attributed to the use of a specific method or medium. All laboratories stated that they performed some type of confirmation.

The majority of the laboratories followed ISO 10273 (different versions) or NMKL 117:1996. Half of the laboratories that used the ISO method followed the new ISO 10273:2017, which contains several important changes compared to the previous version. These include that characteristic *Y. enterocolitica* can be confirmed either by the traditional biochemical methods or by detection of the chromosomal virulence-associated gene *ail* by real-time PCR. Here, it can also be mentioned that NMKL 117:1996 is currently being revised – there is however no estimated date for when a new version will be available.

The method in ISO 10273:2017 is based on parallel enrichment in peptone sorbitol bile salts broth (PSB) and irgasan ticarcillin potassium chlorate broth (ITC). Samples are subsequently streaked onto cefsulodin irgasan novobiocin agar (CIN) as well as (optionally) on a second chromogenic medium selected by the laboratory. Characteristic colonies are confirmed by biochemical methods or by real-time PCR. Cold enrichment can also be performed, but is not mandatory. The method in NMKL 117:1996 differs somewhat and is instead based on pre- and cold enrichment in PSB, as well as selective enrichment in modified Rappaport broth (MRB). After the enrichment steps, samples are inoculated onto CIN, but *Salmonella/Shigella* sodium deoxycholate calcium chloride agar (SSDC) can also be used. Presumptive colonies are subcultured onto bromthymol blue saccharose agar (BS) and sucrose-positive colonies (yellow) are selected for confirmation.

On CIN, colonies of *Y. enterocolitica* have a typical appearance; a red “bull’s eye” center and an outer transparent zone. At the National Food Agency, the strain of *Y. enterocolitica* in mixture B formed typical colonies on both CIN and BS. The strain was also oxidase-negative in the confirmation. All laboratories in this proficiency

testing reported incubating on CIN. Chromogenic media that can be used in parallel with CIN are e.g. YECA (2), YeCM (3) and CHROMagar™ Yersinia.

Laboratories that use NMKL methods can also choose a method based on real-time PCR, NMKL 163:2013. The sample is here enriched in semi-selective PSB or in non-selective tryptone soya broth with yeast extract (TSBY). The enrichment step is followed by DNA extraction and real-time PCR aimed at the *ail* gene in *Y. enterocolitica*, in a similar way as in ISO 10273:2017. Inoculation from the enrichment broth onto CIN is optional. NMKL 163:2013 is suitable when high contamination levels are suspected, and the use of NMKL 117:1996 or ISO 10273:2003 is recommended for samples with low suspected levels of *Y. enterocolitica*.

Results from qualitative analysis of Yersinia enterocolitica

Method	N	Mixture A			Mixture B			Mixture C		
		n	+/-	F	n	+/-	F	n	+/-	F
All results	14	14	Neg	0	13	Pos	1	13	Neg	1
ISO 10273:2017	4	4	Neg	0	4	Pos	0	4	Neg	0
ISO 10273:2003	4	4	Neg	0	4	Pos	0	3	Neg	1
NMKL 117:1996	3	3	Neg	0	3	Pos	0	3	Neg	0
Other*	3	3	Neg	0	2	Pos	1	3	Neg	0

* The group Other includes national and/or company-specific methods.

Outcome of the results of individual laboratory - assessment

The reported results of all participating laboratories are listed in Annex 1, together with the minimum and maximum accepted values for each analysis. Results that received a remark (false results and outliers) are highlighted in yellow, with bold font.

It is the responsibility of the participating laboratories to correctly report results according to the instructions. When laboratories incorrectly report their results, for example by stating “pos” or “neg” for quantitative analyses, the results cannot be correctly processed. Such incorrectly reported results are normally excluded. Inclusion and further processing of such results may still be done, after manual assessment in each individual case.

Z-scores (see below) for individual analyses are shown in Annex 2 and can be used as a tool by laboratories when following up on the results.

The laboratories are not grouped or ranked based on their results. The performance of a laboratory as a whole can only be evaluated from the number of false results and outliers that are listed in Annex 1 and below the box plots.

Information on the results processing and recommendations for follow-up work are given in the Scheme Protocol (4). Samples for follow-up can be ordered, free of charge via our website: www.livsmedelsverket.se/en/PT-extra

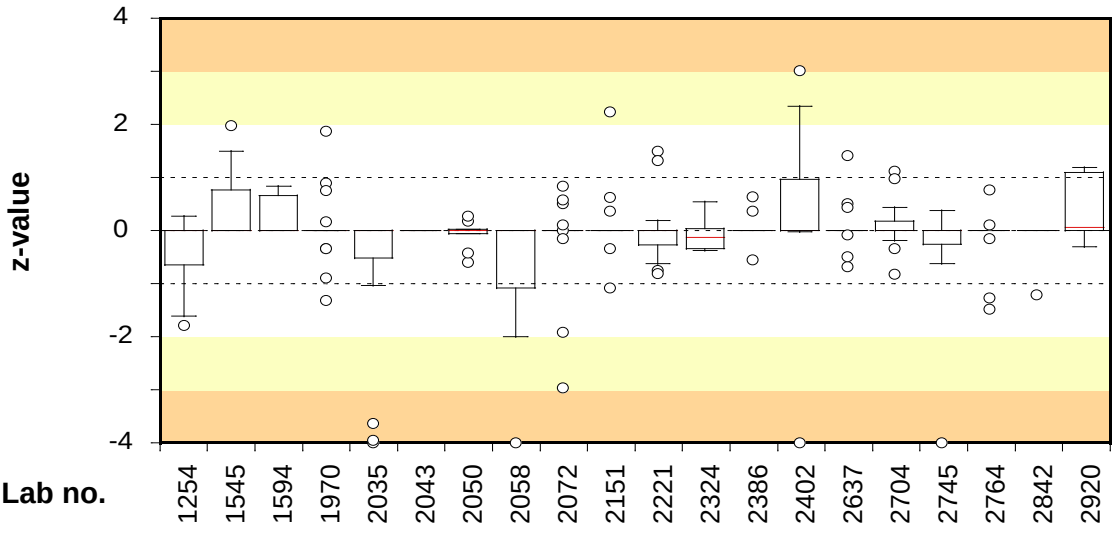
In order to allow comparison of the results from different analyses and mixtures, all results are transformed into standard values (z-scores). For quantitative analyses, a z-score is either positive or negative, depending on whether the individual result is higher or lower than the mean value calculated from all laboratory results for each analysis.

The box plots are based on the z-scores listed in Annex 2, and give a comprehensive view of the achievement of each laboratory. A small box, centred around zero, indicates the results of that individual laboratory, with false results excluded, are close to the general mean values calculated for all laboratory results. The range of z-scores is indicated by the size of the box and, for most laboratories, by lines and/or circles above and beneath the box. For each laboratory, the number of false results and outliers are also listed in the tables below the box plots.

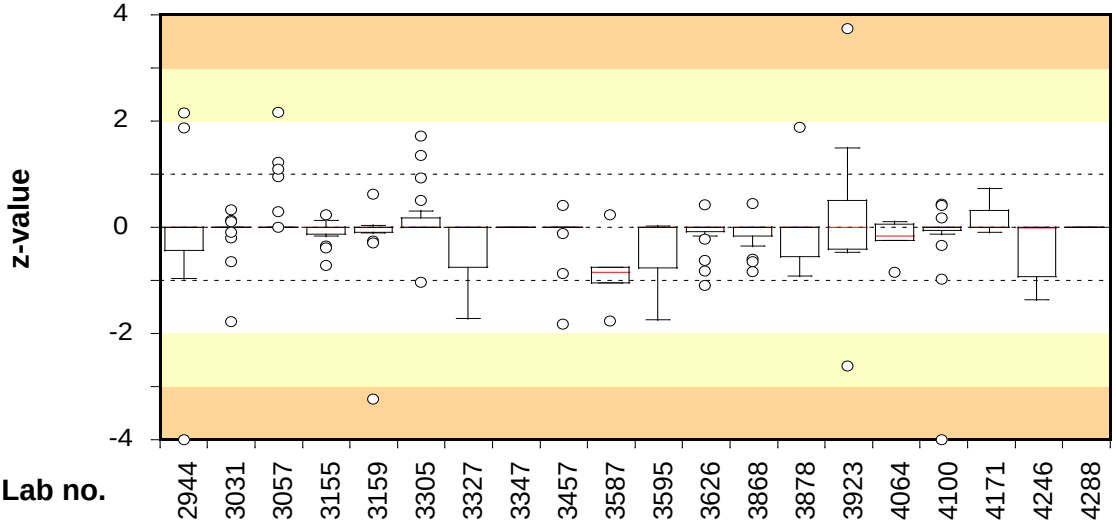
Box plots and numbers of deviating results for each laboratory

- *Z-scores are calculated according to the formula: z = (x-m)/s, where x is the result of the individual laboratory, m is the mean of the results of all participating laboratories, and s is the standard deviation of the participating laboratories, after removing outliers and false results.*
- *Outliers are included in the figures after being calculated to z-scores in the same way as for other results.*
- *False results do not generate any z-scores, and are not included in "No. of results".*
- *Correct results for qualitative analyses and correct negative results for quantitative analyses without target organism generate a z-score of 0.*
- *The laboratory median value is illustrated by a horizontal red line in the box.*
- *The box includes 50 % of a laboratory's results (25 % of the results above the median and 25 % of the results below the median). The remaining 50 % are illustrated by lines and circles outside the box.*
- *A circle is for technical reasons shown in the plot when a value deviates to certain degree* from the other values. This does not by itself indicate that the value is an outlier.*
- *z-scores >+4 and <−4 are positioned at +4 and −4, respectively, in the plot.*
- *The background is divided by lines and shaded fields to simplify identifying the range in which the results are located.*

* *< [lowest value in the box −1,5 × (highest value in the box− lowest value in the box)]* <u>or</u>
> [highest value in the box + 1,5 × (highest value in the box − lowest value in the box)].



	1254	1545	1594	1970	2035	2043	2050	2058	2072	2151	2221	2324	2386	2402	2637	2704	2745	2764	2842	2920
No. of results	15	15	12	24	15	3	9	12	23	18	15	5	9	9	15	15	15	14	19	9
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	1	-	-	1	-	-	-	-	-	-	2	-
Low outliers	-	-	-	-	2	-	-	2	-	-	-	-	-	1	-	-	1	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



Lab no.	2944	3031	3057	3155	3159	3305	3327	3347	3457	3587	3595	3626	3868	3878	3923	4064	4100	4171	4246	4288
No. of results	12	18	23	15	15	21	15	3	14	6	17	19	21	5	10	6	15	12	12	-
False positive	-	-	1	-	-	-	-	-	-	-	1	-	-	-	1	-	-	-	-	-
False negative	-	-	3	-	-	-	-	-	1	-	-	-	-	1	1	-	-	-	-	-
Low outliers	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
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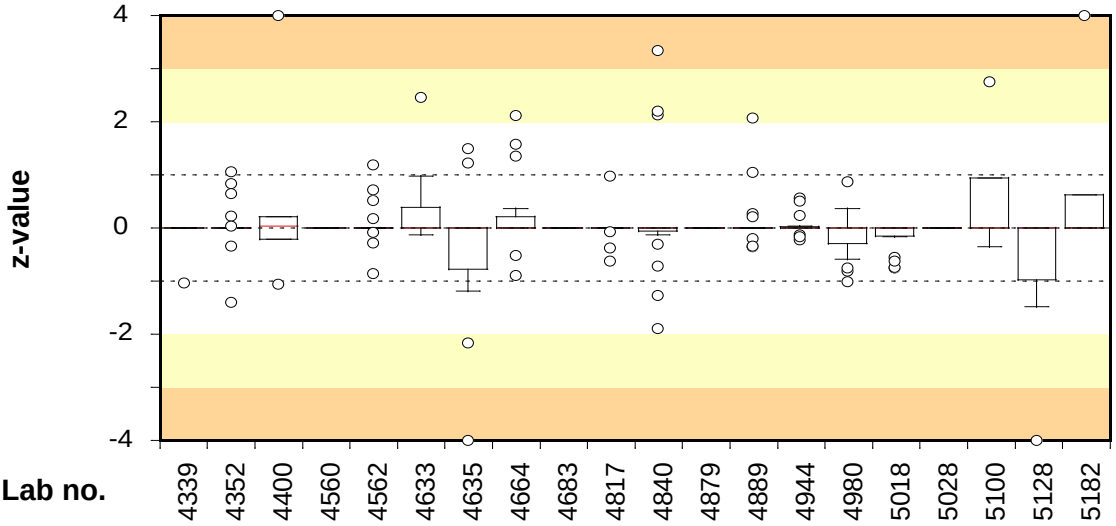
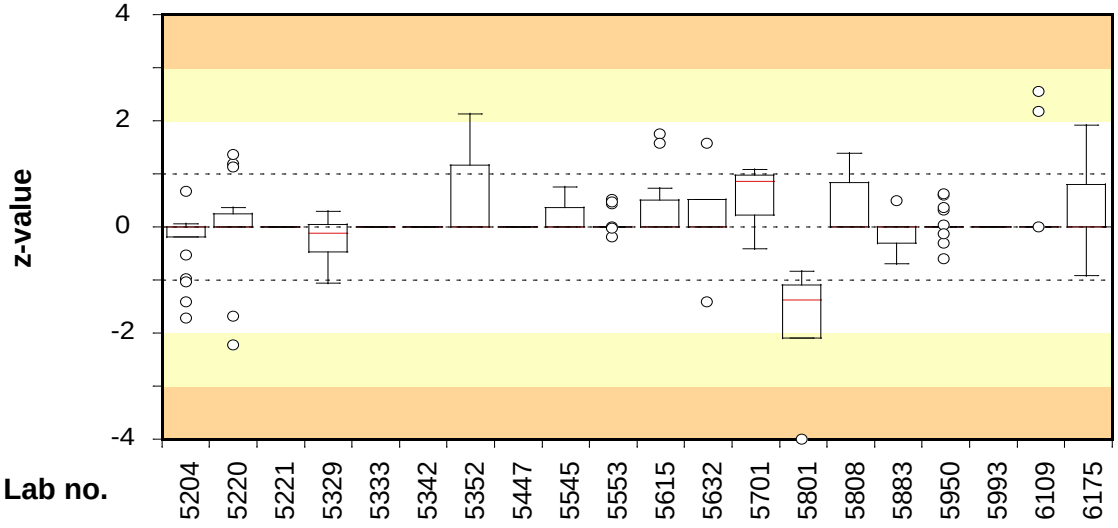
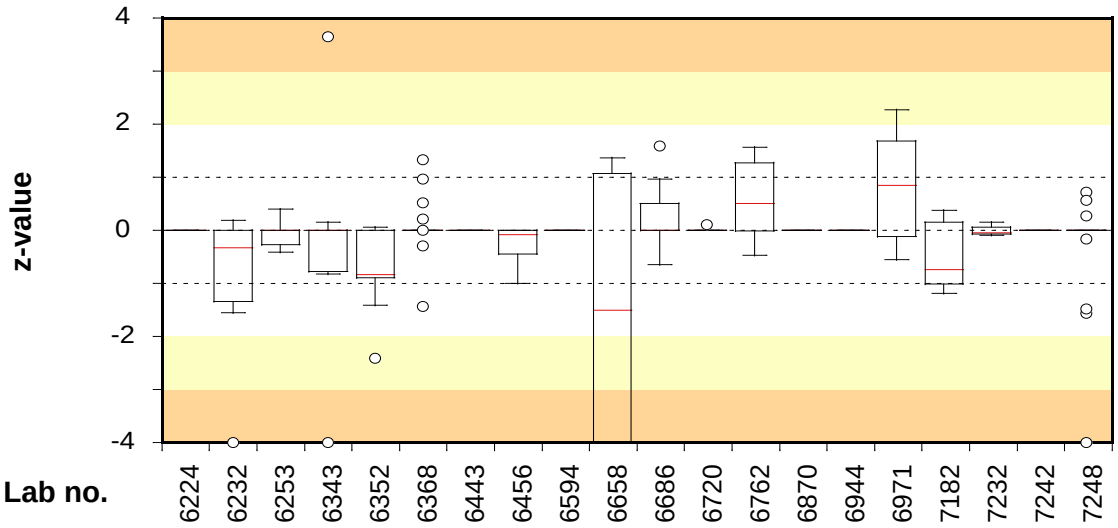


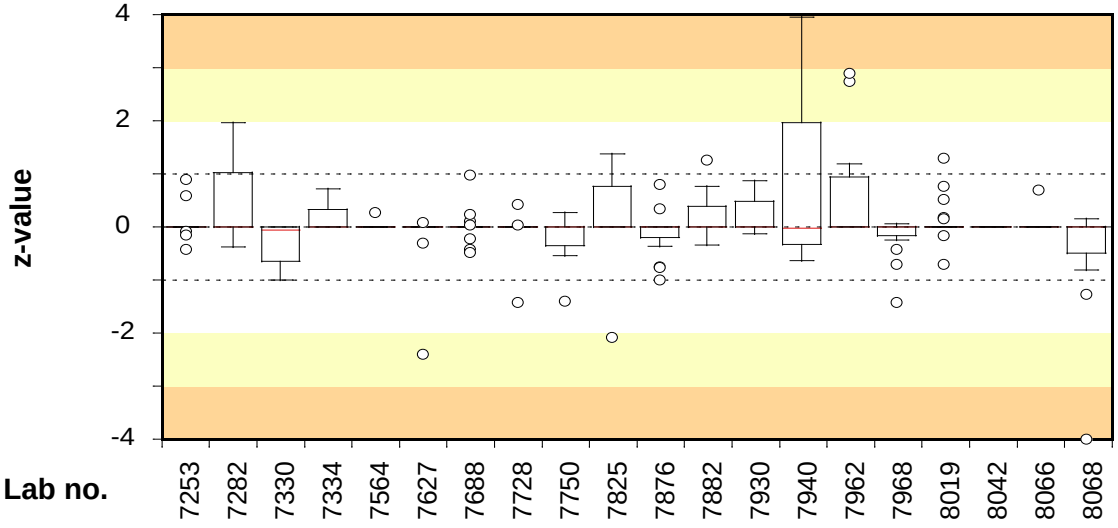
Lab no.	4339	4352	4400	4560	4562	4633	4635	4664	4683	4817	4840	4879	4889	4944	4980	5018	5028	5100	5128	5182
No. of results	15	24	5	6	27	15	12	18	-	21	20	-	18	15	15	21	3	6	9	5
False positive	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
False negative	-	-	1	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Low outliers	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-
High outliers	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1



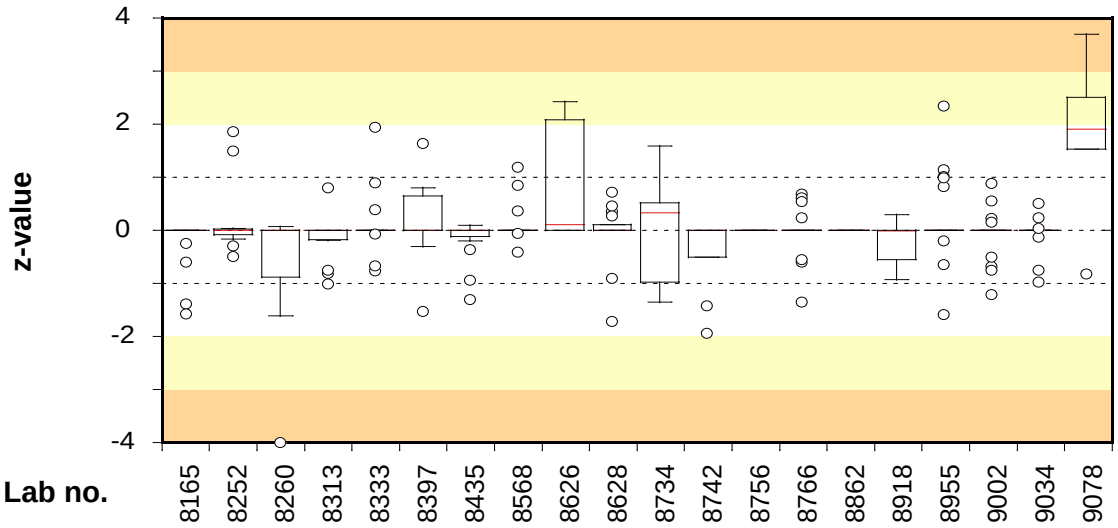
Lab no.	5204	5220	5221	5329	5333	5342	5352	5447	5545	5553	5615	5632	5701	5801	5808	5883	5950	5993	6109	6175
No. of results	21	15	-	6	6	-	15	3	8	20	12	5	3	6	6	14	30	3	9	11
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	-	-	1
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



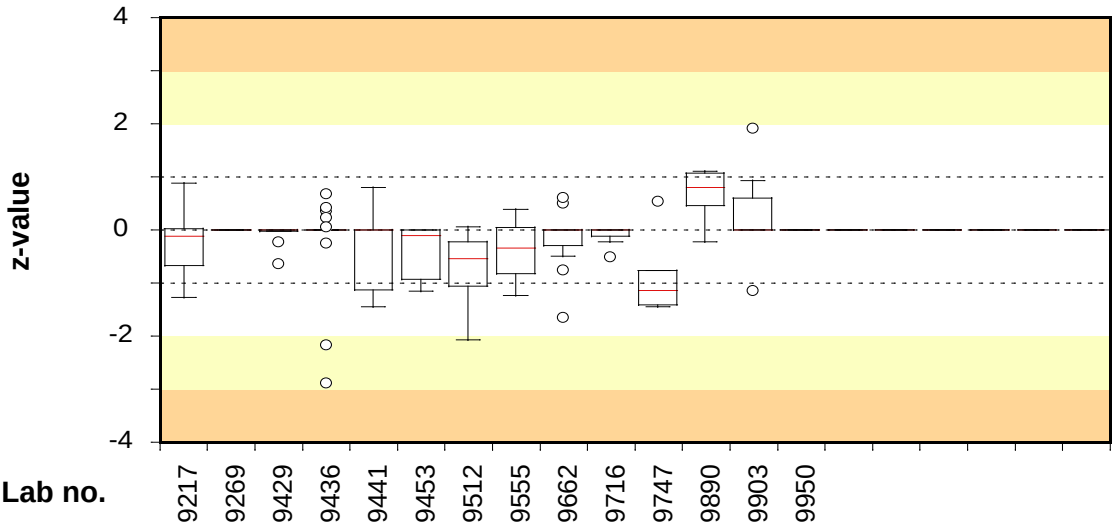
Lab no.	6224	6232	6253	6343	6352	6368	6443	6456	6594	6658	6686	6720	6762	6870	6944	6971	7182	7232	7242	7248
No. of results	-	8	12	12	9	18	3	12	-	6	14	9	5	3	3	6	6	3	-	17
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
False negative	-	1	-	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-
Low outliers	-	1	-	2	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	1
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



Lab no.	7253	7282	7330	7334	7564	7627	7688	7728	7750	7825	7876	7882	7930	7940	7962	7968	8019	8042	8066	8068
No. of results	18	9	12	8	6	9	24	12	9	15	15	8	15	3	15	17	24	3	9	15
False positive	-	-	-	1	-	-	-	-	1	-	-	-	-	-	-	1	-	-	-	-
False negative	-	-	-	-	-	-	-	-	2	-	-	1	-	-	-	-	-	-	-	-
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-



Lab no.	8165	8252	8260	8313	8333	8397	8435	8568	8626	8628	8734	8742	8756	8766	8862	8918	8955	9002	9034	9078
No. of results	21	12	15	15	15	12	15	14	11	18	6	9	-	18	3	12	30	17	15	6
False positive	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	1	-	-
False negative	-	-	-	-	-	-	-	1	2	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1



Lab no.	9217	9269	9429	9436	9441	9453	9512	9555	9662	9716	9747	9890	9903	9950
No. of results	7	3	9	24	15	12	6	6	15	12	6	6	11	-
False positive	1	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	1	-	-	-	-	-	-	-	-	-	-	-	1	-
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Test material and quality control

Test material

Each laboratory received three manufactured freeze-dried microbial mixtures, designated A-C. The test material was freeze-dried in portions of 0.5 ml in vials, as described by Peterz and Steneryd (5). Before analysing the samples, the contents of each vial had to be dissolved in 254 ml of sterile diluent. The organisms present in the mixtures are listed in Table 2.

Table 2. *Microorganisms present in mixtures A-C.*

Mixture[1]	Microorganism	Strain	
		SLV[2]	Reference[3]
A	*Campylobacter jejuni*	SLV-540	chicken, 2003
	Proteus mirabilis	SLV-374	CCUG 43605
	Salmonella Enteritidis	SLV-436	-
	Vibrio parahaemolyticus	SLV-529	CCUG 38981
B	*Escherichia coli*	SLV-558	-
	Kocuria rhizophila	SLV-055	ATCC 9341
	Salmonella Stockholm	SLV-390	chocolate powder
	Yersinia enterocolitica	SLV-408	CCUG 45643
C	*Escherichia coli O157*	SLV-528	CCUG 47557
	Hafnia alvei	SLV-015	CCUG 45642
	Listeria monocytogenes	SLV-361	raw spiced salmon
	Staphylococcus saprophyticus	SLV-013	CCUG 45100
	Vibrio cholerae	SLV-507	CCUG 34649
	Yersinia intermedia	SLV-472	CCUG 39927

[1] The links between the mixtures and the randomised sample numbers are shown in Annex 1.
[2] Internal strain identification no. at the National Food Agency.
[3] Origin or culture collection (CCUG: Culture Collection University of Gothenburg, Sweden ; ATCC: American Type Culture Collection)

Quality control of the mixtures

It is essential to have aliquots of homogeneous mixture and equal volume in all vials in order to allow comparison of all freeze-dried samples from one mixture. Quality control is performed on 10 randomly chosen vials in conjunction with manufacturing of the mixtures or on 5 vials if an "old" mixture was used and the last quality control was performed more than 6 months ago. Homogeneity of a mixture is approved if, for each analysis, the values obtained for the test of reproducibility (T) and the test "Index of dispersion" between vials (I_2) do not simultaneously exceed 2.6 and 2.0, respectively. (For definitions of T and I_2, see references 6 and 7 respectively.)

Table 3. *Concentration mean (m), T and I_2 values from the quality control of the mixtures; m is expressed in log_{10} cfu (colony forming units) per ml of sample.*

Analysis and method	A[1]			B[1]			C[2]		
	m	**T**	**I_2**	**m**	**T**	**I_2**	**m**	**T**	**I_2**
Aerobic microorganisms 30 ˚C NMKL method no. 86	4.316	1.39	0.573	4.546	1.36	0.931	4.910	1.44	2.733
Enterobacteriaceae NMKL method no. 144	4.308	1.14	0.839	4.207	1.61	5.164	4.542	1.43	1.088
Thermotolerant *Campylobacter*, quant. NMKL method no. 119	2.595	1.29	0.613	-	-	-	-	-	-
Thermotolerant *Campylobacter*, qual. NMKL method no. 119	Pos.	-	-	Neg.	-	-	Neg.	-	-
Listeria monocytogenes, quant. NMKL method no. 136	-	-	-	-	-	-	2.461	1.53	1.313
Listeria monocytogenes, qual. NMKL method no. 136	Neg.	-	-	Neg.	-	-	Pos.	-	-
Salmonella NMKL method no. 71	2.060	1.49	0.121	0.660	1.27	0.803	Neg.	-	-
Escherichia coli O157 NMKL method no. 164	Neg.	-	-	Neg.	-	-	0.810	1.24	0.936
Pathogenic *Vibrio* spp. NMKL method no. 156	2.621	1.36	0.233	Neg.	-	-	3.276	1.37	11.786
Yersinia enterocolitica NMKL method no. 117	Neg.	-	-	1.513	1.18	0.553	0.707	1.29	2.021

– No target organism and therefore no value
[1] n = 5 vials analysed in duplicate
[2] n = 10 vials analysed in duplicate

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4. Anonymous, 2015. Protocol, Microbiology. Drinking Water & Food, The National Food Agency, Sweden.
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Annex 1 ***Results of the participating laboratories - January 2018***

All results are in log_{10} cfu per ml sample. Results reported as "< value" have been regarded as zero. Results reported as "> value" are exluded from the calculations. A dash indicates the analysis was not performed. Outliers and false results are highlighted and summarized for each analysis at the end of the table

Lab no.	Vial	Aerobic micro-organisms 30 °C			Enterobacteriaceae			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			*Salmonella*			*Escherichia coli* O157 (VT-neg)			Pathogenic *Vibrio* spp.			*Yersinia enterocolitica*			Lab no.
	A B C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
1254	1 3 2	4.18	4.41	4.57	3.91	4.04	3.93	-	-	-	<1	<1	2.45	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	**1254**
1545	3 2 1	4.28	4.76	5.04	4.19	4.54	4.69	-	-	-	<0	<0	2.48	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	**1545**
1594	3 1 2	4.23	4.6	4.94	4.2	4.34	4.53	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	**1594**
1970	3 1 2	4.11	4.45	4.95	3.79	4.52	4.52	1.97	<1	<1	<1	<1	2.38	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	Pos	Neg	Pos	-	-	-	**1970**
2035	3 1 2	-	-	-	**2**	**3.5**	3.5	-	-	-	<1	<1	2.3	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	Pos	Neg	Pos	Neg	Pos	Neg	**2035**
2043	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2043**
2050	3 2 1	4.15	4.43	4.84	4.09	4.24	4.33	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2050**
2058	1 2 3	**3.1**	4.06	**3.78**	-	-	-	-	-	-	<1	<1	2.4	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2058**
2072	2 1 3	4.23	4.65	4.79	4.11	4.34	4.48	0.95	<1	<1	<1	<1	2.08	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	**Neg**	Neg	Pos	-	-	-	**2072**
2151	1 3 2	4.53	4.45	4.65	-	-	-	2.2	0	0	0	0	2.46	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2151**
2221	2 3 1	4.43	4.4	4.7	4.38	4.05	4.2	-	-	-	<2	<2	2.44	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2221**
2324	1 3 2	4.18	4.45	4.82	**<1**	4.17	4.47	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**2324**
2386	3 1 2	4.28	4.4	4.91	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2386**
2402	1 2 3	4.34	5.08	4.96	**1.9**	4.72	4.34	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2402**
2637	3 1 2	4.22	4.53	4.71	4.2	4.27	4.23	-	-	-	<1	<1	2.58	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2637**
2704	2 3 1	4.38	4.45	4.88	3.9	4.16	4.57	-	-	-	<1	<1	2.46	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2704**
2745	1 2 3	4.15	4.41	4.72	4.17	4.19	4.41	-	-	-	0	0	**1.34**	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2745**
2764	3 1 2	-	4.71	4.79	4.11	3.97	4	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**2764**
2842	3 1 2	-	-	-	-	-	-	**<1**	<1	<1	<1	<1	2.28	Pos	Neg	Neg	Neg	Neg	Pos	-	-	-	Neg	Neg	Pos	Pos	Neg	Pos	Neg	**Neg**	Neg	**2842**
2920	2 1 3	4.19	4.68	4.98	4.1	4.4	4.61	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2920**
2944	2 3 1	4.14	4.97	5.14	**3.15**	4.16	4.12	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**2944**
3031	2 3 1	4.2	4.11	4.86	4.11	4.08	4.32	-	-	-	<1	<1	2.43	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	Pos	Neg	Pos	-	-	-	**3031**
3057	3 1 2	4.23	4.6	5	4.57	4.36	4.6	-	-	-	<1	<1	**<1**	Pos	Neg	Neg	Neg	Neg	**Neg**	Pos	Pos	**Pos**	Neg	Neg	Pos	Pos	Neg	**Neg**	Neg	Pos	Neg	**3057**
3155	1 2 3	4.25	4.49	4.76	4.06	4.13	4.18	-	-	-	0	0	2.45	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**3155**
3159	3 2 1	4.22	4.47	4.77	3.36	4.2	4.32	-	-	-	<1	<1	2.49	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**3159**
3305	3 2 1	4.46	4.57	4.86	4.2	4.43	4.56	-	-	-	0	0	2.3	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**3305**
3327	2 1 3	4	4.36	4.63	3.91	3.9	4.28	-	-	-	0	0	2.37	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**3327**
3347	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**3347**
3457	1 2 3	-	-	-	4.06	4.04	4.44	-	-	-	0	0	2.21	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	**Neg**	Neg	Pos	-	-	-	**3457**
3587	2 3 1	4.09	4.35	4.7	3.69	4.03	4.4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**3587**
3595	2 1 3	4.19	4.35	4.65	3.95	4.04	4.35	1.28	<1	<1	<1	<1	2.22	-	-	-	Neg	Neg	Pos	Pos	Pos	**Pos**	-	-	-	-	-	-	-	-	-	**3595**
3626	2 1 3	4.2	-	-	3.9	4	4.2	2.1	<1	<1	<1	<1	2.4	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**3626**
3868	1 2 3	4.15	4.39	4.76	4.08	4.08	4.15	2.11	0	0	0	0	2.4	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**3868**
3878	2 1 3	4.16	4.97	4.68	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	**Neg**	Neg	-	-	-	-	-	-	-	-	-	**3878**
3923	3 1 2	4.43	5.41	4.89	3.5	4.11	4.25	-	-	-	-	-	-	-	-	-	-	-	-	Pos	**Neg**	**Pos**	-	-	-	Pos	Neg	Pos	-	-	-	**3923**
4064	2 3 1	4.2	4.33	4.8	4.1	4.15	4.37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4064**
4100	2 3 1	4.1	4.5	4.84	**2**	4.27	4.44	-	-	-	<1	<1	2.38	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4100**
4171	2 1 3	4.3	4.56	4.8	4.11	4.32	4.49	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**4171**
4246	3 1 2	4.21	4.21	4.63	4.08	4.05	4.1	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4246**
4288	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4288**
4339	2 3 1	-	-	-	-	-	-	-	-	-	<1	<1	2.3	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	Neg	Pos	Neg	**4339**
4352	1 3 2	4.26	4.2	4.94	4.23	4.2	4.59	-	-	-	<1	<1	2.38	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	Pos	Neg	Pos	-	-	-	**4352**
4400	2 1 3	**4.78**	4.48	4.82	**0**	4.23	4.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4400**
4560	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4560**
4562	1 2 3	4.3	4.51	4.84	**<2**	4.4	4.28	1.47	<1	<1	<1	<1	2.5	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	**Neg**	Pos	Neg	Pos	Neg	Pos	**Pos**	**4562**
4633	1 3 2	4.23	4.76	4.89	4.15	4.17	4.52	-	-	-	<1	<1	2.7	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4633**
4635	3 1 2	3.94	4.88	5	**1.78**	4.13	4.07	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4635**
4664	3 1 2	4.11	4.58	4.87	4.56	4.43	4.71	-	-	-	0	0	2.36	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	Pos	Neg	Pos	-	-	-	**4664**
4683	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4683**
4817	3 1 2	4.18	4.76	4.72	-	-	-	-	-	-	<1	<1	2.41	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	Pos	Neg	Pos	Neg	Pos	Neg	**4817**
4840	1 3 2	4.06	4.5	5.32	3.66	4.14	4.84	1.54	<1	<1	<1	<1	2.67	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	**Pos**	-	-	-	-	-	-	-	-	-	**4840**
4879	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4879**
4889	1 3 2	4.2	4.45	4.97	4.15	4.23	4.83	-	-	-	0	0	2.38	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	Pos	Neg	Pos	-	-	-	**4889**
4944	3 1 2	4.2	4.5	4.9	4.2	4.2	4.4	-	-	-	<0	<0	2.4	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4944**
4980	2 3 1	4.28	4.34	4.7	4.28	4.09	4.11	-	-	-	<1	<1	2.44	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**4980**
m		4.230	4.529	4.814	4.085	4.193	4.345	1.890	0	0	0	0	2.418	pos	neg	neg	neg	neg	pos	pos	pos	neg	neg	neg	pos	pos	neg	pos	neg	pos	neg	**m**
s		0.134	0.235	0.152	0.224	0.175	0.232	0.492	0	0	0	0	0.114	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**s**

Lab no.	Vial	Aerobic micro-organisms 30 °C			Enterobacteriaceae			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			*Salmonella*			*Escherichia coli* O157 (VT-neg)			Pathogenic *Vibrio* spp.			*Yersinia enterocolitica*			Lab no.
	A B C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
5018	2 3 1	4.13	4.4	4.79	3.92	4.18	4.2	-	-	-	<1	<1	2.4	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	Neg	Pos	Neg	**5018**
5028	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Pos	Neg	**5028**
5100	3 2 1	4.6	4.75	4.76	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5100**
5128	2 3 1	**3.36**	4.3	4.59	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5128**
5182	1 2 3	-	-	-	**<2**	**5.02**	4.49	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5182**
5204	3 1 2	4	4.3	4.6	4.1	4.1	4.5	1.8	<1	<1	<1	<1	2.3	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5204**
5220	2 3 1	4.39	4.56	4.56	4.39	4.39	3.83	-	-	-	0	0	2.46	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5220**
5221	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5221**
5329	2 3 1	4.23	4.54	4.78	4.15	4.11	4.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5329**
5333	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5333**
5342	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5342**
5352	1 2 3	4.39	4.91	5.03	4.34	4.36	4.84	-	-	-	<1	<1	2.49	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5352**
5447	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Neg	Neg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5447**
5545	2 3 1	-	-	-	>1	4.32	4.52	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5545**
5553	3 1 2	4.3	4.53	4.88	4.19	4.16	4.34	-	<1	<1	-	-	-	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**5553**
5615	2 3 1	4.23	4.54	5.08	4.15	4.32	4.71	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5615**
5632	3 1 2	4.3	4.9	4.6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**Neg**	Pos	Neg	-	-	-	-	-	-	-	-	-	**5632**
5701	1 3 2	4.18	4.73	4.98	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5701**
5801	2 3 1	3.95	4.2	4.61	**2.9**	4	4.15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5801**
5808	3 2 1	4.23	4.86	4.94	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5808**
5883	3 1 2	4.19	4.39	4.79	**<2**	4.13	4.46	-	-	-	0	0	2.34	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5883**
5950	2 3 1	4.19	4.39	4.82	4.22	4.17	4.42	2.2	<1	<1	<1	<1	2.46	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	Pos	Neg	Pos	Neg	Pos	Neg	**5950**
5993	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**5993**
6109	3 1 2	4.23	5.04	5.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**6109**
6175	3 1 2	4.22	4.98	4.95	3.88	4.5	4.51	-	-	-	-	-	-	-	-	-	Neg	Neg	**Neg**	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6175**
6224	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**6224**
6232	1 3 2	4.26	4.4	4.58	**2.65**	4	4.32	-	-	-	-	-	-	-	-	-	-	-	-	Pos	**Neg**	Neg	-	-	-	-	-	-	-	-	-	**6232**
6253	1 2 3	4.18	4.59	4.76	4.18	4.15	4.28	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6253**
6343	3 1 2	4.72	**2.46**	4.69	3.92	**2.19**	4.38	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6343**
6352	1 2 3	4.11	4.33	4.6	4.1	3.77	4.15	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6352**
6368	1 3 2	4.23	4.46	4.89	4.3	4.23	4.65	-	-	-	<1	<1	2.26	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	Pos	Neg	Pos	-	-	-	**6368**
6443	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6443**
6456	1 3 2	4.21	4.43	4.78	3.86	4.11	4.19	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6456**
6594	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**6594**
6658	2 3 1	4.04	4.85	**3.6**	3.73	4.38	**2.47**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**6658**
6686	2 3 1	4.36	4.56	4.92	4.2	4.08	4.36	-	-	-	<1	<1	2.6	-	-	-	Neg	Neg	Pos	**Neg**	Pos	Neg	-	-	-	-	-	-	-	-	-	**6686**
6720	2 3 1	-	-	-	-	-	-	-	-	-	<1	<1	2.43	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**6720**
6762	1 3 2	4.44	4.42	4.89	4.37	4.19	**<1**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**6762**
6870	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	-	-	-	-	-	-	**6870**
6944	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	-	-	-	-	-	-	**6944**
6971	3 2 1	4.35	4.4	5.07	4.06	4.59	4.53	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**6971**
7182	2 3 1	4.25	4.25	4.66	4.17	4.02	4.23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**7182**
7232	3 2 1	4.25	4.52	4.8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**7232**
7242	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**7242**
7248	1 3 2	4.02	4.7	4.9	**2.78**	4.24	4	-	-	-	<1	<1	2.4	Pos	**Pos**	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7248**
7253	1 2 3	4.35	4.51	4.79	-	-	-	2.18	<1	<1	<1	<1	2.37	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7253**
7282	3 1 2	4.18	4.99	4.97	4.01	4.3	4.67	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	-	-	-	-	-	-	**7282**
7330	1 2 3	4.1	4.4	4.7	3.86	4.1	4.32	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7330**
7334	2 3 1	4.27	4.62	4.92	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	Neg	**Pos**	Pos	-	-	-	-	-	-	**7334**
7564	2 3 1	-	-	-	-	-	-	-	-	-	<0	<0	2.45	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	-	-	-	-	-	-	**7564**
7627	1 2 3	4.19	4.55	4.45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**7627**
7688	2 1 3	4.2	4.43	4.74	4.11	4.2	4.4	-	-	-	<1	<1	2.53	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	Neg	Pos	Neg	**7688**
7728	2 3 1	4.04	4.63	4.82	-	-	-	-	-	-	-	-	-	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7728**
7750	2 3 1	4.23	4.2	4.76	4.13	4.24	4.22	-	-	-	-	-	-	-	-	-	-	-	-	Pos	**Neg**	Neg	Neg	**Pos**	**Neg**	-	-	-	-	-	-	**7750**
7825	1 2 3	4.33	4.82	4.93	4.35	3.83	4.38	-	-	-	<1	<1	2.58	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7825**
7876	1 2 3	4.13	4.61	4.81	3.86	4.06	4.26	-	-	-	<1	<1	2.51	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7876**
7882	2 3 1	4.4	4.45	4.93	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	**Neg**	Neg	-	-	-	-	-	-	-	-	-	**7882**
7930	3 2 1	4.32	4.5	4.88	4.28	4.3	4.32	-	-	-	<1	<1	2.48	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7930**
7940	3 1 2	**4.76**	4.38	4.81	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**7940**
7962	2 1 3	4.24	4.61	4.99	4.7	4.7	4.62	-	-	-	0	0	2.5	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7962**
m		4.230	4.529	4.814	4.085	4.193	4.345	1.890	0	0	0	0	2.418	pos	neg	neg	neg	neg	pos	pos	pos	neg	neg	neg	pos	pos	neg	pos	neg	pos	neg	**m**
s		0.134	0.235	0.152	0.224	0.175	0.232	0.492	0	0	0	0	0.114	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**s**

Lab no.	Vial	Aerobic micro-organisms 30 °C			Enterobacteriaceae			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			*Salmonella*			*Escherichia coli* O157 (VT-neg)			Pathogenic *Vibrio* spp.			*Yersinia enterocolitica*			Lab no.
	A B C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
7968	2 1 3	4.04	4.52	4.75	4.03	4.07	4.36	-	-	-	<1	<1	2.4	Pos	**Pos**	Neg	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**7968**
8019	3 2 1	4.3	4.71	4.84	4.12	4.42	4.18	-	-	-	<1	<1	2.4	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	Pos	Neg	Pos	-	-	-	**8019**
8042	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8042**
8066	1 2 3	-	-	-	-	-	-	-	-	-	<1	<1	2.5	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8066**
8068	2 1 3	4.06	4.4	4.76	3.99	4.05	4.38	-	-	-	0	0	**1.86**	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8068**
8165	2 3 1	-	-	-	3.95	3.95	3.98	1.77	<1	<1	-	-	-	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	Neg	Pos	Neg	**8165**
8252	2 3 1	4.48	4.49	4.77	4.42	4.2	4.23	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8252**
8260	3 1 2	4.24	4.34	4.67	**1.75**	3.98	3.97	-	-	-	<1	<1	2.4	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8260**
8313	1 2 3	4.21	4.34	4.7	4.06	4.16	4.11	-	-	-	0	0	2.51	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8313**
8333	2 3 1	4.49	4.62	4.95	4.07	4.06	4.19	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**8333**
8397	3 1 2	4.45	4.17	4.9	4.25	4.14	4.53	-	-	-	<1	<1	2.43	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	-	-	-	-	-	-	**8397**
8435	3 2 1	4.23	4.45	4.67	4.11	4.16	4.04	-	-	-	0	0	2.43	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8435**
8568	1 2 3	4.39	4.73	4.87	**<2**	4.12	4.33	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**8568**
8626	1 3 2	4.51	5.1	5.09	4.11	4.56	4.83	-	-	-	**2.13**	0	**0**	-	-	-	**Pos**	Neg	**Neg**	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8626**
8628	1 3 2	4.33	4.13	4.87	4.15	4.03	4.37	-	-	-	0	0	2.47	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	Pos	Neg	Pos	**8628**
8734	1 3 2	4.3	4.3	4.61	4.44	4.23	4.45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8734**
8742	3 2 1	4.04	4.41	4.52	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8742**
8756	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8756**
8766	3 1 2	4.15	4.69	4.85	3.96	4.3	4.03	-	-	-	0	0	2.48	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	Neg	Pos	Neg	**8766**
8862	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**8862**
8918	1 2 3	4.17	4.32	4.81	4.15	4.08	4.13	-	-	-	0	0	2.41	-	-	-	Neg	Neg	Pos	-	-	-	-	-	-	-	-	-	-	-	-	**8918**
8955	1 2 3	4.2	4.16	4.94	4.34	4.08	4.58	3.04	<2	<2	<1	<1	2.53	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	Pos	Neg	Pos	Neg	Pos	Neg	**8955**
9002	1 2 3	4.26	4.37	4.7	4.21	3.98	4.38	1.64	**4.13**	0	0	0	2.52	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**9002**
9034	2 1 3	4.1	4.5	4.7	4.2	4.2	4.4	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	Neg	Pos	Neg	**9034**
9078	2 1 3	4.48	5.12	5.11	3.9	**4.84**	4.7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9078**
9217	3 2 1	4.06	4.35	4.82	4.06	4.09	4.55	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	**Pos**	**Neg**	-	-	-	-	-	-	**9217**
9269	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**9269**
9429	3 1 2	4.2	4.38	4.81	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**9429**
9436	3 1 2	4.28	4.69	4.85	3.6	4.15	4.36	2.1	<1	<1	<1	<1	2.09	Pos	Neg	Neg	Neg	Neg	Pos	Pos	Pos	Neg	Neg	Neg	Pos	-	-	-	-	-	-	**9436**
9441	1 3 2	4.08	4.43	4.62	3.82	3.94	4.08	-	-	-	<1	<1	2.51	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**9441**
9453	1 2 3	4.08	4.31	4.64	4.04	4.14	4.13	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**9453**
9512	3 2 1	4.2	4.4	4.5	4.1	4.1	4.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9512**
9555	2 3 1	4.12	4.54	4.8	3.81	4.26	4.21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9555**
9662	3 2 1	4.18	4.48	4.7	4.2	4.3	4.23	-	-	-	<1	<1	2.23	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	-	-	-	**9662**
9716	1 3 2	4.2	4.41	4.78	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	Pos	Pos	Neg	-	-	-	-	-	-	Pos	Neg	Pos	**9716**
9747	2 3 1	4.06	4.29	4.6	3.76	4.06	4.47	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9747**
9890	2 1 3	4.2	4.79	4.91	4.3	4.38	4.45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9890**
9903	2 3 1	4.29	4.63	4.93	3.83	4.53	4.56	-	-	-	-	-	-	-	-	-	Neg	Neg	Pos	**Neg**	Pos	Neg	-	-	-	-	-	-	-	-	-	**9903**
9950	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9950**
N		120	120	120	104	105	105	16	17	17	67	67	67	25	25	25	98	98	98	114	114	114	24	24	24	19	19	19	14	14	14	**N**
Min		3.1	2.46	3.6	0	2.19	0	0	0	0	0	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**Min**
Max		4.78	5.41	5.32	4.7	5.02	4.84	3.04	4.13	0	2.13	0	2.7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**Max**
Med		4.22	4.49	4.81	4.11	4.16	4.36	1.97	0	0	0	0	2.43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**Med**
m		4.230	4.529	4.814	4.085	4.193	4.345	1.890	0	0	0	0	2.418	pos	neg	neg	neg	neg	pos	pos	pos	neg	neg	neg	pos	pos	neg	pos	neg	pos	neg	**m**
s		0.134	0.235	0.152	0.224	0.175	0.232	0.492	0	0	0	0	0.114	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**s**
F+		0	0	0	0	0	0	0	1	0	1	0	0	0	2	0	1	0	0	0	0	4	0	3	0	0	0	0	0	0	1	**F+**
F-		0	0	0	6	0	1	1	0	0	0	0	2	0	0	0	0	0	3	3	5	0	0	0	3	2	0	1	0	1	0	**F-**
<		2	1	2	9	2	1	0	0	0	0	0	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**<**
>		2	0	0	0	2	0	0	0	0	0	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**>**
< OK		3.94	4.06	4.45	3.36	3.77	3.50	0.95	0	0	0	0	2.08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**< OK**
> OK		4.72	5.41	5.32	4.70	4.72	4.84	3.05	0	0	0	0	2.70	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**> OK**

N = number of analyses performed
Min = lowest reported result
Max = highest reported result
Median = median value
m = mean value
s = standard deviation
F+ = false positive
F- = false negative
< = low outlier
> = high outlier
< OK = lowest accepted value
>OK = highest accepted value

Annex 2 Z-scores of all participants - January 2018

Z-scores are calculated according to the formula: z = (x-m)/s, where x = result of the individual laboratory, m = mean of the results of all participating laboratories, s = standard deviation of the results from all participating laboratories. Correct negative results in quantitative analyses and correct results in qualitative analyses have obtained a z-score of zero. False results did not generate a z-score. Z-scores from outliers are not real z-scores, but are a practical means to express the results from the outliers. Very low and high z-scores are here limited to -4 and +4 respectively.

2 < |z| ≤ 3, |z|>3

Lab no.	Vial			Aerobic micro-organisms 30 °C			Enterobacteriaceae			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			*Salmonella*			*Escherichia coli* O157 (VT-neg)			Pathogenic *Vibrio* spp.			*Yersinia enterocolitica*			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
1254	1	3	2	-0.374	-0.509	-1.609	-0.781	-0.871	-1.786				0.000	0.000	0.277				0	0	0	0	0	0										**1254**
1545	3	2	1	0.372	0.981	1.492	0.469	1.982	1.489				0.000	0.000	0.540				0	0	0	0	0	0										**1545**
1594	3	1	2	-0.001	0.300	0.833	0.514	0.841	0.799													0	0	0	0	0	0							**1594**
1970	3	1	2	-0.896	-0.338	0.899	-1.317	1.868	0.756	0.163	0.000	0.000	0.000	0.000	-0.336	0	0	0	0	0	0	0	0	0				0	0	0				**1970**
2035	3	1	2				**-4.000**	**-3.952**	**-3.639**				0.000	0.000	-1.037				0	0	0							0	0	0	0	0	0	**2035**
2043	3	2	1																			0	0	0										**2043**
2050	3	2	1	-0.598	-0.423	0.173	0.023	0.270	-0.063													0	0	0										**2050**
2058	1	2	3	**-4.000**	-1.998	**-4.000**							0.000	0.000	-0.161				0	0	0	0	0	0										**2058**
2072	2	1	3	-0.001	0.513	-0.157	0.112	0.841	0.584	-1.912	0.000	0.000	0.000	0.000	**-2.964**	0	0	0	0	0	0	0	0	0					0	0				**2072**
2151	1	3	2	**2.237**	-0.338	-1.081				0.630	0.000	0.000	0.000	0.000	0.365	0	0	0	0	0	0	0	0	0										**2151**
2221	2	3	1	1.491	-0.551	-0.751	1.317	-0.814	-0.623				0.000	0.000	0.189				0	0	0	0	0	0										**2221**
2324	1	3	2	-0.374	-0.338	0.041		-0.129	0.541																									**2324**
2386	3	1	2	0.372	-0.551	0.635													0	0	0	0	0	0										**2386**
2402	1	2	3	0.820	**2.343**	0.965	**-4.000**	**3.009**	-0.020													0	0	0										**2402**
2637	3	1	2	-0.076	0.002	-0.685	0.514	0.442	-0.494				0.000	0.000	1.416				0	0	0	0	0	0										**2637**
2704	2	3	1	1.118	-0.338	0.437	-0.826	-0.186	0.972				0.000	0.000	0.365				0	0	0	0	0	0										**2704**
2745	1	2	3	-0.598	-0.509	-0.619	0.380	-0.015	0.282				0.000	0.000	**-4.000**				0	0	0	0	0	0										**2745**
2764	3	1	2		0.768	-0.157	0.112	-1.270	-1.485										0	0	0	0	0	0	0	0	0							**2764**
2842	3	1	2								0.000	0.000	0.000	0.000	-1.212	0	0	0	0	0	0				0	0	0	0	0	0	0		0	**2842**
2920	2	1	3	-0.299	0.641	1.097	0.067	1.183	1.144													0	0	0										**2920**
2944	2	3	1	-0.672	1.875	**2.152**	**-4.000**	-0.186	-0.968										0	0	0	0	0	0										**2944**
3031	2	3	1	-0.194	-1.768	0.327	0.129	-0.647	-0.096				0.000	0.000	0.114				0	0	0	0	0	0				0	0	0				**3031**
3057	3	1	2	-0.001	0.300	1.228	**2.165**	0.955	1.101				0.000	0.000		0	0	0	0	0		0	0	0	0	0	0	0	0		0	0	0	**3057**
3155	1	2	3	0.133	-0.160	-0.349	-0.098	-0.386	-0.722				0.000	0.000	0.233				0	0	0	0	0	0										**3155**
3159	3	2	1	-0.076	-0.253	-0.289	**-3.236**	0.042	-0.106				0.000	0.000	0.627				0	0	0	0	0	0										**3159**
3305	3	2	1	1.715	0.172	0.305	0.514	1.355	0.928				0.000	0.000	-1.037	0	0	0	0	0	0	0	0	0	0	0	0							**3305**
3327	2	1	3	-1.716	-0.721	-1.213	-0.781	-1.670	-0.278				0.000	0.000	-0.424				0	0	0	0	0	0										**3327**
3347	3	2	1																			0	0	0										**3347**
3457	1	2	3				-0.111	-0.871	0.411				0.000	0.000	-1.825				0	0	0	0	0	0					0	0				**3457**
3587	2	3	1	-1.045	-0.764	-0.751	-1.763	-0.928	0.239																									**3587**
3595	2	1	3	-0.299	-0.764	-1.081	-0.602	-0.871	0.024	-1.241	0.000	0.000	0.000	0.000	-1.737				0	0	0	0	0											**3595**
3626	2	1	3	-0.225			-0.826	-1.099	-0.623	0.427	0.000	0.000	0.000	0.000	-0.161	0	0	0	0	0	0	0	0	0										**3626**
3868	1	2	3	-0.598	-0.594	-0.355	-0.022	-0.643	-0.838	0.447	0.000	0.000	0.000	0.000	-0.161	0	0	0	0	0	0	0	0	0										**3868**
3878	2	1	3	-0.545	1.888	-0.916																0		0										**3878**
3923	3	1	2	1.491	**3.747**	0.503	**-2.611**	-0.471	-0.407													0						0	0	0				**3923**
4064	2	3	1	-0.225	-0.849	-0.091	0.067	-0.243	0.110																									**4064**
4100	2	3	1	-0.971	-0.126	0.173	**-4.000**	0.442	0.411				0.000	0.000	-0.336				0	0	0	0	0	0										**4100**
4171	2	1	3	0.521	0.130	-0.091	0.112	0.727	0.627													0	0	0	0	0	0							**4171**
4246	3	1	2	-0.150	-1.360	-1.213	-0.022	-0.814	-1.054										0	0	0	0	0	0										**4246**
4288	1	3	2																															**4288**
4339	2	3	1										0.000	0.000	-1.037				0	0	0	0	0	0	0	0	0							**4339**
4352	1	3	2	0.223	-1.402	0.833	0.648	0.042	1.058				0.000	0.000	-0.336	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				**4352**
4400	2	1	3	**4.000**	-0.211	0.041		0.213	-1.054																									**4400**
4560	1	3	2																0	0	0	0	0	0										**4560**
4562	1	2	3	0.521	-0.083	0.173		1.183	-0.278	-0.854	0.000	0.000	0.000	0.000	0.715	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0		**4562**
4633	1	3	2	-0.001	0.981	0.503	0.290	-0.129	0.756				0.000	0.000	**2.467**				0	0	0	0	0	0										**4633**

Lab no.	Vial			Aerobic micro-organisms 30 °C			Enterobacteriaceae			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			*Salmonella*			*Escherichia coli* O157 (VT-neg)			Pathogenic *Vibrio* spp.			*Yersinia enterocolitica*			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
4635	3	1	2	-2.164	1.492	1.228	-4.000	-0.357	-1.183										0	0	0	0	0	0									4635
4664	3	1	2	-0.896	0.215	0.371	2.121	1.355	1.575				0.000	0.000	-0.511				0	0	0	0	0	0				0	0	0				4664
4683	2	3	1																														4683
4817	3	1	2	-0.374	0.981	-0.619							0.000	0.000	-0.073				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4817
4840	1	3	2	-1.269	-0.126	3.340	-1.897	-0.300	2.135	-0.712	0.000	0.000	0.000	0.000	2.204	0	0	0	0	0	0	0	0											4840
4879	1	3	2																														4879
4889	1	3	2	-0.195	-0.351	1.050	0.273	0.213	2.075				0.000	0.000	-0.336				0	0	0	0	0	0				0	0	0				4889
4944	3	1	2	-0.225	-0.126	0.569	0.514	0.042	0.239				0.000	0.000	-0.161				0	0	0	0	0	0										4944
4980	2	3	1	0.372	-0.806	-0.751	0.871	-0.586	-1.011				0.000	0.000	0.189				0	0	0	0	0	0										4980
5018	2	3	1	-0.747	-0.551	-0.157	-0.736	-0.072	-0.623				0.000	0.000	-0.161	0	0	0	0	0	0	0	0	0							0	0	0	5018
5028	2	3	1																											0	0	0	5028
5100	3	2	1	2.759	0.938	-0.355																0	0	0										5100
5128	2	3	1	-4.000	-0.977	-1.477													0	0	0	0	0	0										5128
5182	1	2	3					4.000	0.627													0	0	0										5182
5204	3	1	2	-1.716	-0.977	-1.411	0.067	-0.528	0.670	-0.183	0.000	0.000	0.000	0.000	-1.037	0	0	0	0	0	0	0	0	0										5204
5220	2	3	1	1.192	0.130	-1.675	1.362	1.126	-2.217				0.000	0.000	0.365				0	0	0	0	0	0										5220
5221	2	3	1																														5221
5329	2	3	1	-0.001	0.045	-0.223	0.290	-0.471	-1.054																								5329
5333	1	2	3																0	0	0	0	0	0										5333
5342	2	1	3																														5342
5352	1	2	3	1.192	1.619	1.426	1.139	0.955	2.135				0.000	0.000	0.627				0	0	0	0	0	0										5352
5447	2	3	1													0	0	0															5447
5545	2	3	1					0.727	0.756										0	0	0	0	0	0										5545
5553	3	1	2	0.521	0.002	0.437	0.469	-0.186	-0.020		0.000	0.000				0	0	0	0	0	0	0	0	0	0	0	0							5553
5615	2	3	1	-0.001	0.045	1.756	0.290	0.727	1.575										0	0	0	0	0	0										5615
5632	3	1	2	0.521	1.577	-1.411																	0	0										5632
5701	1	3	2	-0.404	0.862	1.083																												5701
5801	2	3	1	-2.089	-1.402	-1.345	-4.000	-1.099	-0.838																									5801
5808	3	2	1	-0.001	1.394	0.833																0	0	0										5808
5883	3	1	2	-0.299	-0.594	-0.157		-0.357	0.498				0.000	0.000	-0.686				0	0	0	0	0	0										5883
5950	2	3	1	-0.299	-0.594	0.041	0.603	-0.129	0.325	0.630	0.000	0.000	0.000	0.000	0.365	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5950
5993	1	2	3																			0	0	0										5993
6109	3	1	2	-0.001	2.173	2.548																0	0	0	0	0	0							6109
6175	3	1	2	-0.076	1.917	0.899	-0.915	1.754	0.713										0	0		0	0	0										6175
6224	1	2	3																														6224
6232	1	3	2	0.186	-0.564	-1.550	-4.000	-1.128	-0.097													0		0										6232
6253	1	2	3	-0.404	0.262	-0.382	0.407	-0.266	-0.282										0	0	0	0	0	0										6253
6343	3	1	2	3.654	-4.000	-0.817	-0.736	-4.000	0.153										0	0	0	0	0	0										6343
6352	1	2	3	-0.896	-0.849	-1.411	0.067	-2.411	-0.838													0	0	0										6352
6368	1	3	2	-0.001	-0.287	0.516	0.965	0.213	1.329				0.000	0.000	-1.431				0	0	0	0	0	0				0	0	0				6368
6443	1	3	2																			0	0	0										6443
6456	1	3	2	-0.150	-0.423	-0.223	-1.004	-0.471	-0.666										0	0	0	0	0	0										6456
6594	2	1	3																														6594
6658	2	3	1	-1.418	1.364	-4.000	-1.585	1.069	-4.000																								6658
6686	2	3	1	0.969	0.130	0.701	0.514	-0.643	0.067				0.000	0.000	1.591				0	0	0		0	0										6686
6720	2	3	1										0.000	0.000	0.102				0	0	0	0	0	0										6720
6762	1	3	2	1.565	-0.466	0.503	1.273	-0.015																										6762
6870	3	2	1																0	0	0													6870
6944	2	1	3																0	0	0													6944
6971	3	2	1	0.894	-0.551	1.690	-0.111	2.267	0.799																									6971
7182	2	3	1	0.148	-1.189	-1.015	0.380	-0.985	-0.494																									7182
7232	3	2	1	0.148	-0.040	-0.091																												7232
7242	2	1	3																															7242
7248	1	3	2	-1.567	0.726	0.569	-4.000	0.270	-1.485				0.000	0.000	-0.161	0		0	0	0	0	0	0	0										7248

Lab no.	Vial			Aerobic micro-organisms 30 °C			Enterobacteriaceae			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			Thermotolerant *Campylobacter*			*Listeria monocytogenes*			*Salmonella*			*Escherichia coli* O157 (VT-neg)			Pathogenic *Vibrio* spp.			*Yersinia enterocolitica*			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
7253	1	2	3	0.894	-0.083	-0.157				0.590	0.000	0.000	0.000	0.000	-0.424	0	0	0	0	0	0	0	0	0									**7253**
7282	3	1	2	-0.374	1.960	1.031	-0.335	0.613	1.402										0	0	0												**7282**
7330	1	2	3	-0.971	-0.551	-0.751	-1.004	-0.528	-0.106										0	0	0	0	0	0									**7330**
7334	2	3	1	0.303	0.369	0.720																0	0	0	0		0						**7334**
7564	2	3	1										0.000	0.000	0.277				0	0	0												**7564**
7627	1	2	3	-0.299	0.087	**-2.401**																0	0	0	0	0	0						**7627**
7688	2	1	3	-0.225	-0.423	-0.487	0.112	0.042	0.239				0.000	0.000	0.978	0	0	0	0	0	0	0	0	0	0	0	0						0	0	0	**7688**
7728	2	3	1	-1.418	0.428	0.041										0	0	0	0	0	0	0	0	0										**7728**
7750	2	3	1	-0.001	-1.402	-0.355	0.201	0.270	-0.537													0		0	0									**7750**
7825	1	2	3	0.730	1.228	0.793	1.161	**-2.086**	0.149				0.000	0.000	1.381				0	0	0	0	0	0									**7825**
7876	1	2	3	-0.747	0.343	-0.025	-1.004	-0.757	-0.364				0.000	0.000	0.803				0	0	0	0	0	0									**7876**
7882	2	3	1	1.267	-0.338	0.767													0	0	0	0		0									**7882**
7930	3	2	1	0.670	-0.126	0.437	0.871	0.613	-0.106				0.000	0.000	0.540				0	0	0	0	0	0									**7930**
7940	3	1	2	**3.952**	-0.636	-0.025																											**7940**
7962	2	1	3	0.074	0.343	1.162	**2.746**	**2.895**	1.187				0.000	0.000	0.715				0	0	0	0	0	0									**7962**
7968	2	1	3	-1.418	-0.040	-0.421	-0.245	-0.700	0.067				0.000	0.000	-0.161	0		0	0	0	0	0	0	0									**7968**
8019	3	2	1	0.521	0.768	0.173	0.157	1.297	-0.709				0.000	0.000	-0.161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				**8019**
8042	1	3	2																			0	0	0									**8042**
8066	1	2	3										0.000	0.000	0.697				0	0	0	0	0	0									**8066**
8068	2	1	3	-1.269	-0.551	-0.355	-0.424	-0.814	0.153				0.000	0.000	**-4.000**				0	0	0	0	0	0									**8068**
8165	2	3	1				-0.602	-1.384	-1.571	-0.244	0.000	0.000				0	0	0	0	0	0	0	0	0	0	0	0				0	0	0	**8165**
8252	2	3	1	1.864	-0.168	-0.289	1.496	0.042	-0.494										0	0	0	0	0	0									**8252**
8260	3	1	2	0.074	-0.806	-0.949	**-4.000**	-1.213	-1.614				0.000	0.000	-0.161				0	0	0	0	0	0									**8260**
8313	1	2	3	-0.150	-0.806	-0.751	-0.111	-0.186	-1.011				0.000	0.000	0.803				0	0	0	0	0	0									**8313**
8333	2	3	1	1.938	0.385	0.899	-0.067	-0.757	-0.666										0	0	0	0	0	0	0	0	0							**8333**
8397	3	1	2	1.640	-1.530	0.569	0.737	-0.300	0.799				0.000	0.000	0.102				0	0	0												**8397**
8435	3	2	1	-0.036	-0.357	-0.935	0.099	-0.195	-1.306				0.000	0.000	0.100				0	0	0	0	0	0									**8435**
8568	1	2	3	1.192	0.853	0.371		-0.414	-0.063										0	0	0	0	0	0	0	0	0							**8568**
8626	1	3	2	**2.087**	**2.428**	1.822	0.112	**2.096**	**2.092**					0.000						0		0	0	0										**8626**
8628	1	3	2	0.715	-1.718	0.351	0.273	-0.904	0.101				0.000	0.000	0.464				0	0	0	0	0	0						0	0	0			**8628**
8734	1	3	2	0.521	-0.977	-1.345	1.585	0.213	0.454																									**8734**
8742	3	2	1	-1.418	-0.509	-1.939													0	0	0	0	0	0									**8742**
8756	1	2	3																															**8756**
8766	3	1	2	-0.598	0.683	0.239	-0.558	0.613	-1.355				0.000	0.000	0.540				0	0	0	0	0	0									**8766**
8862	2	3	1																			0	0	0									**8862**
8918	1	2	3	-0.448	-0.892	-0.025	0.290	-0.643	-0.925				0.000	0.000	-0.073				0	0	0												**8918**
8955	1	2	3	-0.195	-1.581	0.826	1.148	-0.648	1.015	**2.341**	0.000	0.000	0.000	0.000	0.986	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**8955**
9002	1	2	3	0.223	-0.679	-0.751	0.558	-1.213	0.153	-0.509		0.000	0.000	0.000	0.890				0	0	0	0	0	0									**9002**
9034	2	1	3	-0.971	-0.126	-0.751	0.514	0.042	0.239										0	0	0	0	0	0							0	0	0	**9034**
9078	2	1	3	1.864	**2.513**	1.954	-0.826	**3.694**	1.532																									**9078**
9217	3	2	1	-1.269	-0.764	0.041	-0.111	-0.586	0.885																0									**9217**
9269	3	1	2																			0	0	0									**9269**
9429	3	1	2	-0.225	-0.636	-0.025													0	0	0	0	0	0									**9429**
9436	3	1	2	0.372	0.683	0.239	**-2.165**	-0.243	0.067	0.427	0.000	0.000	0.000	0.000	**-2.876**	0	0	0	0	0	0	0	0	0	0	0	0							**9436**
9441	1	3	2	-1.120	-0.423	-1.279	-1.183	-1.441	-1.140				0.000	0.000	0.803				0	0	0	0	0	0									**9441**
9453	1	2	3	-1.120	-0.934	-1.147	-0.201	-0.300	-0.925										0	0	0	0	0	0									**9453**
9512	3	2	1	-0.225	-0.551	**-2.071**	0.067	-0.528	-1.054																									**9512**
9555	2	3	1	-0.821	0.045	-0.091	-1.227	0.385	-0.580																									**9555**
9662	3	2	1	-0.374	-0.211	-0.751	0.514	0.613	-0.494				0.000	0.000	-1.650				0	0	0	0	0	0									**9662**
9716	1	3	2	-0.225	-0.509	-0.223													0	0	0	0	0	0						0	0	0	**9716**
9747	2	3	1	-1.269	-1.019	-1.411	-1.451	-0.757	0.541																									**9747**
9890	2	1	3	-0.225	1.109	0.635	0.960	1.069	0.454																									**9890**
9903	2	3	1	0.447	0.428	0.767	-1.138	1.925	0.928										0	0	0		0	0									**9903**
9950	3	1	2																															**9950**

Internal and external control for microbiological analyses of food and drinking water

All analytical activities require work of a high standard that is accurately documented. For this purpose, most laboratories carry out some form of internal quality assurance, but their analytical work also has to be evaluated by an independent party. Such external quality control of laboratory competence is commonly required by accreditation bodies and can be done by taking part in proficiency testing (PT).

In a proficiency test, identical test material is analysed by a number of laboratories using their routine methods. The organiser evaluates the results and compiles them in a report.

The National Food Agency's PT program offers

- External and independent evaluation of laboratories analytical competence.
- Improved knowledge of analytical methods with respect to various types of organisms.
- Expert support.
- Tool for inspections regarding accreditation.
- Free extra material for follow-up analyses.

For more information visit our website: www2.slv.se/absint

The National Food Agency's reference material

As a complement to the proficiency testing, but without specific accreditation, the National Food Agency also manufactures a number of reference materials (RM) for internal quality control of food and drinking water microbiological analyses, including pathogens.

More information is available on our website: www.livsmedelsverket.se/en/RM-micro