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***AFNOR validation following the ISO 16140 standard
of the Assurance GDS™ Salmonella method method***

SUMMARY REPORT

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1 Introduction

1.1 Validation references

The Assurance GDS™ *Salmonella* method (BioControl Systems) has been realized according to the reference method EN ISO 16140:2003, with respect to the reference method EN ISO 6579:2002.

1.2 Protocol and principle of the alternative method

1.2.1 Protocol

The method protocol is:

- **1st step** - an enrichment in buffered peptone water (BPW), incubated 18h–24h at 35°C – 38°C, for most foods and environmental samples

Note:

- *for raw seafood, the enrichment broth is buffered peptone water with Novobiocin (1mL of 0,4% Novobiocin solution), incubated 18h–24h at 35°C – 38°C*
- *for non-fat dry milk, the enrichment broth is brilliant green water, incubated 20h–24h at 35°C – 38°C*

- **2nd step** - a preparation sample step: 1mL of sample is transferred in a sample block well containing Sample Concentrating Reagent (immuno-concentration step) and the sample block is agitated at 600 rpm for 10 – 20 min.

Note:

- *for the low microbial foods, raw seafood and environmental samples, samples are then transferred in Wash Solution before the Amplification and Detection step*
- *for the high microbial foods, (and more particularly raw meat/poultry, raw fruits/vegetables and petfood/animal feeds) and non-fat dry milk, samples are then transferred in BHI broth distributed in a second sample block and incubated for 2–4h at 35°C – 38°C before the Amplification and Detection step*

- **3rd step** - a PCR test using an Assurance Rotor-Gene™

Confirmations of positive samples:

With traditional method following ISO method :

- Transfer 100 µl of the culture broth incubated 22 – 24 hours at 37°C to 10 ml of RVS broth and incubate at 41.5 ± 0.5°C for 24 ± 3h or 1 mL to MKTTn broth and incubate at 37 ± 1°C for 24 ± 3h,
- Streak RVS or MKTTn broths on selective media plates and follow up with biochemical identification, according to the reference method.

Enriched BPW broths may be stored for up to 72 hours at 2°C – 8°C before initiation of confirmation of positive samples.

The protocol is presented in Appendix A.

1.2.2 Principle of Assurance GDS™ *Salmonella* method

GDS is an automated gene-based assay that incorporates multiple levels of specificity to ensure highly accurate results. The method utilizes proprietary probes and specific primers directed against a highly conserved DNA sequence of the target organism. GDS also utilizes a proprietary device and reagents that concentrate populations of target microorganisms and eliminate potential competitive microflora. The method is designed to be highly selective, and does not detect microorganisms that are potential cross-reactors in antibody-based assays.

A 1mL aliquot of the enrichment broth is agitated with magnetic beads, and after 10 – 20 min, the bead-bacteria complexes are collected with a PickPen® tool.

The collected and washed bead-bacteria complexes are transferred into amplification tubes containing Polymerase Buffer solution and loaded in an Assurance Rotor-Gene™.

Results are presented as positive or negative.

1.3 Application scope

All human food
Animal feed stuffs
Environmental samples

1.4 Reference method

The validation study was carried out by reference to the EN ISO 6579:2002 (#) standard method.
The diagram summarising the method is shown in annex A.

2 Comparative study of methods

2.1 Relative accuracy, relative specificity and relative sensitivity

The aim of this study, according to the reference document ISO 16140, is to evaluate the performances of the two methods:

- reference method EN ISO 6579 :2002,
 - Assurance GDS™ *Salmonella* method,
- on naturally contaminated or non-contaminated samples.

2.1.1 Number and nature of the samples

According to the ISO 16140 standard, a minimum of 60 products per category must be analysed, with around 50% of positive products (at least 30 results) and 50% of negative products.

Each category was divided into different types and the results are displayed as follows:

Category	Types	Positive*	Negative	Total
Meat products	Raw meats	13	26	39
	Poultry	12	14	26
	Delicatessen	7	9	16
	Total	32	49	81
Dairy products	Cheeses	10	9	19
	Pastries	10	10	20
	Milks and milk powders	10	11	21
	Total	30	30	60
Miscellaneous	Eggs products	9	11	20
	Egg-based products (mayonnaise, pastries)	11	9	20
	Ready-to-eat meals	10	10	20
	Total	30	30	60
Seafood products and vegetables	Fish fillets and shellfish	11	10	21
	Raw vegetables, spices and herbs	10	11	21
	Ready-to eat vegetables	10	10	20
	Total	31	31	62
Feed	Cattle cakes	7	8	15
	Meals and dry pet foods	13	12	25
	Wet pet foods and raw meat for animals	12	11	23
	Total	32	31	63
Environment	Various waters	12	17	29
	Surface samplings	9	9	18
	Residues and scraps	11	12	23
	Total	32	38	70
TOTAL		187	209	396

* these are positive results by one or other of the methods

2.1.2 Artificial contaminations of the samples and percentage

Artificial contamination was achieved by using stressed contaminating suspensions, the stress treatment and efficiency of which have been determined according to EN ISO 16140 and AFNOR validation rules.

138 samples were positive after artificial contamination.

In total, of 187 positive results of *Salmonella*, 74% were obtained as a result of artificial contamination.

2.1.3 Results of assays

The analyses have been conducted singly using the two methods.

The results of analysed samples were presented in appendix B.

The table of the 396 results of samples is below:

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 183	Positive deviation (R-/A+) PD = 0	183
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 4*	Negative agreement (A-/R-) NA = 209*	213
Total	187	209	396

Legend:

A+ = positives confirmed

A- = immediate negatives **and** negatives after confirmation when presumed positive

* not including any non-confirmed positive result

2.1.4 Calculation of relative accuracy (AC), relative specificity (SP) and relative sensitivity (SE)

All of these results help calculate the relative accuracy, relative sensitivity and relative specificity for each of the categories and for all of the categories, according to the formulae of the EN ISO 16140 standard.

Category	PA	NA	ND	PD	Sum N	Relative accuracy AC (%) [100x(PA+NA)]/N	N+ PA + ND	Relative sensitivity SE (%) [100xPA]/N+	N- NA + PD	Relative specificity SP (%) [100xNA]/N-
Meat products	31	49	1	0	81	98.8	32	96.9	49	100
Dairy products	30	30	0	0	60	100	30	100	30	100
Miscellaneous	30	30	0	0	60	100	30	100	30	100
Seafood & Vegetables	30	31	1	0	62	98.4	31	96.8	31	100
Feed	30	31	2	0	63	96.8	32	93.8	31	100
Environment	32	38	0	0	70	100	32	100	38	100
TOTAL	183	209	4	0	396	99.0	187	97.9	209	100

For the alternative method, the values as a percentage calculated for the following three criteria according to the EN ISO 16140 standard were:

<i>Relative accuracy</i> : AC	99.0 %
<i>Relative specificity</i> : SP	100 %
<i>Relative sensitivity</i> : SE	97.9 %

The AFNOR Technical Board asks the sensitivity of the two methods to be recalculated with consideration of all the confirmed positives (this includes the additional positives of the alternative method):

	Alternative method :	Reference method :
Sensitivity	$(PA + PD) / (PA + PD + ND) = 97.9 \%$	$(PA + ND) / (PA + PD + ND) = 100 \%$

2.1.5 Analysis of discordances

The number of discordances between the reference method and the alternative method was 4.

According to annex F of the NF EN ISO 16140 standard, the number of discordances for which a statistical test must be conducted in order to compare the two methods is 6.

No statistic test has been done.

The Assurance GDS™ *Salmonella* method and the reference method EN ISO 6579 can be considered as equivalent.

2.1.6 Comments on the confirmation protocol

The strains were found for all positive samples, streaking on XLD agar, after enrichment in RVS broth or MKTTn broth.

In case of discordance between the Assurance GDS™ *Salmonella* test result and the confirmation, it's recommended to repeat the confirmation by performing a new subculture in the alternative selective broth (MKTTn if RVS was initially used or vice versa).

2.1.7 Comments on inhibitions

Among the 396 results, two samples of cheese and a residue from cheese plant have presented some inhibition:

- a pasteurized cheese and the residues, for which the inhibition disappeared when the BPW was transferred in BHI broth distributed in a second sample block and incubated for 2–4h at 35°C – 38°C before the Amplification and Detection step
- a raw milk cheese sample for which the inhibition disappeared when the lysate was diluted in 1/10

An example of curve is presented in appendix F (sample C13).

2.1.8 Comments on protocol choice

Low Microbial Protocol - this protocol has been designed to take advantage of situations in which the general bioburden of the sample is relatively low, allowing for faster growth detection of the presence of *Salmonella*. These conditions are most often found in processed samples. In general, the Low Microbial protocol is recommended for samples in which the total aerobic plate count is <10,000 CFU/g and/or the product undergoes a processing step known to reduced or control the bioburden of the product.

High Microbial Protocol - this protocol is more robust than the Low Microbial protocol. As such, it is better able to recover *Salmonella* from raw, unprocessed products or products with high bioburdens exceeding 10,000 CFU/g. However, this protocol can also be utilized with low bioburden or processed samples.

2.2 Relative detection level

The objective was to determine the level of contamination for which less than 50% of the responses obtained are positive and that for which more than 50% of the responses obtained are positive.

Different food matrix/strain pairs were studied in parallel with the reference method and the Assurance GDS™ *Salmonella* method, for six product categories.

The artificial contaminations have been realised according to EN ISO 16140 and AFNOR validation rules.

The levels of detection, calculated according to the Spearman – Kärber* method (LOD₅₀), obtained for each combination « matrix – strain » are the following:

Matrix	Strain	Relative detection level for the reference method (CFU / 25 g or 25 mL)	Relative detection level for the alternative method (CFU / 25 g or 25 mL)
Mincéd poultry meat	<i>Salmonella</i> Hadar	0,2 [0,2 – 0,4]	0,3 [0,2 – 0,4]
Non-fat dry milk	<i>Salmonella</i> Typhimurium	0,6 [0,4 – 1,1]	0,7 [0,5 – 1,2]
Raw liquid egg	<i>Salmonella</i> Enteritidis	0,4 [0,2 – 0,7]	0,4 [0,2 – 0,7]
Fish filet	<i>Salmonella</i> Virchow	0,3 [0,2 – 0,5]	0,4 [0,2 – 0,6]
Dog petfood	<i>Salmonella</i> Senftenberg	0,6 [0,4 – 0,9]	0,6 [0,4 – 0,9]
Process water	<i>Salmonella</i> Newport	0,9 [0,6 – 1,4]	0,9 [0,6 – 1,4]

* "Hitchins A. Proposed Use of a 50 % Limit of Detection Value in Defining Uncertainty Limits in the Validation of Presence-Absence Microbial Detection Methods, Draft 10th December, 2003".

The level of detection obtained for the Assurance GDS™ *Salmonella* method is between 0.2 and 1.4 cells per 25 grams. It is identical to the one obtained for the reference method (0.2 to 1.4 cells per 25 grams).

2.3 Inclusivity / exclusivity

The inclusivity and the exclusivity of the method are defined by analysis, respectively, of 50 positive strains and 30 negative strains.

2.3.1 Protocols

Protocol for inclusivity

For each of the strains of *Salmonella*, a culture in buffered peptone water was made over 24 hours at 37°C. An enrichment broth was inoculated with around 10 *Salmonella* cells per 225 mL and incubated at 37°C, then the complete protocol of the alternative method was realised.

Protocol for exclusivity

The different negative strains were cultivated in nutritional broth and diluted to obtain levels of around 10⁵ cells per mL. A buffered peptone water was then inoculated and the immunomagnetic concentration step, followed by the PCR assay, was performed for each strain.

2.3.2 Results and conclusion

Results are presented in appendix C.

The study of the 32 non-*Salmonella* strains by the Assurance GDS™ *Salmonella* test, did not detect the presence of any cross-reaction.

Among the 60 strains of *Salmonella*, most were detected with the Assurance GDS™ *Salmonella* method.

Two strains of *Salmonella* Amsterdam and two strains of *Salmonella* Westhampton among three of each serovar were not detected.

Further molecular analysis of all 3 strains of *Salmonella* Westhampton with multiple DNA primer sets^{1,2} revealed that the two negative strains do not contain the targeted *invA* gene. However the gene was present in the positive *S.*Westhampton strain. It is widely recognized that the *invA* gene is a key pathogenicity marker for defining the *Salmonella* genus.¹⁻⁶ While these strains may be serologically and biochemically identified as *Salmonella*, they lack the required pathogenicity gene. At best, these strains would be considered highly atypical and non-pathogenic.

Investigation of the *Salmonella* Amsterdam strains is also being conducted.

The strain *Salmonella* Amsterdam S2, which gave a negative result with the complete protocol, was inoculated in nutrient broth, with a level of 1.4. 10⁵ cells / mL. After an overnight incubation, the strain was tested with the Assurance GDS™ *Salmonella* test and the result was positive.

Another strain of *Salmonella* Amsterdam (origin: meat product) was tested with the complete protocol and gave a negative result, but in pure culture in nutrient broth, the result was positive.

¹Rahn K, De Grandis SA, Clarke RC, McEwen SA, Galán JE, Ginocchio C, Curtiss R 3rd, Gyles CL. 1992. Amplification of an *invA* gene sequence of *Salmonella* typhimurium by polymerase chain reaction as a specific method of detection of *Salmonella*. Mol. Cell. Probes. 6(4):271-9.

²Hoorfar J, Ahrens P, Rådström P. 2000. Automated 5' nuclease PCR assay for identification of *Salmonella* enterica. J Clin Microbiol. 38(9):3429-35.

³Collazo CM, Galán JE. 1997. The invasion-associated type-III protein secretion system in *Salmonella*--a review. Gene. 11;192(1):51-9. Review.

⁴Ginocchio CC, Galán JE. 1995. Functional conservation among members of the *Salmonella* typhimurium *InvA* family of proteins. Infect Immun. 63(2):729-32.

⁵Malorny B, Hoorfar J, Bunge C, and Helmuth R. 2003. Multicenter Validation of the Analytical Accuracy of *Salmonella* PCR: towards an International Standard. Appl Environ Microbiol. 69(1): 290–296.

⁶Steele-Mortimer O, Brumell JH, Knodler LA, Méresse S, Lopez A, Finlay BB. 2002. The invasion-associated type III secretion system of *Salmonella* enterica serovar Typhimurium is necessary for intracellular proliferation and vacuole biogenesis in epithelial cells. Cell Microbiol. 2002 Jan;4(1):43-54.

3 Interlaboratory study

3.1 Study organization

- Number of participating laboratories

13 laboratories received samples. The laboratories list is presented in appendix D.

- Matrix used

A "vanilla ice-cream" matrix was used to perform the interlaboratory study.

- Strain used

The strain used for contaminations is a strain of *Salmonella* Typhimurium (origin « dairy products »).

- Number of samples per laboratory

24 samples were prepared per laboratory, and were distributed in 3 levels, with 8 samples per level and method.

3.2 Control of experimental parameters

3.2.1 Contamination rates obtained after artificial contamination

Because of the matrix nature (ice-cream) and of the time between the spiking day and the analyses day, some assays were made to follow the evolution of the *Salmonella* contamination in this type of samples.

Samples of 25g ice-cream were spiked at different levels of *Salmonella* and stored in freezing conditions:

- 24 hours in dry ice and 14 days at – 20°C, to simulate the shipping and storage conditions for the European labs
- 7 days in dry ice and 7 days at – 20°C, to simulate the shipping and storage conditions for the north – American labs.

Then enumerations were done, using a MPN method and in parallel, assays with the reference method and with the alternative method were performed.

The results indicated that the number of viable cells decreased after the conditions of storage in dry ice and at –20°C, by a factor of 10.

The following table shows the contamination rates obtained and estimated precisions:

Level	Samples	Real rate (spiking day) (b/25g sample)	Estimated lower contamination limit per 25g sample	Estimated upper contamination limit per 25g sample	Real rate (analyses day) (b/25g sample)
Level 0 (L0)	1-2-11-12-13-14-19-20	0			0
Low level (L1)	3-4-9-10-15-16-21-22	35	24	48	1.5 – 2.8 – 2.8
High level (L2)	5-6-7-8-17-18-23-24	175	150	203	57 – 18 – 23

3.2.2 Problems of temperature recorded during transport, temperature on reception and reception times

3.2.2.1 Analysis of temperature monitoring curves during transport

The temperature curves obtained from thermobutton data recorders show that temperatures were stable during transport (below – 40°C) and during storage (below – 15°C) for most of the laboratories.

3.2.2.2 Temperatures on reception and reception times

The temperatures obtained are recorded in the following tables:

Laboratory	Temperatures (°C)		Comments
	Reception day	Analyse day	
a	- 40.7°C	- 40.2°C	/
b	- 40.9°C	/	Data recorder sent the day of reception
c	- 40.2°C	- 30°C	/
d	- 40.4°C	- 18°C	/
e	- 40.7°C	- 22°C	/
f	- 40.4°C	/	Data recorder sent the day of reception
g	- 40.8°C	- 16°C	/
h	- 39.1°C	- 18°C (given by the lab)	Data recorder sent the day of reception
i	- 40.1°C	- 20°C	/
j	- 40.9°C	- 18°C	/
k	- 40.1°C	- 21°C	/
l	Not received	Not received	/
m	- 40.6°C	- 32°C	/

3.2.2.3 Conclusion

All the results from the 13 participating laboratories could be analyzed after considering the conditions of shipment and delivery. All labs have received frozen samples.

3.3 Results

3.3.1 Results obtained by cooperating laboratories

The detailed results are presented in appendix D and the following tables give a synthesis of the results obtained by all the laboratories.

Positive results obtained by the reference method

Laboratories	Levels of contamination					
	L0		L1		L2	
	Obtained	Nr samples	Obtained	Nr samples	Obtained	Nr samples
Lab c	5	8	8	8	8	8
Lab d	0	8	8	8	8	8
Lab e	2	8	8	8	8	8
Lab g	0	8	8	8	8	8
Lab f	0	8	8	8	8	8
Lab b	0	8	8	8	8	8
Lab a	0	8	8	8	8	8
Lab h	0	8	8	8	8	8
Lab i	1	8	8	8	8	8
Lab j	0	8	8	8	8	8
Lab k	0	8	8	8	8	8
Lab l	2	8	8	8	8	8
Lab m	0	8	8	8	8	8
Total	10	104	104	104	104	104

Positive results obtained by the alternative method

Laboratories	Levels of contamination					
	L0		L1		L2	
	Obtained	Nr samples	Obtained	Nr samples	Obtained	Nr samples
Lab c	3	8	8	8	8	8
Lab d	0	8	8	8	8	8
Lab e	1	8	8	8	8	8
Lab g	0	8	8	8	8	8
Lab f	0	8	8	8	8	8
Lab b	0	8	8	8	8	8
Lab a	0	8	8	8	8	8
Lab h	0	8	8	8	8	8
Lab i	1	8	8	8	8	8
Lab j	0	8	8	8	8	8
Lab k	0	8	8	8	8	8
Lab l	0	8	8	8	8	8
Lab m	0	8	8	8	8	8
Total	5	104	104	104	104	104

The results of the reference method and the alternative method **were in agreement** for 9 laboratories: the non-spiked samples were negative and the spiked samples were positive.

Four laboratories may have possible contamination problems:

- the laboratory C found with the reference method five of the non contaminated samples as positive and with the alternative method, three of them positive as well. Some problems of cross-contaminations were revealed. The laboratory has confirmed with a molecular identification method that the strain was the same in all the positive samples.
- the laboratory E found with the reference method, two of the non contaminated samples as positive and with the alternative method, one of them positive as well.
For the sample 19, positive by the Assurance GDS test, the Ct value was higher than the values obtained for the spiked samples. The lab has recorded a positive result for the confirmation, but it couldn't confirm that a new selective plate was stroke after obtaining the PCR test result. And all the media and plates were destroyed, avoiding further investigations.
- the laboratory I found one non contaminated sample positive with both methods. The sample was re-tested with the alternative method and the result remained positive. The Ct value was higher than the values obtained for the spiked samples. The labs informed us that the typical colonies were scarce on the selective plates and that the strain was the same as the spiking strain, so it was probably an inter-contamination.
- the laboratory L found two non contaminated samples positive only with the reference method, one after MKTTn broth and one after RVS broth. This laboratory didn't give explanations and didn't keep the plates, so further investigations were impossible.

3.3.2 Conclusion with comments

Regarding the different cases of possible contaminations, the results of the laboratory C could be excluded from the interpretation.

Finally, the results of 12 laboratories could be considered.

But, due to cross-contamination problems, we can discuss the possible exclusion of other labs among the labs E, I and L.

3.4 Calculations

The results of the 12 considered laboratories are summarized in appendix G

Note: the positive results of the alternative method were all confirmed.

3.4.1 Calculation of specificity percentage (%SP) and sensitivity percentage (%SE) for both methods

The percentages of specificity (SP) and sensitivity (SE) have been calculated with the EN ISO 16140 formulas.

For level L0, it is requested that the specificity percentage (%SP) should be calculated using each of the methods:

$$SP = \{1 - (FP/N_-)\} \times 100$$

where FP, number of false positives
N-, total number of tests L0

For levels L1 and L2, it is requested that the sensitivity percentage (%SE) should be calculated for each of the methods, compared with the number of expected positive results:

$$SE = (TP/N_+) \times 100$$

where TP, number of true positives
N+, total number of tests L1 or L2

The results are given in the following table:

Level	Reference method		Alternative method	
	SP/SE	LCL* %	SP/SE	LCL* %
L0	SP% = 95	90	SP% = 98	96
L1	SE% = 100	98	SE% = 100	98
L2	SE% = 100	98	SE% = 100	98
L1+L2	SE% = 100	98	SE% = 100	98

* LCL : low critical value, defined in standard ISO 16140

3.4.2 Calculation of the relative precision (AC)

The relative precision is calculated using the following formula:

$$AC = \{(PA + NA) / N\} \times 100$$

where PA, number of positive agreements
NA, number of negative agreements

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 193	Positive deviation (R-/A+) PD = 1	(N+) = 194
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 4*	Negative agreement (A-/R-) NA = 90*	(N-) = 94
Total	(N+) = 197	(N-) = 91	N = 288

* including no positive samples (not confirmed)

For this study, the relative accuracy is 98.3%.

It's important to note that the discordances observed for positive result with the reference method which was negative with the alternative method was due to inter-contaminations of non-spiked samples.

3.4.3 Analysis of discordances

As defined in appendix F in standard EN ISO 16140, the number of disagreements beyond which a statistical test must be carried out to compare the two methods is 6. Therefore, this statistical test is not used because the number of disagreements observed between the two methods was 5.

Both methods would be considered as equivalent.

3.5 Interpretation

3.5.1 Comparison of relative precision (AC), specificity (SP) and sensitivity (SE) values

The values obtained in the two parts of the validation study are given in the following table:

	Interlaboratory study	Comparative study
Relative accuracy (AC)	98.3 %	99.0 %
Sensitivity (SE)	100 %	97.9 %
Specificity (SP)	98 %	100 %

The values obtained after the interlaboratory study were comparable to the values obtained in the comparative study.

The AFNOR Technical Bureau asks that the sensitivity of the two methods be recalculated with consideration of all the confirmed positives (confirmed positive results):

	Alternative method	Reference method
sensitivity	$(PA + PD) / (PA + PD + ND) = 98.0 \%$	$(PA + ND) / (PA + PD + ND) = 99.5 \%$

The sensitivity value for the reference method is higher, but it's due to the inter-contaminations of non-spiked samples.

3.5.2 Accordance (DA)

The accordance is the percentage chance of finding the same result from two identical test portions analyzed in the same laboratory under repeatability conditions, in other words a single operator using the same instrument and the same reagents within the shortest feasible time interval.

The first step to calculate the accordance is to calculate the probability that two identical samples give the same result for each of the participating laboratories, and then to determine the average of the probabilities of all laboratories.

The different tables used to deduce the accordance are given in appendix E and the accordance for each of the methods at each of the levels are given in the following table:

Level	Reference method	Alternative method
L0	DA % = 92 %	DA % = 96 %
L1	DA % = 100 %	DA % = 100 %
L2	DA % = 100 %	DA % = 100 %

The values are different between both methods for the L0 level because of the positive results for the reference method and for the alternative method, due to inter-contamination of non-spiked samples (6 for the reference method and 2 for the alternative method).

3.5.3 Concordance

The concordance is the percentage chance of finding the same result for two identical samples analyzed in two different laboratories.

The objective is to calculate the percentage of all pairs giving the same results on all possible pairs of results.

Result tables used to make these calculations are given in appendix F and the concordance for each of the methods and for each of the levels are given in the following table:

Level	Reference method	Alternative method
L0	Concordance % = 90 %	Concordance % = 96.9 %
L1	Concordance % = 100 %	Concordance % = 100 %
L2	Concordance % = 100 %	Concordance % = 100 %

The values are different between both methods for the L0 level because of the positive results for the reference method and for the alternative method, due to inter-contamination of non-spiked samples (6 for the reference method and 2 for the alternative method).

3.5.4 Odds Ratio (COR)

The concordance odds ratio is calculated using the following formula:

$$\text{COR} = \frac{\text{accordance} \times (100 - \text{concordance})}{\text{concordance} \times (100 - \text{accordance})}$$

The concordance odds ratio for each of the methods and for each of the levels is given in the following table:

Level	Alternative method	Reference method
L0	COR % = 1.14	COR % = 1.27
L1	COR % = 1.00	COR % = 1.00
L2	COR % = 1.00	COR % = 1.00

A value of 1.00 for the Odds ratio means that the degree of agreement and the agreement are equal. When the Odds ratio increases, the interlaboratory variation becomes more predominant.

4 Practicability

Practicability is studied as a function of the 13 criteria defined by the technical bureau in comparing the reference method EN ISO 6579 to the Assurance GDS™ *Salmonella* method.

1. <i>Packaging mode of the components of the method (cf package insert)</i> 2. <i>Reagent volumes (cf package insert and vial packaging)</i>	The Assurance GDS™ <i>Salmonella</i> kit contains the quantity of reagent necessary for 100 analyses : - one vial of wash solution - one vial of resuspension buffer - one vial of concentration reagent - one vial of polymerase dilution buffer - amplification tubes
3. <i>Storage conditions of the elements method (cf package insert) – Expiry of products not opened (cf package insert)</i>	The storage temperature is of 2-8°C. The kit expiry date is shown on the box label and on the different vials.
4. <i>Modalities of use after first use (cf package insert)</i>	The kit components should be stored at 2-8°C. The TAQ polymerase enzyme should be stored at – 18°C before use and then at 2-8°C up to 6 weeks..
5. <i>Equipment or necessary specific premises (cf package insert)</i>	Among the required equipment, - an air incubator at 37°C ± 1°C - Microplate shaker - Pipette 1mL - Pickpen - Multichannel pipette - Assurance Rotor-Gene
6. <i>Reagents ready for use or to be reconstituted (cf package insert)</i>	/
7. <i>Duration of training of the operator not familiar with the method</i>	For an operator trained in standard techniques of microbiology, training in the technique requires less than 2 days.

8. Real time handling - Flexibility of the technique relative to the number of samples to be analysed

Steps	Average time for a sample (min)		Average time for 30 samples (min)	
	Standard ISO 6579	Assurance GDS <i>Salmonella</i>	Standard ISO 6579	Assurance GDS <i>Salmonella</i>
Preparation, weighing, dilution in BPW and crushing	7	7	90	90
Transfer to selective broths (RVS and MKTTn°)	3	/	45	/
Assurance GDS™ <i>Salmonella</i> test (transfert and PCR)	/	2	/	15
Streaking of RVS and MKTTn broths, on two selective media	10	/	150	/
Average total time (per sample)	20 minutes	9 minutes	9.5 minutes	3.5 minutes

These times correspond to negative samples for which no confirmation is necessary.

In the case of positive samples, the necessary time for isolation of the enrichment broth on selective media must be added to the confirmations (around 1 minute).

And the average time for the confirmation of a typical colony by reference method tests can be evaluated at around 5 minutes.

The advantage of the alternative method particularly lies in the possibility to sort negative samples from the suspicious samples and thus reducing the number of confirmations.

9. Time-to-result

Steps	Time required	
	Assurance GDS <i>Salmonella</i> method	ISO 6579 reference method
Realisation of pre-enrichment	D0	D0
Transfer to selective broths (Rappaport-Vassiliadis Soya, MKTTn)	D1	D1
Assurance GDS™ <i>Salmonella</i> procedure	D1	/
Test result	D1	/
Obtaining negative result (if test is negative)		
Transfer to selective broths (Rappaport-Vassiliadis Soya, MKTTn)	D1	/
Streaking of selective broths on selective media	D2	D2
Reading the plates		
Confirmation tests : identification strips, serology	D3 to D4	D3 to D4
Obtaining negative result (after streaking and negative confirmation if done)	D3 to D6	D3 to D6
Obtaining positive result		
Confirmation by reference method tests (including purification)	D5 to D6	D5 to D6

10. Type of qualification of the operator:	level identical to that necessary for the reference method
11. Steps common to the reference method	Confirmations
12. Traceability of the analysis results	All the results are saved in a history file. A result sheet is printed with the reagents lot numbers, time, test result, and sample identification. The results can be exported to a LIMS.
13. Maintenance by the laboratory	Routine cleaning of optics and filters with water and 70% alcohol solution

5 Conclusion

The validation study of the methods was conducted according to the reference document EN ISO 16140.

The **comparative study** conducted according to the reference document EN ISO 16140, allows assessing:

- the relative accuracy, the relative sensitivity and the relative specificity,
- the relative detection level,
- the inclusivity and the exclusivity.

The performances of the Assurance GDS™ *Salmonella* method are equivalent to those of the reference method EN ISO 6579:2002. They were determined by analysis of 396 samples distributed over five categories of products.

The relative accuracy obtained was 99.0%, the relative sensitivity 97.9% and the relative specificity 100%, according to the calculations required by the EN ISO 16140 standard.

4 discordant results were obtained, all false negative.

Because the positive samples by the alternative method are positive confirmed samples, the sensitivities were recalculated relative to all positive results and are:

- 97.9% sensitivity for the alternative method,
- 100% sensitivity for the reference method.

The relative level of detection of the Assurance GDS™ *Salmonella* method and of the reference method was evaluated by artificial contaminations of five different products, representative of the five categories tested.

It is between 0.2 and 1.4 cells of *Salmonella* per 25 g or mL of sample and is identical to the one of the reference method.

The specificity of the method is satisfactory since the strains of *Salmonella* were detected (inclusivity) and no cross-reactions were observed in the non *Salmonella* strains tested (exclusivity).

The **interlaboratory study results** obtained for all of the 12 selected laboratories show that the alternative method and the reference method have comparable values of relative accuracy, specificity and sensitivity as those obtained during the preliminary study.

The variability of the alternative method (accordance, concordance, Odds ratio) is better than the variability of the reference method.

Lille, October, the 21th 2009



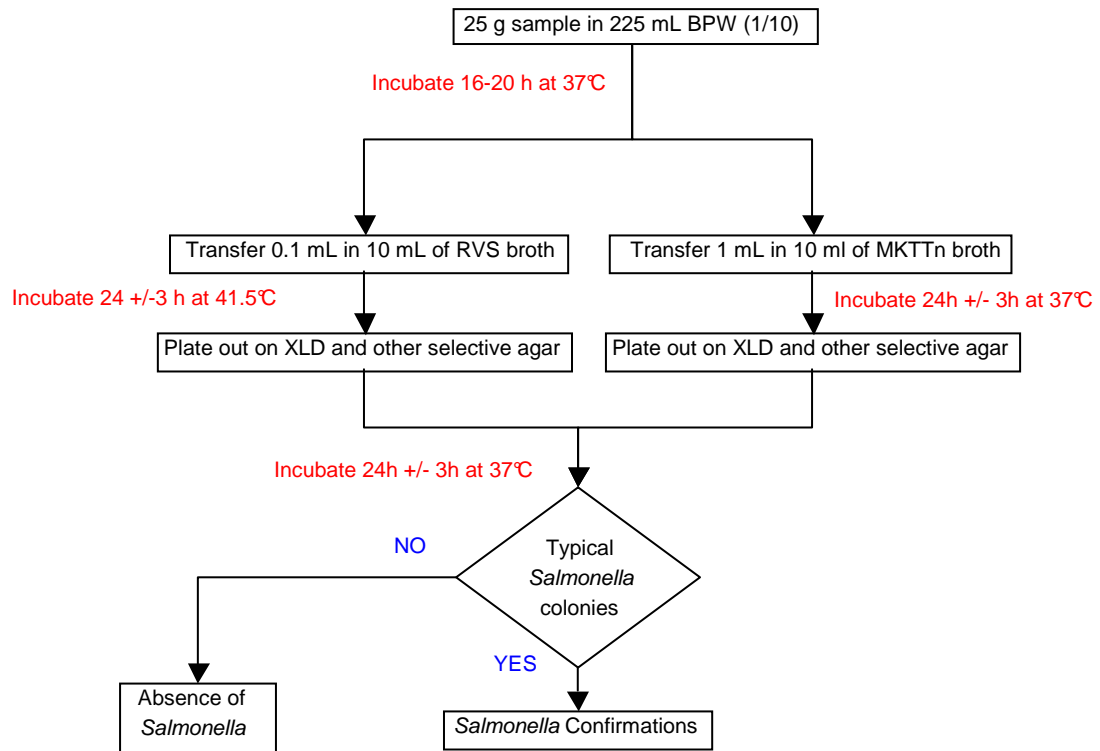
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Responsable Etudes

APPENDICES

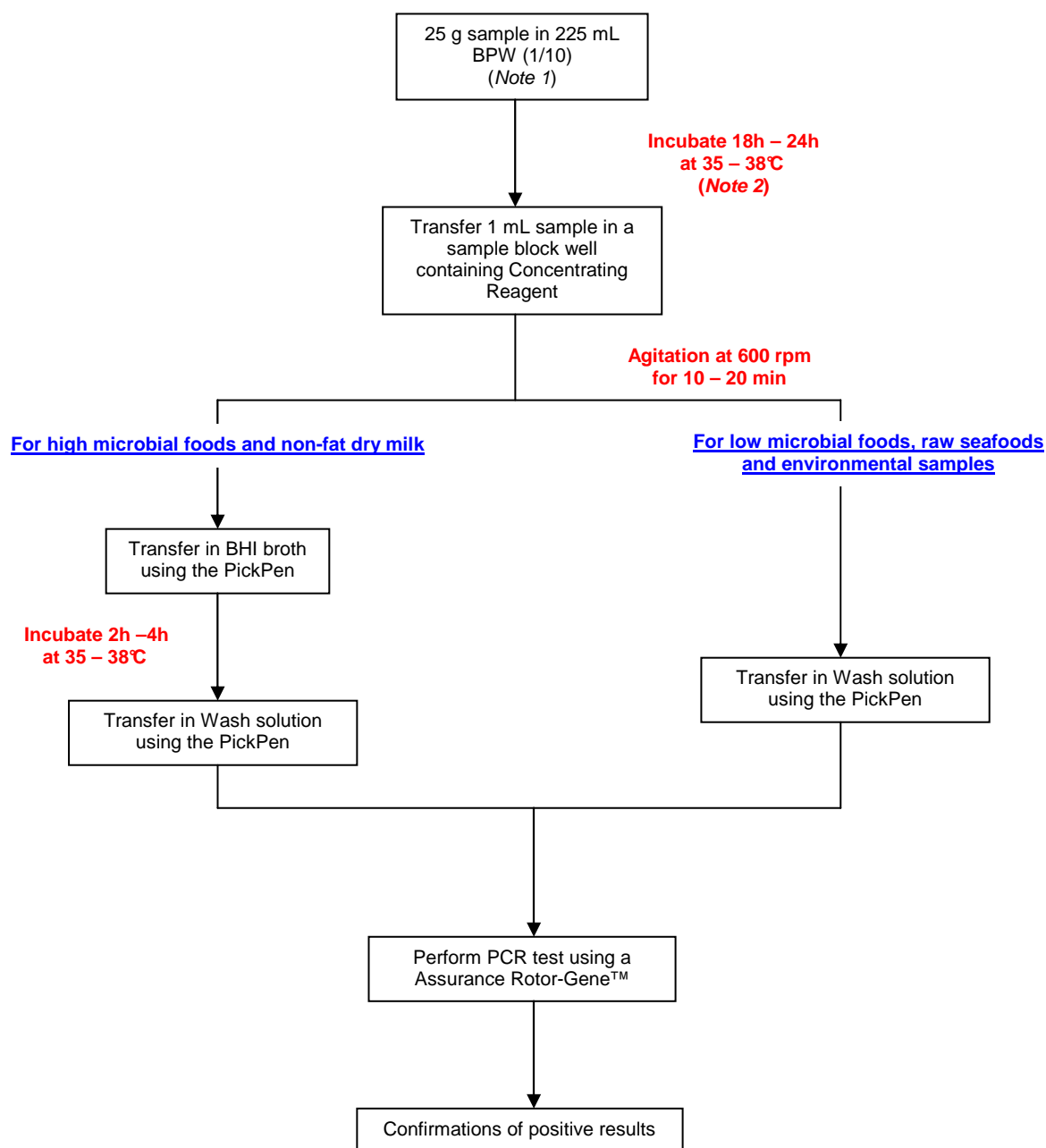
APPENDIX A:

ANALYTICAL PROTOCOLS

STANDARD EN ISO 6579 :2002



ASSURANCE GDS™ Salmonella method



Note 1:

- for raw seafood, the enrichment broth is BPW + novobiocin
- for non-fat dry milk, enrichment broth is brilliant green water

Note 2:

- for non-fat dry milk, incubate 20h–24h at 35°C – 38°C

APPENDIX B:

RELATIVE ACCURACY, RELATIVE SPECIFICITY,
RELATIVE SENSITIVITY

-

DETAILED RESULTS TABLES
FOR EACH SAMPLE CATEGORY

LEGEND

Total bacteria growth

∅ : no growth

L = low

M = medium

H = high

Distribution of flora

A = pure culture of suspicious colonies

B = mix with a majority of suspicious colonies

C = mix with a minority of suspicious colonies

D = mix with rare suspicious colonies

E = absence of suspicious colonies

(x) : x characteristic colonies of *Salmonella* if $x \leq 5$

Meat products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS Salmonella method					Comparison
					RVS		MKTtn		Identification	Result	PCR result	RVS	Mktn	Identification	Result	
					XLD	Edel	XLD	Edel				XLD	XLD			
A1	Beef liver	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
A2	Boar stew	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
A3	Boar stew	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
J1	Sauté of pork	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
L3	Beef kidneys	high	MP1	no	-ME	-LE	-ME	-HE	/	-	-	/	/	/	-	=
L6	Liver calf	high	MP1	no	-LE	-LE	-HE	-HE	/	-	-	/	/	/	-	=
M1	Minced pork	high	MP1	no	-LE	Ø	-ME	Ø	/	-	-	/	/	/	-	=
M4	Pork fillet	high	MP1	no	-LE	Ø	-HE	-HE	/	-	-	/	/	/	-	=
N16	Liver calf	10 e8 high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
N17	Calf kidneys	10 e8 high	MP1	no	+MB	+MB	+HC	+HC	Salmonella spp	+	+	-ME	+MB	Salmonella spp	+	=
P1	Pork ham	high	MP1	no	-LE	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P2	Fat of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P3	Gorge of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P4	Pork ham	high	MP1	no	+MB	+MB	+HC	+HC	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
P5	Gorge of pork	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
P6	Gorge of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P7	Gorge of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P8	Fat of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P9	Pork ham	high	MP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
P10	Pork ham	high	MP1	no	+MB	+MB	+HC	+HC	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
P11	Gorge of pork	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
P12	Fat of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P13	Fat of pork	high	MP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
P14	Fat of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
P15	Pork ham	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
Q2	Pork tongue	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+LB	+HB	Salmonella spp	+	=
Q3	Pork kidneys	high	MP1	no	-LE	-LE	-ME	-HE	/	-	-	/	/	/	-	=
R10	Pork tongue	high	MP1	non	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
R14	Liver beef	high	MP1	no	+MB	+MB	+HB	+HC	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
R15	Liver beef	high	MP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
R16	Gorge of pork	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
R17	Pork ham	high	MP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
R18	Pork ham	high	MP1	no	-LE	-LE	-HE	-HE	/	-	-	-ME	-ME	/	-	=
R19	Gorge of pork	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+HB	+MB	Salmonella spp	+	=
S5	Rumsteak	high	MP1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
S6	Hampe	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
S7	Rumsteak	high	MP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
U5	Pork tenderloin	high	MP1	no	-ME	-LE	-HE	-ME	/	-	-	/	/	/	-	=
U6	Liver pork	high	MP1	no	-ME	-LE	-HE	-ME	/	-	-	/	/	/	-	=
O1	Chicken	high	MP2	no	-LE	Ø	-HE	Ø	/	-	-	/	/	/	-	=
O2	Chicken	high	MP2	no	-LE	Ø	-HE	Ø	/	-	-	/	/	/	-	=
O3	Chicken	high	MP2	no	-LE	Ø	-HE	Ø	/	-	-	/	/	/	-	=
O4	Chicken	high	MP2	no	-ME	Ø	-HE	Ø	/	-	-	/	/	/	-	=
O5	Chicken	high	MP2	no	-ME	-LE	-ME	-LE	/	-	-	/	/	/	-	=
O6	Poultry neck skin	high	MP2	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
O7	Poultry neck skin	high	MP2	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
O8	Poultry neck skin	high	MP2	no	+HB	+HB	+HB	+HB	Salmonella spp	+	+	+HC	+HB	Salmonella spp	+	=
O9	Poultry neck skin	high	MP2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
O10	Poultry neck skin	high	MP2	no	+HB	+MB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
O11	Poultry neck skin	high	MP2	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
O12	Poultry neck skin	high	MP2	no	-LE	Ø	-HE	Ø	/	-	-	/	/	/	-	=
Q1	Rabbit leg	high	MP2	no	-LE	Ø	-HE	-ME	/	-	-	/	/	/	-	=
R1	Poultry neck skin	high	MP2	no	-HE	-ME	-HE	-HE	/	-	-	/	/	/	-	=
R2	Poultry neck skin	high	MP2	no	-ME	-HE	-HE	-HE	/	-	-	/	/	/	-	=
R3	Poultry neck skin	high	MP2	no	+HB	+HB	+HC	+HC	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
R4	Poultry neck skin	high	MP2	no	+HB	+HC	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
R5	Poultry neck skin	high	MP2	no	+HB	+HB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
R6	Poultry neck skin	high	MP2	no	+HB	+HB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
R7	Turkey filet	high	MP2	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
R8	Turkey filet	high	MP2	no	-ME	-ME	-HE	-HE	/	-	-	-ME	-HE	/	-	=
R9	Chicken leg	high	MP2	no	-ME	-LE	-HE	-HE	/	-	-	-ME	-HE	/	-	=
U1	Chicken leg	high	MP2	yes	+MB	+HC	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
U2	Duck breast	high	MP2	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
V1	Poultry neck skin	high	MP2	no	+HB	+HB	+HB	+HC	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=
V2	Poultry neck skin	high	MP2	no	+HB	+HB	+HB	+HB	Salmonella spp	+	+	+HB	+HB	Salmonella spp	+	=

Meat products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS <i>Salmonella</i> method						Comparison	
					RVS		MKTtn		Identification	Result	PCR result	RVS		Mktn		Identification		Result
					XLD	Edel	XLD	Edel				XLD	XLD					
G1	Rind sausage	230000000 high	MP3	no	+MB	+HB	+MB	+HC	<i>Salmonella spp</i>	+	+	+MC	-HE	<i>Salmonella spp</i>	+	=		
G2	Rind sausage	180000000 high	MP3	no	+MB	+MB	+HC	+HD	<i>Salmonella spp</i>	+	+	+MB	+MC	<i>Salmonella spp</i>	+	=		
G3	Rind sausage	150000000 high	MP3	no	+MB	+MB	+HC	+HC	<i>Salmonella spp</i>	+	+	+HC	+HC	<i>Salmonella spp</i>	+	=		
L1	Pig's caul	high	MP3	no	-HE	-HE	-ME	-ME	/	-	-	/	/	/	-	=		
L2	Ham	high	MP3	no	-LE	Ø	-LE	Ø	/	-	-	/	/	/	-	=		
L4	Roast turkey	high	MP3	no	-LE	-ME	-HE	-HE	/	-	-	/	/	/	-	=		
L5	Raw ham	high	MP3	no	-HE	-LE	-HE	-ME	/	-	-	/	/	/	-	=		
R11	Toulouse sausage	high	MP3	no	+MB	+MB	+HB	+HC	<i>Salmonella spp</i>	+	-	+HB	+HB	<i>Salmonella spp</i>	-	FN		
R12	Seasoned minced pork	high	MP3	no	-ME	+HB	-HE	-HE	/	-	-	/	/	/	-	=		
R13	Toulouse sausage	high	MP3	no	+HE	-HE	-HE	-HE	/	-	-	-HE	-HE	/	-	=		
S1	Seasoned minced pork	high	MP3	no	+MB	+HC	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+HB	<i>Salmonella spp</i>	+	=		
S2	Rind sausage	high	MP3	no	+MB	+MB	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+HB	<i>Salmonella spp</i>	+	=		
S3	Pork belly	high	MP3	no	+MB	+MB	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+HB	<i>Salmonella spp</i>	+	=		
S4	Roasted pork fillet	high	MP3	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=		
U3	Rind sausage	high	MP3	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=		
U4	Chipolata sausage	high	MP3	no	-ME	-ME	-ME	-HE	/	-	-	/	/	/	-	=		

Dairy products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS <i>Salmonella</i> method					Comparison
					RVS		MKTTn		Identification	Result	PCR result	RVS	Mkttn	Identification	Result	
					XLD	Edel	XLD	Edel				XLD	XLD			
B1	Epoisses cheese (pasteurized)	low	DP1	yes	+MA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+HA	+MA	<i>Salmonella spp</i>	+	=
B2	Soumatrain cheese (pasteurized)	low	DP1	yes	+MB	+MB	+MB	+HB	<i>Salmonella spp</i>	+	+	+HB	+HB	<i>Salmonella spp</i>	+	=
B3	Selles sur Cher goat cheese (raw milk)	high	DP1	yes	+HB	+HB	+HD	+HD	<i>Salmonella spp</i>	+	+	+MC	+HD	<i>Salmonella spp</i>	+	=
B4	St Maure cheese (raw milk)	high	DP1	yes	+HB	+HB	+HB	+HB	<i>Salmonella spp</i>	+	+	+HB	+HB	<i>Salmonella spp</i>	+	=
B5	Chabichou goat cheese (raw milk)	high	DP1	yes	+MB	+MB	+HC	+HC	<i>Salmonella spp</i>	+	+	+MB	+HB	<i>Salmonella spp</i>	+	=
B6	St Chevrier ashy goat cheese (pasteurized)	low	DP1	yes	+MA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
B7	Beaufort cheese (raw milk)	high	DP1	yes	+HA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
B8	Brie cheese (pasteurized)	low	DP1	yes	+HA	+HB	+HB	+HB	<i>Salmonella spp</i>	+	+	+HA	+HA	<i>Salmonella spp</i>	+	=
B9	Epoisses cheese (pasteurized)	low	DP1	yes	+MB	+HB	+HB	+HB	<i>Salmonella spp</i>	+	+	+HB	+HB	<i>Salmonella spp</i>	+	=
B10	Beaufort cheese (raw milk)	high	DP1	yes	+HA	+HA	+MA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
B22	Selles sur Cher goat cheese (raw milk)	high	DP1	no	-HE	-ME	-HE	-ME	/	-	-	/	/	/	-	=
B23	Chabichou goat cheese (raw milk)	high	DP1	no	-HE	-HE	-HE	-ME	/	-	-	/	/	/	-	=
B24	Brie cheese (pasteurized)	low	DP1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
B25	St Maure cheese (raw milk)	high	DP1	no	-HE	-ME	-HE	-LE	/	-	-	/	/	/	-	=
C11	Epoisses cheese (pasteurized)	low	DP1	no	-ME	-HE	-ME	-HE	/	-	-	/	/	/	-	=
C12	Soumatrain cheese (pasteurized)	low low 1/10	DP1 DP1	no	-HE	-HE	-HE	-HE	/	-	NO AMP	/	/	/	-	=
C13	Reblochon cheese (raw milk)	high high 1/10	DP1 DP1	no	-HE	-HE	-HE	-HE	/	-	NO AMP	/	/	/	-	=
C14	Beaufort cheese (raw milk)	high	DP1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
C15	Soft cheese with garlic & herbs (pasteurized)	low	DP1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
B11	Pastry with raspberry mousse	low	DP2	yes	+MA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+HA	+MA	<i>Salmonella spp</i>	+	=
B12	Strawberry tart	low	DP2	yes	+HB	+HB	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+MB	<i>Salmonella spp</i>	+	=
B13	Pastry	low	DP2	yes	+MB	+HB	+MB	+HB	<i>Salmonella spp</i>	+	+	+MB	+MB	<i>Salmonella spp</i>	+	=
B14	Paris-Brest (baked almond-topped choux pastry ring + praline flavored butter cream)	low	DP2	yes	+MB	+MB	+HC	+MB	<i>Salmonella spp</i>	+	+	+MB	+HC	<i>Salmonella spp</i>	+	=
B15	Noiselia hazelnut sweet spread	high	DP2	yes	+MA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+HA	+MA	<i>Salmonella spp</i>	+	=
B16	Opéra cake	high	DP2	yes	+HA	+MA	+HB	+HB	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
B17	Religieuse chocolat (choux pastry + chocolate custard)	high	DP2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
B18	Fraisier cake (chocolate genoise filled with fresh strawberries)	high	DP2	yes	+MA	+HA	+HB	+HB	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
B19	Chocolate éclair	high	DP2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MB	+MA	/	+	=
B20	Noiselia hazelnut sweet spread	high	DP2	yes	+HA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
C1	Chocolate éclair	low	DP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
C2	Strawberry tart	low	DP2	no	-ME	-HE	-HE	-HE	/	-	-	/	/	/	-	=
C3	Pastry with raspberry mousse	low	DP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
C4	Noiselia hazelnut sweet spread	low	DP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
C5	Fraisier cake (chocolate genoise filled with fresh strawberries)	low	DP2	no	Ø	Ø	-ME	-ME	/	-	-	/	/	/	-	=
C6	Miroir exotique (iced passion fruit mousse + almonds biscuits)	low	DP2	no	-HE	-HE	-HE	-HE	/	-	-	/	/	/	-	=
C7	St Honoré pastry	low	DP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
C8	Baba au rhum chocolate flavoured	low	DP2	no	-ME	-HE	Ø	Ø	/	-	-	/	/	/	-	=
C9	Pastry with rhum & kirsh	low	DP2	no	Ø	Ø	-ME	-LE	/	-	-	/	/	/	-	=
C10	Whipped cream-based raspberry dessert	low	DP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=

Dairy products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS <i>Salmonella</i> method						Comparison
					RVS		MKTn		Identification	Result	PCR result	RVS	Mktn	Identification	Result		
					XLD	Edel	XLD	Edel				XLD	XLD				
H1	Nursie premium 2nd age infant formula	milk	DP3	yes	Ø	Ø	Ø	Ø	/	-	-	Ø	Ø	/	-	=	
H2	Guigoz 2nd age infant formula (+ probiotics)	milk	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
H3	Gallia 2nd age infant formula	milk	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
H4	Gallia 1st age infant formula	milk	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
H5	Nursie premium 2nd age infant formula	milk	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H6	Guigoz 2nd age infant formula (+ probiotics)	milk	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H7	Gallia 2nd age infant formula	milk	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H8	Gallia 1st age infant formula	milk	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H9	Nidal natea 2nd age infant formula	milk	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H10	UHT skimmed milk	low	DP3	yes	+MA	+MA	+MA	+MA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
H11	UHT semi-skimmed milk	low	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
H12	UHT semi-skimmed milk	low	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=	
H13	UHT skimmed milk	low	DP3	yes	+MA	+MA	+MA	+MA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
H20	UHT skimmed milk	low	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H21	UHT skimmed milk	low	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H22	UHT skimmed milk	low	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H23	UHT semi-skimmed milk	low	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
H24	UHT semi-skimmed milk	low	DP3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=	
J23	Milk powder	milk	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
J24	Milk powder	milk	DP3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=	
M8	Bledlait croissance milk	milk	DP3	yes	+MA	+MA	+MB	+MB	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=	

Miscellaneous products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #				Assurance GDS <i>Salmonella</i> method					Comparison		
					RVS		MKTtn		Identification	Result	PCR result	RVS	Mkttn		Identification	Result
					XLD	Edel	XLD	Edel				XLD	XLD			
G4	Liquid egg	20000000 high	MS1	no	+HC	+HD	+HB	+HB	<i>Salmonella spp</i>	+	+	+HD	+HD	<i>Salmonella spp</i>	+	=
G5	Liquid egg	90000000 high	MS1	no	+MB	+MC	+HB	+HB	<i>Salmonella spp</i>	+	+	+HB	+HC	<i>Salmonella spp</i>	+	=
G6	Liquid egg	98000000 high	MS1	no	+MC	+HC	+HB	+MB	<i>Salmonella spp</i>	+	+	+HC	+HC	<i>Salmonella spp</i>	+	=
G7	Liquid egg	16000000 high	MS1	no	+MB	+MB	+HB	+MB	<i>Salmonella spp</i>	+	+	+HC	+MB	<i>Salmonella spp</i>	+	=
G8	Liquid egg	30000000 high	MS1	no	+MB	+MB	+MB	+MB	<i>Salmonella spp</i>	+	+	+MC	+HB	<i>Salmonella spp</i>	+	=
I1	Liquid egg	high	MS1	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
I2	Liquid egg	high	MS1	yes	+MA	+LA	+HA	+HA	<i>Salmonella spp</i>	+	+	+HA	+MA	<i>Salmonella spp</i>	+	=
I3	Liquid egg	high	MS1	yes	+MA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
I4	Liquid egg	high	MS1	yes	+MA	+MA	+HB	+HB	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
I9	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
I10	Liquid egg	high	MS1	no	-LE	Ø	Ø	Ø	/	-	-	/	/	/	-	=
I11	Liquid egg	high	MS1	no	-LE	-LE	-ME	-LE	/	-	-	/	/	/	-	=
I12	Liquid egg	high	MS1	no	-LE	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J2	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K5	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K6	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K7	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K8	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K9	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K10	Liquid egg	high	MS1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F11	Confectioner's custard	85000 low	MS2	yes	+MB	+MB	+HA	+HA	<i>Salmonella spp</i>	+	+	+MB	+HA	<i>Salmonella spp</i>	+	=
F12	Confectioner's custard	850000 low	MS2	yes	+MB	+MC	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+HA	<i>Salmonella spp</i>	+	=
F13	Crème brûlée	4200 low	MS2	yes	+MB	+MC	+HB	+MB	<i>Salmonella spp</i>	+	+	+LB	+MA	<i>Salmonella spp</i>	+	=
G9	Egg cream	46000000 high	MS2	no	+MB	+MB	-HE	+HD	<i>Salmonella spp</i>	+	+	+MC	-HE	<i>Salmonella spp</i>	+	=
G10	Egg cream	50000000 high	MS2	no	+MB	+MB	+HB	+HB	<i>Salmonella spp</i>	+	+	+HC	+HC	<i>Salmonella spp</i>	+	=
G11	Egg cream	36000000 high	MS2	no	+MC	+MC	+HC	+HC	<i>Salmonella spp</i>	+	+	+HB	+HC	<i>Salmonella spp</i>	+	=
G12	Confectioner's custard	high	MS2	no	-ME	-ME	-ME	-LE	/	-	-	/	/	/	-	=
G13	Confectioner's custard	high	MS2	no	-ME	-ME	-HE	-LE	/	-	-	/	/	/	-	=
G14	Confectioner's custard	high	MS2	no	-ME	-LE	-HE	-ME	/	-	-	/	/	/	-	=
G15	Confectioner's custard	high	MS2	no	-ME	-LE	-ME	-LE	/	-	-	/	/	/	-	=
G16	Confectioner's custard	high	MS2	no	-ME	Ø	-HE	-LE	/	-	-	/	/	/	-	=
N1	Mayonnaise	<10 low	MS2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
N2	Mayonnaise	<10 low	MS2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
N3	Mayonnaise	<10 low	MS2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
N4	Mayonnaise	<10 low	MS2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
N5	Mayonnaise	<10 low	MS2	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
N18	Mayonnaise	<10 low	MS2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N19	Mayonnaise	<10 low	MS2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N20	Mayonnaise	<10 low	MS2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N21	Mayonnaise	<10 low	MS2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F1	Goat/spinach pastry	10 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F2	Salmon/carrot cake	10 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F3	Endive with ham	10 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F4	Sauté of veal	13000 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F5	Veal kidneys + pasta	70 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F6	Tarte flambée (Flammenküche)	4500 low	MS3	yes	+MA	+MA	+MA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
F7	Sauté of pork	150 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
F8	Blanquette of veal	95000 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F9	Omelette	480 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+HA	<i>Salmonella spp</i>	+	=
F10	Filet de morette	530000 low	MS3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
F14	Goat/spinach pastry	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F15	Salmon/carrot cake	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F16	Endive with ham	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F17	Sauté of veal	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F18	Veal kidneys + pasta	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F19	Tarte flambée (Flammenküche)	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F20	Sauté of pork	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F21	Blanquette of veal	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F22	Omelette	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
F23	"Filet de morette" (white fish fillet with sauce)	low	MS3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=

Seafood & Vegetables products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS Salmonella method					Comparison
					RVS		MKTTn		Identification	Result	PCR result	RVS	Mkttn	Identification	Result	
					XLD	Edel	XLD	Edel				XLD	XLD			
D1	Filleted whiting	seafood	SP1	yes	+LB	+MB	+MB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
D2	Filleted scabbardfish	seafood	SP1	yes	+MB	+MB	+MB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
D3	Filleted pouting	seafood	SP1	yes	+MB	+LB	+HB	+HB	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
D4	Filleted whiting	seafood	SP1	yes	+LB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
D5	Filleted Haddock	seafood	SP1	yes	+MB	+LB	+HB	+HB	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
D16	Filleted whiting	seafood	SP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
D17	Filleted scabbardfish	seafood	SP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
E1	Filleted cod	seafood	SP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
E2	Filleted scabbardfish	seafood	SP1	yes	+MC	+MC	+HB	+HB	Salmonella spp	+	+	+MC	+MB	Salmonella spp	+	=
E3	Filleted perch	seafood	SP1	yes	+MB	+MB	+HB	+HC	Salmonella spp	+	+	+MB	+HC	Salmonella spp	+	=
E4	Filleted pouting	seafood	SP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
E5	Filleted red snapper	seafood	SP1	yes	+LC	+LC	+HD	+HC	Salmonella spp	+	+	+MC	+HC	Salmonella spp	+	=
E16	Filleted cod	seafood	SP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
E17	Filleted scabbardfish	seafood	SP1	no	-ME	-HE	-HE	-HE	/	-	-	/	/	/	-	=
E18	Filleted perch	seafood	SP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
E19	Filleted pouting	seafood	SP1	no	-ME	-LE	-HE	-LE	/	-	-	/	/	/	-	=
E20	Filleted red snapper	seafood	SP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
I15	Filleted ling	seafood	SP1	no	Ø	Ø	-ME	-ME	/	-	-	/	/	/	-	=
I16	Filleted perch	seafood	SP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
I17	Filleted perch	seafood	SP1	no	-ME	-ME	-HE	-LE	/	-	-	/	/	/	-	=
I18	Filleted whiting	seafood	SP1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
E6	Beet root	70000 low	VP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
E7	Red cabbage	50000 low high	VP1 VP1	yes	Ø	Ø	Ø	Ø	/	-	-	Ø	Ø	/	-	=
E8	Cucumber	960 low	VP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
E9	Grated carrots	high	VP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MC	+MB	Salmonella spp	+	=
E10	Tomato	5200000 high	VP1	yes	+MB	+MB	+MB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
E21	Beet root	70000 low	VP1	no	-ME	-LE	-ME	-ME	/	-	-	/	/	/	-	=
E22	Red cabbage	50000 low	VP1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
E23	Cucumber	960 low	VP1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
E24	Grated carrots	2500 low	VP1	no	-ME	-ME	-LE	-LE	/	-	-	/	/	/	-	=
E25	Tomato	5200000 low	VP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
I5	Endive	high	VP1	yes	+MB	+MB	+MC	+MB	Salmonella spp	+	-	+LB	+MB	Salmonella spp	-	FN
I6	Zucchini / Pepper mix	high	VP1	yes	-ME	-ME	-HE	-HE	/	-	-	-LE	-ME	/	-	=
I7	Grated carrots	high	VP1	yes	+MC	+LC	+HC	+HC	Salmonella spp	+	+	+LB	+MB	Salmonella spp	+	=
I8	Beet root	high	VP1	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
I13	Yeast	low	VP1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
I14	Yeast	low	VP1	no	Ø	Ø	-LE	Ø	/	-	-	/	/	/	-	=
J3	Salad	high	VP1	no	-ME	-ME	-ME	-HE	/	-	-	/	/	/	-	=
J4	Tomatoes	high	VP1	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
M9	Ciboulette	low	VP1	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+LA	+LA	Salmonella spp	+	=
M10	Paprika	low	VP1	yes	+MB	+MB	+HA	+MA	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
T1	Grated carrots	high	VP1	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
C21	Carrots	low high	VP2 VP2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
C22	Green peas	low	VP2	yes	+MA	+MA	+MA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
C23	Brussels sprouts	low	VP2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
C24	Beans	low	VP2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
C25	Green beans	low	VP2	yes	+MA	+HA	+MA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
E11	Rice	9500000 low high	VP2 VP2	yes	+MB	+MC	+MB	+HB	Salmonella spp	+	+	+MC	+HC	Salmonella spp	+	=
E12	Green cabbage	100 low	VP2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+MA	Salmonella spp	+	=
E13	Ratatouille	500 low	VP2	yes	+MB	+MA	+HB	+HA	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
E14	Carrot/rutabaga mix	200 low	VP2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
E15	Green beans	8000000 low	VP2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
J5	Tomato sauce	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J6	Lenses	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J7	Leeks and turnips	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J8	Carrots	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J9	Potatoes	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J10	Peas and green beans	low	VP2	no	-ME	-ME	-ME	-ME	/	-	-	/	/	/	-	=
J11	Cauliflower	low	VP2	no	-ME	-ME	Ø	Ø	/	-	-	/	/	/	-	=
J12	Green beans	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J13	Courgettes	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
J14	Brocolis	low	VP2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=

Feed products

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #				Assurance GDS Salmonella method					Comparison		
					RVS		MKTIn		Identification	Result	PCR result	RVS	Mkttn		Identification	Result
					XLD	Edel	XLD	Edel				XLD	XLD			
A6	Cattle cake	low	AF1	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
A7	Cattle cake	low	AF1	yes	+MA	+MA	+HB	+HB	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
D15	Cattle cake	10 low	AF1	yes	+MA	+LA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
D25	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K12	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K13	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K14	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L21	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L22	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L23	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L24	Cattle cake	low	AF1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
M13	Cattle cake	low	AF1	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+MA	Salmonella spp	+	=
M14	Cattle cake	low	AF1	yes	+MA	+MA	+HA	+MA	Salmonella spp	+	+	+MA	+MA	Salmonella spp	+	=
M15	Cattle cake	high	AF1	yes	+MA	+MA	+MA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
M16	Cattle cake	low	AF1	yes	+MA	+MA	+MA	+HA	Salmonella spp	+	+	+HA	+MA	Salmonella spp	+	=
A4	Flour	high	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A8	Half white middlings	low	AF2	yes	+MB	+MB	+HA	+HA	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
A9	Dry dog food	low	AF2	yes	+HA	+HA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
A10	Dry dog food	low	AF2	yes	+HA	+HA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
A11	Fishmeal	low	AF2	yes	+HA	+HA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
A12	Dry dog food	low	AF2	yes	+HA	+HA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
A16	Dry dog food	low	AF2	no	-HE	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A17	Dry dog food	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A18	Half white middlings	low	AF2	no	Ø	Ø	-ME	-HE	/	-	-	/	/	/	-	=
A19	Fishmeal	low	AF2	no	-LE	-LE	-ME	-LE	/	-	-	/	/	/	-	=
A20	Soya flour	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A21	Meat flour	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
D11	Dry cat food	10 low	AF2	yes	+MA	+MA	+MA	+MA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
D12	Dry dog food	10 low	AF2	yes	+MA	+HA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
D13	Soya flour	<10 low	AF2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
D14	Rabbit food	330000 high	AF2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
D23	Dry cat food	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
D24	Soya flour	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
H14	Hen food	240000 High low	AF2	yes	+MB	+MC	+HB	+HB	Salmonella spp	+	-	+MB	+HB	Salmonella spp	-	FN FN
H15	Dry cat food	low	AF2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
K11	Dry cat food	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L19	Dry cat food	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L20	Seeds for birds	low	AF2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
M11	Bran flour	low	AF2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
M12	Dry food	low	AF2	yes	+MA	+HA	+MA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
A13	Wet dog food (beef)	low	AF3	yes	+HA	+HA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
A14	Wet dog food (beef)	low	AF3	yes	+HA	+HA	+HA	+HA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=
A15	Wet dog food (beef)	low	AF3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A22	Wet dog food (poultry)	low	AF3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A23	Wet dog food (lamb)	low	AF3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
A24	Wet cat food	low	AF3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
D6	Meat scraps for animals	20000000 high	AF3	yes	+MB	+LB	+HB	+HB	Salmonella spp	+	+	+MB	+MB	Salmonella spp	+	=
D7	Meat scraps for animals	85000000 high	AF3	yes	+LB	+LB	+HB	+HB	Salmonella spp	+	+	+MC	+HB	Salmonella spp	+	=
D8	Meat scraps for animals	90000000 high	AF3	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
D9	Meat scraps for animals	180000000 high	AF3	yes	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
D10	Meat scraps for animals	700000 high	AF3	yes	+MB	+MA	+HA	+HA	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
D18	Meat scraps for animals	20000000 high	AF3	no	-LE	Ø	-HE	-HE	/	-	-	/	/	/	-	=
D19	Meat scraps for animals	85000000 high	AF3	no	-LE	-LE	-ME	-LE	/	-	-	/	/	/	-	=
D20	Meat scraps for animals	90000000 high	AF3	no	-LE	Ø	-ME	Ø	/	-	-	/	/	/	-	=
D21	Meat scraps for animals	180000000 high	AF3	no	-ME	Ø	-HE	-LE	/	-	-	/	/	/	-	=
D22	Meat scraps for animals	700000 high	AF3	no	-ME	-ME	-ME	-LE	/	-	-	/	/	/	-	=
L17	Meat scraps for animals	high	AF3	no	-LE	-LE	-HE	-HE	/	-	-	/	/	/	-	=
L18	Meat scraps for animals	high	AF3	no	-LE	-LE	-HE	-HE	/	-	-	/	/	/	-	=
M5	Sausages for animals	high	AF3	yes	+MB	+MB	+MB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
M6	Sausages for animals	high	AF3	yes	+MB	+MB	+MB	+HB	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
M7	Meat scraps for animals	high high	AF3	yes	+MB	+MB	+HD	-HE	Salmonella spp	+	-	+MB	+HC	Salmonella spp	-	FN
N6	Wet food (various meats)	10 low	AF3	yes	+MA	+MA	+MA	+MA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
N7	Wet food (various meats)	<10 low	AF3	yes	+MA	+MA	+HA	+MA	Salmonella spp	+	+	+HA	+HA	Salmonella spp	+	=

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS Salmonella method					Comparison
					RVS		MKTtn		Identification	Result	PCR result	RVS	Mktn	Identification	Result	
					XLD	Edel	XLD	Edel				XLD	XLD			
H16	Process water	low	EN1	yes	Ø	Ø	Ø	Ø	/	-	-	Ø	Ø	/	-	=
H17	Process water	low	EN1	yes	+MA	+MA	+MA	+HA	Salmonella spp	+	+	+MA	+MA	Salmonella spp	+	=
H18	Process water	low	EN1	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+MA	Salmonella spp	+	=
H19	Process water	low	EN1	yes	Ø	Ø	Ø	Ø	/	-	-	Ø	Ø	/	-	=
K1	Process water	low	EN1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K2	Process water	low	EN1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K3	Process water	low	EN1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
K4	Process water	low	EN1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N8	Process water	<10 low	EN1	yes	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N9	Process water	<10 low	EN1	yes	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N10	Process water	<10 low	EN1	yes	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N11	Process water	<10 low	EN1	yes	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N22	Process water	<10 low	EN1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
N23	Process water	<10 low	EN1	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
O13	Process water	low	EN1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
O14	Process water	low	EN1	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
O15	Process water	low	EN1	no	-LE	-LE	-ME	-HE	/	-	-	/	/	/	-	=
O16	Process water	low	EN1	no	-HE	-ME	-HE	-ME	/	-	-	/	/	/	-	=
Q4	Process water	low	EN1	no	+MB	+MB	+HB	+HB	Salmonella spp	+	+	+LB	+MB	Salmonella spp	+	=
Q5	Process water	low	EN1	no	-LE	-LE	-HE	-HE	/	-	-	/	/	/	-	=
S11	Water rinse from carving booth	high	EN1	no	+MB	+MB	+HC	+HC	Salmonella spp	+	+	+MB	+HC	Salmonella spp	+	=
S12	Water rinse from carving booth	high	EN1	no	+MC	+LC	+HC	+HC	Salmonella spp	+	+	+MB	+HC	Salmonella spp	+	=
T2	Process water	high	EN1	yes	+MA	+LA	+MA	+MA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
T3	Process water	high	EN1	yes	+MA	+MA	+MA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
T4	Process water	high	EN1	yes	+MA	+MA	+MA	+MA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
T5	Process water	high	EN1	yes	+MC	+MC	+HD	+HC	Salmonella spp	+	+	+MC	+HD	Salmonella spp	+	=
T6	Process water	high	EN1	yes	+MB	+MB	+HC	+HB	Salmonella spp	+	+	+MB	+HD	Salmonella spp	+	=
T7	Process water	high	EN1	yes	+MC	+MC	+HD	+HD	Salmonella spp	+	+	+MD	-HE	Salmonella spp	+	=
T8	Process water	high	EN1	yes	+MD	+MC	+HD	+HC	Salmonella spp	+	+	+MD	+HC	Salmonella spp	+	=
I23	Sausage preparation booth	low	EN2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
I24	Butcher's shop	low	EN2	no	-ME	-LE	-HE	-HE	/	-	-	/	/	/	-	=
J19	White tank	low	EN2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
J21	Floor of sample fridge	low	EN2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
J22	Shelf in cold room	low	EN2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
L9	Knife from a cheese booth	low	EN2	no	-LE	Ø	-LE	Ø	/	-	-	/	/	/	-	=
S13	Surface of meat cutting board	high	EN2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
S14	Surface of working area	high	EN2	no	+MB	+MC	+HC	+HC	Salmonella spp	+	+	+MB	+HC	Salmonella spp	+	=
S15	Surface of meat cutting board	high	EN2	no	+MC	+MC	+HB	+HC	Salmonella spp	+	+	+MC	+HB	Salmonella spp	+	=
S16	Surface of knife for meat carving	high	EN2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
S17	Surface of knife for meat carving	high	EN2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
S18	Surface from meat cutting board	high	EN2	no	-ME	-LE	-HE	-LE	/	-	-	/	/	/	-	=
U7	Stainless steel shelf of a fish booth	high	EN2	yes	+MA	+MA	+HA	+HA	Salmonella spp	+	+	+MA	+HA	Salmonella spp	+	=
U8	Surface	high	EN2	yes	+MB	+MB	+HB	+HC	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
U9	Surface	high	EN2	yes	+MB	+MC	+HB	+HC	Salmonella spp	+	+	+MB	+HB	Salmonella spp	+	=
U10	Floor of cold room	high	EN2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
U11	Trolley workshop fish supply	high	EN2	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
U12	Laundry floor	high	EN2	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=

Environment

Code	Product	Total count flora / Protocol	Cat.	Artif. Cont.	Reference method ISO 6579 #						Assurance GDS <i>Salmonella</i> method					Comparison
					RVS		MKTTn		Identification	Result	PCR result	RVS	Mktn	Identification	Result	
					XLD	Edel	XLD	Edel				XLD	XLD			
I19	Scraps from a meat carving plant	low	EN3	no	-LE	-LE	-HE	-HE	/	-	-	/	/	/	-	=
I20	Scraps from sausages	low	EN3	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
I21	Scraps from a butcher's shop	low	EN3	no	-ME	-ME	-ME	-LE	/	-	-	/	/	/	-	=
J15	Scraps from meat	low	EN3	no	-LE	-LE	-ME	-HE	/	-	-	/	/	/	-	=
K17	Scraps from a butcher's shop	low	EN3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
K18	Scraps from a butcher's shop (pâté)	low	EN3	yes	+MA	+MA	+MA	+MA	<i>Salmonella spp</i>	+	+	+HA	+MA	<i>Salmonella spp</i>	+	=
K19	Scraps from cutting machine	low	EN3	yes	+HA	+HA	+HA	+HA	<i>Salmonella spp</i>	+	+	+HA	+MA	<i>Salmonella spp</i>	+	=
K20	Vegetables scraps	low	EN3	yes	+MB	+MB	+MB	+HB	<i>Salmonella spp</i>	+	+	+MB	+MB	<i>Salmonella spp</i>	+	=
K21	Sauce residues from catering booth	low	EN3	yes	+MA	+MA	+MA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
K22	Scraps from a catering booth	low	EN3	yes	+MA	+MA	+HA	+HA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
K23	Scraps from a delicatessen's shop	low	EN3	yes	+HB	+HB	+HB	+HB	<i>Salmonella spp</i>	+	+	+HB	+HB	<i>Salmonella spp</i>	+	=
K24	Scraps from a delicatessen's shop	low	EN3	yes	+MA	+MA	+MA	+MA	<i>Salmonella spp</i>	+	+	+MA	+MA	<i>Salmonella spp</i>	+	=
L12	Scraps from cutting machine	low	EN3	no	-LE	Ø	Ø	Ø	/	-	-	/	/	/	-	=
L13	Scraps from cutting machine	low	EN3	no	-LE	Ø	-ME	Ø	/	-	-	/	/	/	-	=
L14	Scraps from cheese	low	EN3	no	-ME	-ME	-HE	-ME	/	-	NO AMP	/	/	/	-	=
		low	EN3								NO AMP					=
		high	EN3													=
L15	Scraps découpe végétaux	low	EN3	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
L16	Scraps from a catering booth	low	EN3	no	Ø	Ø	Ø	Ø	/	-	-	/	/	/	-	=
M3	Scraps from meat	low	EN3	no	-LE	Ø	-ME	-ME	/	-	-	/	/	/	-	=
N14	Scraps from meat	low	EN3	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
N15	Scraps from meat	low	EN3	no	+MB	+MB	+HC	-HE	<i>Salmonella spp</i>	+	+	-HE	+MB	<i>Salmonella spp</i>	+	=
S8	Scraps from meat	high	EN3	no	-ME	-ME	-HE	-HE	/	-	-	/	/	/	-	=
S9	Scraps from meat	high	EN3	no	+MB	+LB	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+HC	<i>Salmonella spp</i>	+	=
S10	Scraps from meat	high	EN3	no	+MB	+MB	+HB	+HB	<i>Salmonella spp</i>	+	+	+MB	+HB	<i>Salmonella spp</i>	+	=

APPENDIX C:

INCLUSIVITY / EXCLUSIVITY

Strain	Origin	TSA	Test GDS		
			nb of cells in 225 mL BPW before incubation	Test Result (low protocol)	
S86	<i>Salmonella Anatum</i>	Chocolate	6,0E+08 2,7E+08	4.8 10.8	+ +
S24	<i>Salmonella Montevideo</i>	Beef liver	8,0E+08	6.4	+
S55	<i>Salmonella Typhimurium</i>	Milk	2,5E+08	2.0	+
S15	<i>Salmonella Hadar</i>	Chicken meat	1,1E+09	8.8	+
S10	<i>Salmonella Derby</i>	Horse meat	1,2E+09	9.6	+
S123	<i>Salmonella Agona</i>	Milk powder	2,3E+08	9.2	+
S2	<i>Salmonella Amsterdam</i>	Vegetable	2,3E+08 2,0E+08	9.2 0.8	- -
S141	<i>Salmonella Amsterdam</i>	Poultry	2,3E+08	11.5	+
S142	<i>Salmonella Amsterdam</i>	Poultry feed	2,8E+08	1.4	-
S68	<i>Salmonella Illb 38:r:z</i>	Turkey battery farming	1,3E+08	5.2	+
S74	<i>Salmonella Illb 61:-:-</i>	Turkey	8,0E+07	3.2	+
S79	<i>Salmonella Illb 61:z:1,5</i>	Turkey Blanquette	9,0E+07 1,2E+08	3.6 4.8	+ +
S4	<i>Salmonella Brandenburg</i>	Heifer liver	1,9E+08	7.6	+
S5	<i>Salmonella Brandenburg</i>	Pig liver	1,4E+08	5.6	+
S6	<i>Salmonella Brandenburg</i>	Kangaroo meat	3,1E+08	12.4	+
S8	<i>Salmonella Bredeney</i>	Pig offal	1,8E+08	7.2	+
S103	<i>Salmonella Cerro</i>	Cream bun	1,2E+08	4.8	+
S11	<i>Salmonella Derby</i>	Pig liver	8,00E+07	3.2	+
S14	<i>Salmonella Enteritidis</i>	Pastry	2,4E+08	9.6	+
S38	<i>Salmonella Enteritidis</i>	Egg product	3,4E+08	13.6	+
S43	<i>Salmonella Enteritidis</i>	Egg product	1,0E+08	0.4	+
S122	<i>Salmonella Enteritidis</i>	Egg product	1,6E+08	6.4	+
S66	<i>Salmonella Havana</i>	Goose flock	1,3E+08	2.5	+
S87	<i>Salmonella Blockley</i>	Basil	2,8E+08	11.2	+
S113	<i>Salmonella Senftenberg</i>	Animal feed	1,5E+08	0.6	+
S16	<i>Salmonella Hadar</i>	Poultry meat	2,1E+08	8.4	+
S19	<i>Salmonella Infantis</i>	Poultry meat	2,2E+08	8.8	+
S50	<i>Salmonella Heidelberg</i>	Poultry	1,5E+08	0.6	+
S10	<i>Salmonella Derby</i>	Viande de cheval	1,2E+08	4.8	+
S22	<i>Salmonella Michigan</i>	Viande de cheval	2,9E+08	11.6	+
S21	<i>Salmonella Mbandaka</i>	Veal heart	1,7E+08	6.8	+
S13	<i>Salmonella Saintpaul</i>	Meat product	1,6E+08	6.4	+
S15	<i>Salmonella Hadar</i>	Poultry meat	1,7E+08	6.8	+
S25	<i>Salmonella Newport</i>	Poultry meat	2,1E+08	8.4	+
S23	<i>Salmonella Montevideo</i>	Poultry meat	3,2E+08	12.8	+
S81	<i>Salmonella Kedougou</i>	Animal feed	2,0E+08	0.8	+
S80	<i>Salmonella Kedougou</i>	Tuna fish	2,2E+08	8.8	+
S45	<i>Salmonella Indiana</i>	Brie cheese	1,3E+08	5.2	+
S70	<i>Salmonella Illb 61:k:1,5,7</i>	Lamb brain	1,4E+08	5.6	+
S85	<i>Salmonella Liverpool</i>	Animal feed	2,8E+08	11.2	+
S67	<i>Salmonella Llandoff</i>	Animal feed	2,1E+08	8.4	+
S90	<i>Salmonella Oranienburg</i>	Animal feed	1,6E+08	6.4	+
S75	<i>Salmonella Illb 61:i:z5,3</i>	Chicken leg	1,3E+08	5.2	+
S26	<i>Salmonella Typhimurium</i>	Pig liver	2,3E+08	9.2	+
S31	<i>Salmonella Virchow</i>	Cockle	2,1E+08	8.4	+
S59	<i>Salmonella Sandiego</i>	Dry herbs	2,8E+08	11.2	+
S69	<i>Salmonella Illa 48;z4;z23</i>	Goose battery farming	3,3E+08	13.2	+
S71	<i>Salmonella Seftenberg</i>	Fish	3,4E+08	13.6	+
S83	<i>Salmonella Westhampton</i>	Animal feed	3,1E+08	12.4	-
S143	<i>Salmonella Westhampton</i>	Poultry	9,0E+07	4.5	+
S144	<i>Salmonella Westhampton</i>	Animal flour	3,5E+08	17.5	-
S97	<i>Salmonella Typhimurium</i>	Saint Nectaire cheese	3,7E+08	14.8	+
S137	<i>Salmonella Pullorum</i>	Collection	3,9E+08	15.6	+
S139	<i>Salmonella Gallinarum</i>	Collection	8,0E+07	3.2	+
S99	<i>Salmonella Paratyphi A</i>	Collection	1,3E+08	5.2	+
S100	<i>Salmonella Paratyphi B</i>	Collection	1,1E+08	4.4	+
S101	<i>Salmonella Paratyphi C</i>	Collection	1,7E+08	6.8	+
S136	<i>Salmonella Typhi Typhi</i>	Collection	3,3E+08	13.2	+
S53	<i>Salmonella Umbilo</i>	Environment water	4,8E+08	19.2	+

Exclusivity

Strain		Origin	TSA	Test GDS	
				nb of cells in 225 mL BPW before incubation	Test Result
CIT 53	<i>Citrobacter diversus</i>	Instant yeast	2,3E+09	2,3E+06	-
CIT52	<i>Citrobacter diversus</i>	Dry herbs	2,5E+09	2,5E+06	-
			1,1E+08	1,1E+05	-
CIT26	<i>Citrobacter freundii</i>	Fish	3,0E+08	3,0E+05	-
			4,8E+08	1,8E+05	-
CIT 27	<i>Citrobacter freundii</i>	Milk	2,6E+08	2,6E+05	-
KL 8	<i>Klebsiella oxytoca</i>	Animal feed	1,2E+08	1,2E+05	-
ENT 17	<i>Enterobacter cloacae</i>	Milk powder	2,5E+08	2,5E+05	-
CIT 23	<i>Citrobacter freundii</i>	Vegetable	1,5E+08	1,5E+05	-
EN 24	<i>Citrobacter freundii</i>	Meat product	6,0E+07	6,0E+04	-
ENT 83	<i>Enterobacter sakazakii</i>	Milk powder	7,0E+07	7,0E+04	-
CIT 30	<i>Citrobacter diversus</i>	Animal feed	1,5E+08	1,5E+05	-
Ha 31	<i>Hafnia alvei</i>	Minced meat	3,7E+08	3,7E+05	-
Ha 54	<i>Hafnia alvei</i>	Reblochon cheese	2,6E+08	2,6E+05	-
KL 63	<i>Klebsiella pneumoniae</i>	Vegetables Céleri	1,0E+08	1,0E+05	-
ENT 59	<i>Enterobacter sakazakii</i>	Pastry Paris Brest	1,1E+08	1,1E+05	-
CIT 65	<i>Citrobacter youngae</i>	Vegetable	8,0E+07	8,0E+04	-
PS30	<i>Pseudomonas aeruginosa</i>	Red mullet filet	5,4E+07	5,4E+04	-
Ec18	<i>Escherichia Coli</i>	Sausage meat	6,0E+08	6,0E+05	-
Ec19	<i>Escherichia Coli</i>	Red cabbage	3,0E+08	3,0E+05	-
Ec20	<i>Escherichia Coli</i>	Tomato	3,0E+08	3,0E+05	-
EN44	<i>Proteus mirabilis</i>	Poultry liver	7,0E+08	7,0E+05	-
PS 33	<i>Pseudomonas fluorescens</i>	Minced meat	1,0E+08	1,0E+05	-
EN 49	<i>Serratia marcescens</i>	Raw milk	4,5E+08	4,5E+05	-
18	<i>Aeromonas hydrophila</i>	Minced meat	4,0E+08	4,0E+05	-
EN73	<i>Shigella sonnei</i>	Collection	2,0E+08	1,5E+05	-
EN72	<i>Shigella flexneri</i>	Collection	1,5E+08	2,0E+05	-
EN7	<i>Yersinia enterocolitica</i>	Egg product	8,0E+07	8,0E+04	-
Ba 1	<i>Bacillus cereus</i>	Whole egg	2,5E+06	2,5E+04	-
Ba 8	<i>Bacillus licheniformis</i>	Dairy product	4,0E+06	4,0E+06	-
St 17	<i>Staphylococcus aureus</i>	Frozen yogurt	5,0E+07	5,0E+05	-
St 20	<i>Staphylococcus epidermidis</i>	Smoked salmon	4,0E+07	4,0E+05	-
EN43	<i>Proteus mirabilis</i>	Produit carné	1,0E+07	1,0E+04	-
EN45	<i>Proteus mirabilis</i>	Volaille	4,0E+08	4,0E+05	-

APPENDIX D:
INTERLABORATORY STUDY
-
DETAILED RESULTS OF
PARTICIPANT LABORATORIES

Laboratory A

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			210							

Laboratory B

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			180							

Laboratory C

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	+	+	+	+	+	FP	+	+	+	FP
12	+	+	+	+	+	FP	+	+	+	FP
13	+	+	+	+	+	FP	+	+	+	FP
14	+	+	+	+	+	FP	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	+	+	+	+	+	FP	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			290							

Laboratory D

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			240							

Laboratory E

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	+	+	+	+	+	FP	-	/	-	=
13	+	+	+	+	+	FP	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	+	+	+	FP
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			NC							

Laboratory F

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			140							

Laboratory G

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):					190					

Laboratory H

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):					75					

Laboratory I

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	+	+	+	+	+	FP	+	+	+	FP
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):					120					

Laboratory J

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			29							

Laboratory K

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			400							

Laboratory L

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	+	+	-	-	+	FP	-	/	-	=
20	-	-	+	+	+	FP	-	/	-	=
21	+	+	+	+	+	FP	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):			NC							

Laboratory M

Code sample	Reference method ISO 6579					Comparison / expected results	Alternative method Assurance GDS Salmonella			Comparison / expected results
	RVS		MKTtn		Result		Test result	Confirmation	Result	
	XLD	SM ID2	XLD	SM ID2						
1	-	-	-	-	-	=	-	/	-	=
2	-	-	-	-	-	=	-	/	-	=
3	+	+	+	+	+	=	+	+	+	=
4	+	+	+	+	+	=	+	+	+	=
5	+	+	+	+	+	=	+	+	+	=
6	+	+	+	+	+	=	+	+	+	=
7	+	+	+	+	+	=	+	+	+	=
8	+	+	+	+	+	=	+	+	+	=
9	+	+	+	+	+	=	+	+	+	=
10	+	+	+	+	+	=	+	+	+	=
11	-	-	-	-	-	=	-	/	-	=
12	-	-	-	-	-	=	-	/	-	=
13	-	-	-	-	-	=	-	/	-	=
14	-	-	-	-	-	=	-	/	-	=
15	+	+	+	+	+	=	+	+	+	=
16	+	+	+	+	+	=	+	+	+	=
17	+	+	+	+	+	=	+	+	+	=
18	+	+	+	+	+	=	+	+	+	=
19	-	-	-	-	-	=	-	/	-	=
20	-	-	-	-	-	=	-	/	-	=
21	+	+	+	+	+	=	+	+	+	=
22	+	+	+	+	+	=	+	+	+	=
23	+	+	+	+	+	=	+	+	+	=
24	+	+	+	+	+	=	+	+	+	=
Total flora of milk (UFC/ml):		170								

APPENDIX E:
INTERLABORATORY STUDY
-
ACCORDANCE

ALTERNATIVE METHOD

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Probability of negatives	Probability of negative pairs	Probability of positives	Probability of positive pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory G	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							0,96
Accordance:							96%

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory G	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							1,00
Accordance:							100%

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory G	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							1,00
Accordance:							100%

REFERENCE METHOD

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Probability of negatives	Probability of negative pairs	Probability of positives	Probability of positive pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	6	0,75	0,56	0,25	0,06	0,63
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory G	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	6	0,75	0,56	0,25	0,06	0,63
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							0,92
Accordance:							92%

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory G	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							1,00
Accordance:							100%

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory G	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							1,00
Accordance:							100%

APPENDIX F:

INTERLABORATORY STUDY
-
CONCORDANCE

ALTERNATIVE METHOD

Number of laboratories 12

Number of positives per laboratory 8

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	688	704
Laboratory B	8	8	688	704
Laboratory D	8	8	688	704
Laboratory E	8	7	610	704
Laboratory F	8	8	688	704
Laboratory G	8	8	688	704
Laboratory H	8	8	688	704
Laboratory I	8	7	610	704
Laboratory J	8	8	688	704
Laboratory K	8	8	688	704
Laboratory L	8	8	688	704
Laboratory M	8	8	688	704
Total			8100	8448
Concordance	95,88%			

Number of laboratories 12

Number of positives per laboratory 8

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	704	704
Laboratory B	8	8	704	704
Laboratory D	8	8	704	704
Laboratory E	8	8	704	704
Laboratory F	8	8	704	704
Laboratory G	8	8	704	704
Laboratory H	8	8	704	704
Laboratory I	8	8	704	704
Laboratory J	8	8	704	704
Laboratory K	8	8	704	704
Laboratory L	8	8	704	704
Laboratory M	8	8	704	704
Total			8448	8448
Concordance	100,00%			

Number of laboratories 12

Number of positives per laboratory 8

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	704	704
Laboratory B	8	8	704	704
Laboratory D	8	8	704	704
Laboratory E	8	8	704	704
Laboratory F	8	8	704	704
Laboratory G	8	8	704	704
Laboratory H	8	8	704	704
Laboratory I	8	8	704	704
Laboratory J	8	8	704	704
Laboratory K	8	8	704	704
Laboratory L	8	8	704	704
Laboratory M	8	8	704	704
Total			8448	8448
Concordance	100,00%			

REFERENCE METHOD

Number of laboratories 12

Number of positives per laboratory 8

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	664	704
Laboratory B	8	8	664	704
Laboratory D	8	8	664	704
Laboratory E	8	6	516	704
Laboratory F	8	8	664	704
Laboratory G	8	8	664	704
Laboratory H	8	8	664	704
Laboratory I	8	7	592	704
Laboratory J	8	8	664	704
Laboratory K	8	8	664	704
Laboratory L	8	6	516	704
Laboratory M	8	8	664	704
Total			7600	8448
Concordance	89,96%			

Number of laboratories 12

Number of positives per laboratory 8

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	704	704
Laboratory B	8	8	704	704
Laboratory D	8	8	704	704
Laboratory E	8	8	704	704
Laboratory F	8	8	704	704
Laboratory G	8	8	704	704
Laboratory H	8	8	704	704
Laboratory I	8	8	704	704
Laboratory J	8	8	704	704
Laboratory K	8	8	704	704
Laboratory L	8	8	704	704
Laboratory M	8	8	704	704
Total			8448	8448
Concordance	100,00%			

Number of laboratories 12

Number of positives per laboratory 8

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	704	704
Laboratory B	8	8	704	704
Laboratory D	8	8	704	704
Laboratory E	8	8	704	704
Laboratory F	8	8	704	704
Laboratory G	8	8	704	704
Laboratory H	8	8	704	704
Laboratory I	8	8	704	704
Laboratory J	8	8	704	704
Laboratory K	8	8	704	704
Laboratory L	8	8	704	704
Laboratory M	8	8	704	704
Total			8448	8448
Concordance	100,00%			