

M09

Standard Microbiology Program Without *E.coli* O157:H7 & Listeria

04-15-19 (Shipment Date)

06-04-19 (Report Issue Date)



Proficiency Testing Provider
Certificate 1782.01

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Appendix A- Participating Laboratory's Results

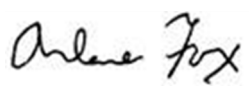
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Report Authorization

This report has been authorized by Arlene Fox, Senior Director of the AOAC laboratory Proficiency Testing Program.



1.0 Introduction

Test materials for the Standard Microbiology Program were shipped to participants on April 15, 2019. Each laboratory was given a site identification number in order to maintain confidentiality. Participants were encouraged to analyze the samples on April 16, 2019 and urged to initiate analyses by April 22, 2019. Instructions on how to use the confidential online data submission system was available upon login. The participants were to submit an electronic response online to: verify the condition of the test materials upon receipt; confirm the safe handling of the test materials containing *Salmonella* and *Staphylococcus* by participants; and indicate sample quantity. Participants were also instructed to report results electronically. Participants were instructed to analyze the test materials according to procedures routinely used in their laboratories. Instructions were provided for all dilutions. The results were recorded and were to be submitted to AOAC on April 30, 2019.

2.0 Preparation of Test Material

Each set of test materials included eight samples, samples 1-4 each were to contain approximately 75 grams of frozen rehydrated mashed potato mixture and samples 5-8 each were to contain approximately 50 grams of frozen rehydrated mashed potato mixture. The samples were shipped in color coded vials to assist in maintaining proper sample identity. Four of the samples were for qualitative testing (Samples 1-4) and four of the samples were for quantitative testing (Samples 5-8). Samples number 5 and 6 were prepared as duplicates and samples 7 and 8 were prepared as duplicates. The matrix was screened prior to spiking. Two samples were randomly selected to verify the presence or absence of pathogens in the qualitative samples. In addition, a set of these samples was analyzed on August 7, 2018. Ten quantitative samples were randomly selected and analyzed in duplicate to verify the homogeneity of the test material prior to shipment. The requirements of Section ISO/IEC Standard 17043:2010(E) Conformity Assessment - General requirements for proficiency testing schemes were met for all other samples used for evaluation. Samples were prepared by the following laboratory:

Silliker Solution Center
3600 Eagles Nest Drive, Bldg. A
Crete, IL 60417

3.0 Analyses Requested

Samples 1-4 Qualitative	<i>Salmonella</i>	Indicate Positive/Negative If positive, report presence/absence of O and H antigens, and antigen identification if applicable.
Samples 5-8 Quantitative	Aerobic Plate Count MPN	Dilution $10^{-2} - 10^{-5}$
	Aerobic Plate Count	Dilution $10^{-2} - 10^{-5}$
	Coliform MPN	Dilution $10^{-2} - 10^{-5}$
	Coliform Plate Count	Dilution $10^{-1} - 10^{-3}$
	<i>E. coli</i> MPN	Dilution $10^{-2} - 10^{-5}$
	<i>E. coli</i> Plate Count	Dilution $10^{-1} - 10^{-3}$
	Coagulase Positive <i>Staphylococcus</i> MPN	Dilution $10^{-2} - 10^{-6}$
	Coagulase Positive <i>Staphylococcus</i> Plate Count	Dilution $10^{-1} - 10^{-3}$
	Yeast & Mold MPN	Dilution $10^{-1} - 10^{-4}$
	Yeast & Mold	Dilution $10^{-1} - 10^{-4}$
	<i>Bacillus cereus</i> MPN	Dilution $10^{-1} - 10^{-3}$
	<i>Bacillus cereus</i> Plate Count	Dilution $10^{-1} - 10^{-3}$
	<i>Enterobacteriaceae</i> MPN	Dilution $10^{-1} - 10^{-3}$
	<i>Enterobacteriaceae</i> Count	Dilution $10^{-1} - 10^{-3}$

Participants had the option of reporting Not Tested for any analysis.

4.0 Calculation and Interpretation of z-score

For each individual result, a z-score was calculated as follows:

$$z = \frac{(x - X)}{s}$$

where:

z = the z score (standard score)

x = the reported value of analyte

X = the assigned value, the best estimate of the true concentration

s = the estimate of variation (standard deviation)

The robust procedure from *ISO 13528:2005 (E), Statistical methods for use in proficiency testing by interlaboratory comparisons* is used in processing the result data. Robust statistics relies on medians rather than means, and uses more information from the central than from the outlying observations. This approach is being used to minimize the effect of extreme results on the calculation of z-scores. There are two types of extreme results in microbial analyses: "Blunders" and "Outliers". Blunder results were likely due to errors, such as transcription errors, incorrect sample identification, or a major problem performing the analysis. Blunders are defined as results that differ from the initial mean of the participant's results prior to log₁₀ transformation, by a factor of 100. These results have been labeled as "pre-screened as an outlier."

The data was log₁₀ transformed prior to the calculation of statistics. The assigned value was determined by the consensus of the majority after the removal of outliers by the robust procedure. Outlier results have been labeled "Outlier: Z beyond 3". The assigned value, standard deviation, and the z-scores were recalculated without the outliers. The blunder results and outlier results were still evaluated within the proficiency scheme and given the appropriate performance rating. Measurement uncertainty (standard uncertainty of the assigned value) has also been provided.

All quantitative data submitted by the participant as 1 to 30 counts per gram of matrix is treated as a zero.

The following interpretation of z-scores for each individual test result is provided in of ISO/IEC Standard 17043:2010(E) Conformity Assessment as common examples of application of z-scores:

Results Obtained	Rating
$ z \leq 2$	Satisfactory
$2 < z < 3$	Questionable
$ z \geq 3$	Unsatisfactory

AOAC has calculated z-scores according to methodology for the Aerobic Plate Count (APC) analyses, Coagulase Positive *Staphylococcus* (CPS), and the Yeast and Mold (Y&M) analyses. All statistics for the APC, CPS, and Y&M analyses have been computed according to methodology when more than 10 participants specified the same method. When participants specified a method used by fewer than 10 participants (X for APC, Y for CPS, V for Y&M), z-scores for their results were based on all results for the specific analysis. Calculations for z scores based on the data presented in the results sheet might be slightly different from the z-scores assigned by AOAC. The z-scores assigned by AOAC are based on calculations that use more decimal places than is possible to display on the results sheet.

5.0 Results

5.1 General Discussion of Results

Confidentiality of results has been maintained by issuing site identification codes to the participants. Results in reports have only been identified by the site identification code. Results were submitted by as many as 184 participants per analysis. Some tests had fewer participants submitting results because some of the laboratories do not routinely perform all the analyses. The assigned value was determined by the consensus of the majority after the removal of outliers. Samples 7 and 8 were negative for *E. coli* MPN and *E. coli* Plate Counts so no statistics were calculated for these samples. Samples 5 and 6 were negative for Coagulase Positive *Staphylococcus* so no statistics were calculated for these samples. Samples 7 and 8 for *Bacillus cereus* plate count analyses were negative so no statistics were calculated for these samples. *Bacillus cereus* MPN did not have enough reported results to process statistics so Z-scores have not been provided. The results for yeast and mold were combined. The data was log10 transformed prior to the calculation of statistics.

AOAC is instituting an approach to provide information on the performance of the different methods used by participants. Results from equivalent methods were grouped together. This report provides this information for Salmonella, APC, Coagulase Positive Staphylococcus, and Yeast and Mold. Future reports will provide additional information.

If a participant would like to appeal against the assessment of their performance in this proficiency testing scheme please contact staff at LPTP@AOAC.org

Salmonella

Results were submitted by as many as 178 participants for the Salmonella qualitative analyses. Greater than ninety eight percent of the results submitted, correctly detected the presence or absence of Salmonella. Reports of false positives and false negatives were tabulated for methods that were specified as the method chosen by greater than 10 participating laboratories. Results from methods that were identified as Vidas were grouped with results from methods identified as AOAC Official Method 996.08. Participants are encouraged to investigate their false positive and false negative results. Also, participants are reminded when using AOAC Official Method 989.13 or 989.14, that if the test is positive, confirmation is required.

***Salmonella* Methods**

Method	# of Participants	False Negatives	False Positives
AOAC Official Method 2001.09 & 996.08, Vidas, SLM, bioMerieux	24	1	1
BAX, RI Performance tested 100201	23	0	1
BAM Method	11	1	0

APC

The table below indicates which methods were grouped together for statistical computation of APC.

APC Method Indicated in Individual Result Section	APC Methods Included
Method A	AOAC 966.23, BAM, and MFHPB-18
Method B	AOAC 990.12 and 3M Petrifilm
Method X*Method	All Methods

*When participants specified a method used by fewer than 10 participants, or when 2 or more methods have been used, z-scores for their results were based on all results for the specific analysis (X for APC).

A table has been provided to compare the standard deviations and assigned values (\log_{10} transformed) for the various methods.

APC	Sample 5	Sample 6	Sample 7	Sample 8
Method A Standard Deviation	0.120	0.110	0.264	0.228
Method B Standard Deviation	0.180	0.173	0.173	0.175
Method X Standard Deviation	0.162	0.160	0.233	0.208
Method A Assigned Value	5.065	4.998	4.936	4.916
Method B Assigned Value	5.103	5.052	5.145	5.101
Method X Assigned Value	5.085	5.039	5.082	5.045

CPS

The table below indicates which methods were grouped together for statistical computation of APC.

CPS Method Indicated in Individual Result Section	CPS Methods Included
Method K	AOAC 975.55, BAM, MFHPB-21, B-P agar, Baird Parker USP, and USDA
Method L	Petrifilm, 3M, 3M Rapid Staph. AOAC 2001.05
Method Y*	All Methods

*When participants specified a method used by fewer than 10 participants, or when 2 or more methods have been used, z-scores for their results were based on all results for the specific analysis (Y for CPS).

A table has been provided to compare the standard deviations and assigned values (\log_{10} transformed) for the various methods.

CPS	Sample 5	Sample 6	Sample 7	Sample 8
Method K Standard Deviation	Negative Sample	Negative Sample	0.196	0.209
Method L Standard Deviation	Negative Sample	Negative Sample	0.224	0.218
Method Y Standard Deviation	Negative Sample	Negative Sample	0.217	0.229
Method K Assigned Value	Negative Sample	Negative Sample	5.017	5.012
Method L Assigned Value	Negative Sample	Negative Sample	4.993	4.959
Method Y Assigned Value	Negative Sample	Negative Sample	5.006	4.974

Y&M

The table below indicates which methods were grouped together for statistical computation of APC.

Y&M Method Indicated in Individual Result Section	Y&M Methods Included
Method R	BAM Method
Method S	Petrifilm, AOAC 997.02
Method U	MFHPB-22
Method V*	All Methods

*When participants specified a method used by fewer than 10 participants, or when 2 or more methods have been used, z-scores for their results were based on all results for the specific analysis (V for Y&M).

A table has been provided to compare the standard deviations and assigned values (\log_{10} transformed) for the various methods.

Y&M	Sample 5	Sample 6	Sample 7	Sample 8
Method R Standard Deviation	0.317	0.279	0.189	0.188
Method S Standard Deviation	0.210	0.191	0.197	0.175
Method V Standard Deviation	0.226	0.216	0.196	0.197
Method R Assigned Value	5.136	5.172	4.280	4.172
Method S Assigned Value	5.221	5.247	4.326	4.272
Method V Assigned Value	5.217	5.236	4.303	4.223

5.2 Discussion of Data Plots

z-Score Plots

z-score plots allow a visual comparison of z-score results from each separate laboratory against the entire distribution of all data for a given test or, where applicable, against the distribution for the same methodology for a given test. These plots are made up of three components. For each sample, the leftmost "stripe" is the entire set of reported z-scores. Each separate value is a thin horizontal line. Tightly clustered values show as dense, dark areas. The entire distribution can be seen spread above and below the mean of zero. A box-whisker plot is included to focus attention on several well known descriptors, notably the median and the upper and lower quartiles (25th and 75th percentiles). The box in these plots itself represents the middle 50% of the data, while the whiskers give a sense of reasonable tails. Inside the box, the median is indicated by a horizontal line. The top whisker goes up to the largest data point which lies no further than 1.5 box-heights from the top of the box. The bottom whisker is analogous. The large black dot locates the individual z-score derived from the original value reported by the lab for each sample.

Distribution of Results Plots

The distribution of results plots provides information on the distribution of results converted to \log_{10} . For a given test, the minimum and maximum of all results (all samples combined) determine the range. For APC and CPS, the minimum and maximum of results for specific methodology determine the range. The values are \log_{10} transformed, and the range is divided into 10 intervals ("bins"). The number of reported results falling into each bin are counted. The bars depict these counts as percentages of the total for each sample.

Instructions -M09 Standard Microbiology Proficiency Testing Program

Enclosed are eight samples, each containing approximately 75 grams of frozen rehydrated mashed potato mixture for samples 1-4 and 50 grams of frozen rehydrated mashed potato mixture for samples 5-8. The stability of potatoes stored frozen adds flexibility to the program by permitting participants to analyze samples at their convenience. Shelf-life studies performed on samples stored frozen demonstrated that the samples remained stable for a period of at least 7 days if stored properly.

Even with this added flexibility, please make every effort to analyze samples as soon as possible. Results are still due within 2 weeks of shipment, so your lab should **initiate analyses by no later than April 22, 2019.**

Results are due on April 30, 2019.

Store samples frozen (-20°C) until analysis date. Thaw quickly when ready to analyze. Place the samples into a plastic bag in a 45 °C water bath for 5 minutes, after 5 minutes in water bath, use sterile tongue depressor or stir rod to break up sample, put back in bath, and repeat after another 5 minutes. Do not place the samples in the 45 °C water bath for longer than 15 minutes. If the samples are still not adequately thawed, refrigerate the samples at 4 °C until thawed. Do not thaw the samples at room temperature.

Please verify that sample #1 is a red vial, #2 Black, #3 purple, #4 green, #5 gold, #6 brown, #7 white and #8 yellow.

Analyze samples numbered 1, 2, 3, and 4 for the following:

Salmonella species - Specify the method. Report as POSITIVE or NEGATIVE or NOT TESTED. If POSITIVE, report O and H antigens .

Please distinguish numbers from letters when reporting groups, factors, and/or complex.

Analyze samples numbered 5, 6, 7, and 8 for the following:

1. **Aerobic Count (MPN Technology) - Dilution 10-2, 10-3, 10-4, and 10-5**
 2. Aerobic Count (Plate Count Technology) - Dilution 10-2, 10-3, 10-4, and 10-5
 3. Coliform (MPN Technology) - Dilution 10-2, 10-3, 10-4, and 10-5
 4. Coliform (Plate Count Technology) - Dilution 10-1, 10-2, and 10-3
 5. E. coli (MPN Technology) - Dilution 10-2, 10-3, 10-4, and 10-5
 6. E. coli (Plate Count Technology) - Dilution 10-1, 10-2, and 10-3
 7. Coagulase Positive Staphylococcus (MPN Technology) - Dilution 10-2, 10-3, 10-4, 10-5 and 10-6
 8. Coagulase Positive Staphylococcus (Plate Count Technology) - Dilution 10-1, 10-2, and 10-3
 9. **Yeast & Mold (MPN Technology) - Dilution 10-1, 10-2, 10-3, and 10 -4**
 10. Yeast & Mold (Plate Count Technology) - Dilution 10-1, 10-2, 10-3, and 10 -4
 11. Bacillus cereus (MPN Technology) - Dilution 10-1, 10-2, and 10-3
 12. Bacillus cereus (Plate Count Technology) - Dilution 10-1, 10-2, and 10-3
 13. Enterobacteriaceae (MPN Technology) - Dilution 10-1, 10-2, and 10-3
 14. Enterobacteriaceae (Plate Count Technology) - Dilution 10-1, 10-2, and 10-3
- Complete Additional Dilutions if Necessary Highlight Indicates a Newly Added Analysis**

Homogeneity Results - Qualitative

Ship Date: April 15, 2019

Results of Homogeneity Testing - *Salmonella* 25g Sample

	Sample 1,2 MO1, MO8, MO9	Sample 3,4 MO1	Sample 3,4 MO8	Sample 3,4 MO9
Rep 1	negative	positive	positive	positive
Rep 2	negative	positive	positive	positive

O antigen	NA	D	D	D
H antigen	NA	G complex	G complex	G complex

Expected	negative	S. Enteritidis D: G comp	S. Enteritidis D: G comp	S. Enteritidis D: G comp
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PASSED

PASSED

PASSED

PASSED

NA = Not applicable.

Homogeneity Results - Quantitative

M01, M08, M09 Proficiency Testing Program

Ship Date: April 15, 2019

Aerobic Plate Count (log cfu/g)

Sample #	APC 5,6 - Rep 1	APC 5,6 - Rep 2
1	5.18	5.26
2	5.40	5.20
3	5.30	5.26
4	5.40	5.34
5	5.36	5.30
6	5.28	5.28
7	5.18	5.11
8	5.26	5.20
9	5.28	5.36
10	5.23	5.23

Average (\bar{x}) 5.27
 S_x 0.0660
 S_w 0.0575
 S_s 0.0520
PASSED

Coagulase Positive Staph (log cfu/g)

Sample #	CPS 5,6 - Rep 1	CPS 5,6 - Rep 2
1	<1.00	<1.00
2	<1.00	<1.00
3	<1.00	<1.00
4	<1.00	<1.00
5	<1.00	<1.00
6	<1.00	<1.00
7	<1.00	<1.00
8	<1.00	<1.00
9	<1.00	<1.00
10	<1.00	<1.00

Average (\bar{x}) NA
 S_x NA
 S_w NA
 S_s NA
PASSED

B. cereus (log cfu/g)

Sample #	B. Cereus 5,6- Rep 1	B. cereus 5,6 - Rep 2
1	4.20	3.86
2	4.18	3.58
3	3.40	4.23
4	3.91	4.23
5	4.18	3.51
6	4.18	4.18
7	3.49	4.18
8	3.79	3.76
9	3.61	3.71
10	4.26	3.66

Average (\bar{x}) 3.90
 S_x 0.1546
 S_w 0.3567
 S_s 0.0000
PASSED

Coliform Plate Count (log cfu/g)

Sample #	Coliform 5,6 - Rep 1	Coliform 5,6 - Rep 2
1	4.71	4.78
2	4.63	4.74
3	4.66	4.76
4	4.85	4.83
5	4.80	4.83
6	4.77	4.70
7	4.66	4.63
8	4.53	4.80
9	4.80	4.86
10	4.65	4.75

Average (\bar{x}) 4.74
 S_x 0.0686
 S_w 0.0768
 S_s 0.0420
PASSED

Aerobic Plate Count (log cfu/g)

Sample #	APC 7,8 - Rep 1	APC 7,8 - Rep 2
1	4.95	4.97
2	4.95	5.00
3	5.08	5.04
4	4.90	5.00
5	4.75	5.08
6	5.08	4.90
7	4.91	5.00
8	5.11	4.87
9	4.87	4.93
10	4.95	4.96

Average (\bar{x}) 4.97
 S_x 0.0446
 S_w 0.1063
 S_s 0.0000
PASSED

Coagulase Positive Staph (log cfu/g)

Sample #	CPS 7,8 - Rep 1	CPS 7,8 - Rep 2
1	4.89	4.83
2	4.94	4.64
3	4.85	4.68
4	4.96	4.85
5	4.83	4.79
6	4.75	4.67
7	4.85	5.00
8	4.66	4.91
9	4.72	4.77
10	4.72	4.66

Average (\bar{x}) 4.80
 S_x 0.0774
 S_w 0.1074
 S_s 0.0152
PASSED

B. cereus (log cfu/g)

Sample #	B. cereus 7,8 - Rep 1	B. cereus 7,8 - Rep 2
1	<1.00	<1.00
2	<1.00	<1.00
3	<1.00	<1.00
4	<1.00	<1.00
5	<1.00	<1.00
6	<1.00	<1.00
7	<1.00	<1.00
8	<1.00	<1.00
9	<1.00	<1.00
10	<1.00	<1.00

Average (\bar{x}) NA
 S_x NA
 S_w NA
 S_s NA
PASSED

Coliform Plate Count (log cfu/g)

Sample #	Coliform 7,8 - Rep 1	Coliform 7,8 - Rep 2
1	4.11	3.98
2	4.20	4.00
3	4.11	4.15
4	4.18	3.95
5	3.96	3.97
6	4.26	4.23
7	4.04	4.11
8	4.30	4.18
9	4.04	4.04
10	4.04	4.04

Average (\bar{x}) 4.09
 S_x 0.0884
 S_w 0.0816
 S_s 0.0669
PASSED

Homogeneity Results - Quantitative

M01, M08, M09 Proficiency Testing Program

Ship Date: April 15, 2019

E. coli Plate Count (log cfu/g)

Sample #	E. coli 5,6 - Rep 1	E. coli 5,6 - Rep 2
1	4.71	4.78
2	4.63	4.74
3	4.66	4.76
4	4.85	4.83
5	4.80	4.83
6	4.77	4.70
7	4.66	4.63
8	4.53	4.80
9	4.80	4.86
10	4.65	4.75

Average (\bar{x}) 4.74

S_x 0.0686

S_w 0.0768

S_s 0.0420

PASSED

Yeast (log cfu/g)

Sample #	Yeast 5,6 - Rep 1	Yeast 5,6 - Rep 2
1	<1.00	<1.00
2	<1.00	<1.00
3	<1.00	<1.00
4	<1.00	<1.00
5	<1.00	<1.00
6	<1.00	<1.00
7	<1.00	<1.00
8	<1.00	<1.00
9	<1.00	<1.00
10	<1.00	<1.00

Average (\bar{x}) NA

S_x NA

S_w NA

S_s NA

PASSED

Mold (log cfu/g)

Sample #	Mold 5,6 - Rep 1	Mold 5,6 - Rep 2
1	5.04	5.15
2	5.11	4.83
3	5.04	5.08
4	5.15	5.15
5	5.08	5.15
6	5.15	5.43
7	5.18	5.15
8	5.04	5.18
9	5.20	5.32
10	5.23	5.30

Average (\bar{x}) 5.15

S_x 0.1006

S_w 0.1038

S_s 0.0688

PASSED

E. coli Plate Count (log cfu/g)

Sample #	E. coli 7,8 - Rep 1	E. coli 7,8 - Rep 2
1	<1.00	<1.00
2	<1.00	<1.00
3	<1.00	<1.00
4	<1.00	<1.00
5	<1.00	<1.00
6	<1.00	<1.00
7	<1.00	<1.00
8	<1.00	<1.00
9	<1.00	<1.00
10	<1.00	<1.00

Average (\bar{x}) NA

S_x NA

S_w NA

S_s NA

PASSED

Yeast (log cfu/g)

Sample #	Yeast 7,8 - Rep 1	Yeast 7,8 - Rep 2
1	4.34	4.36
2	4.28	4.41
3	4.34	4.46
4	4.32	4.20
5	4.11	4.26
6	4.26	4.11
7	4.11	4.28
8	4.04	4.41
9	4.08	4.23
10	4.00	4.30

Average (\bar{x}) 4.25

S_x 0.0906

S_w 0.1355

S_s 0.0000

PASSED

Mold (log cfu/g)

Sample #	Mold 7,8 - Rep 1	Mold 7,8 - Rep 2
1	<1.00	<1.00
2	<1.00	<1.00
3	<1.00	<1.00
4	<1.00	<1.00
5	<1.00	<1.00
6	<1.00	<1.00
7	<1.00	<1.00
8	<1.00	<1.00
9	<1.00	<1.00
10	<1.00	<1.00

Average (\bar{x}) NA

S_x NA

S_w NA

S_s NA

PASSED

Appendix A

04/15/2019

05/28/2019 12:46:58

Qualitative Results: M09 Site ID xxxxx - Set A

Test	Method (Reported)	Corresponding Method	sample	Your reported result	% labs agreeing w/ your reported result*	Expected result
Salmonella	Gene-up (PCR)	Other	1	-	98.9	-
			2	-	100.0	-
			3	+	98.9	+
			4	+	98.9	+
Salmonella O antigen			1	.		Not tested
			2	.		Not tested
			3	.		+
			4	.		+
O antigen ID			1	.		Not tested
			2	.		Not tested
			3	.		D
			4	.		D
Salmonella H antigen			1	.		Not tested
			2	.		Not tested
			3	.		+
			4	.		+
H antigen ID			1	.		Not tested
			2	.		Not tested
			3	.		G complex
			4	.		G complex

* % based on labs reporting results

Appendix A

04/15/2019

05/28/2019 12:46:58

Quantitative Results: M09 Site ID xxxxx - Set A

Test	Sample	Method	Number of reported results	Reported result	log10 of reported result	Min result	Lower quartile	Upper quartile	Max result	Median	Geometric mean	Assigned value (Mean log10)	Std dev	Z-score	Standard uncertainty of the assigned value	Notes
MPN APC	5		12	Not tested	.	4.833	4.999	5.224	5.322	5.169	131927	5.120	0.176	.	0.063	
	6		11	Not tested	.	4.643	4.996	5.230	5.690	Z not computed
	7		11	Not tested	.	4.690	5.176	5.380	5.568	Z not computed
	8		11	Not tested	.	4.690	4.934	5.217	5.322	Z not computed
APC	5	A	40	100000	5.000	4.708	4.989	5.146	5.591	5.074	116274	5.065	0.120	-0.54	0.024	
	6	A	40	58000	4.763	3.959	4.942	5.076	5.462	5.000	99570	4.998	0.110	-2.14	0.022	
	7	A	40	29000	4.462	4.447	4.787	5.161	5.398	4.906	86254	4.936	0.264	-1.79	0.052	
	8	A	40	39500	4.597	4.146	4.760	5.041	5.462	4.927	82406	4.916	0.228	-1.40	0.045	
MPN Coliform	5		69	Not tested	.	2.826	4.097	4.544	5.041	4.380	21025	4.323	0.303	.	0.046	
	6		68	Not tested	.	2.643	3.968	4.380	5.041	4.322	17413	4.241	0.349	.	0.053	
	7		68	Not tested	.	1.756	3.380	3.663	4.380	3.633	3916	3.593	0.315	.	0.048	
	8		68	Not tested	.	1.845	3.380	3.875	4.886	3.633	4080	3.611	0.337	.	0.051	
Coliform plate count	5		156	Not tested	.	0.000	4.035	4.342	4.968	4.194	15649	4.194	0.250	.	0.025	
	6		156	Not tested	.	0.000	3.949	4.301	4.806	4.114	13327	4.125	0.254	.	0.025	
	7		155	Not tested	.	2.431	3.362	3.708	4.315	3.544	3506	3.545	0.255	.	0.026	
	8		155	Not tested	.	2.230	3.380	3.740	4.447	3.602	3707	3.569	0.254	.	0.025	
MPN E. coli	5		73	Not tested	.	2.833	4.176	4.544	5.041	4.380	22117	4.345	0.299	.	0.044	
	6		72	Not tested	.	3.322	3.968	4.380	5.041	4.342	18120	4.258	0.354	.	0.052	
	7		72	Not tested	.	0.000	0.000	0.000	0.000	Negative sample
	8		72	Not tested	.	0.000	0.000	0.000	0.000	Negative sample
E. coli plate count	5		151	12000	4.079	0.000	4.029	4.342	4.991	4.176	15055	4.178	0.255	-0.39	0.026	
	6		151	9300	3.968	0.000	3.924	4.301	4.919	4.086	13039	4.115	0.254	-0.58	0.026	
	7		149	< 1	.	0.000	0.000	0.000	3.934	Negative sample
	8		149	< 1	.	0.000	0.000	0.000	4.041	Negative sample
MPN Coag Pos Staph	5		16	Not tested	.	0.000	0.000	0.000	0.000	Negative sample
	6		15	Not tested	.	0.000	0.000	0.000	0.000	Negative sample
	7		15	Not tested	.	0.000	4.757	5.203	5.380	5.005	110298	5.043	0.284	.	0.092	
	8		15	Not tested	.	4.362	4.968	5.079	5.230	5.041	108419	5.035	0.065	.	0.021	
Coagulase Positive Staph	5		135	Not tested	.	0.000	0.000	0.000	5.230	Negative sample
	6		135	Not tested	.	0.000	0.000	0.000	4.342	Negative sample
	7		134	Not tested	.	0.000	4.886	5.146	5.342	5.000	101396	5.006	0.217	.	0.023	
	8		134	Not tested	.	0.000	4.813	5.146	5.477	4.988	94199	4.974	0.229	.	0.025	
MPN Yeast/Mold	5		6	Not tested	.	4.041	5.146	5.690	5.946	Z not computed
	6		5	Not tested	.	4.935	5.157	5.477	5.568	Z not computed
	7		5	Not tested	.	2.000	3.649	4.362	4.398	Z not computed
	8		5	Not tested	.	0.000	2.845	4.230	4.398	Z not computed
Yeast/Mold	5	R	37	265000	5.423	4.394	4.898	5.362	5.699	5.137	136742	5.136	0.317	0.91	0.065	
	6	R	37	255000	5.407	4.273	4.934	5.380	5.505	5.255	148684	5.172	0.279	0.84	0.057	

Appendix A

04/15/2019

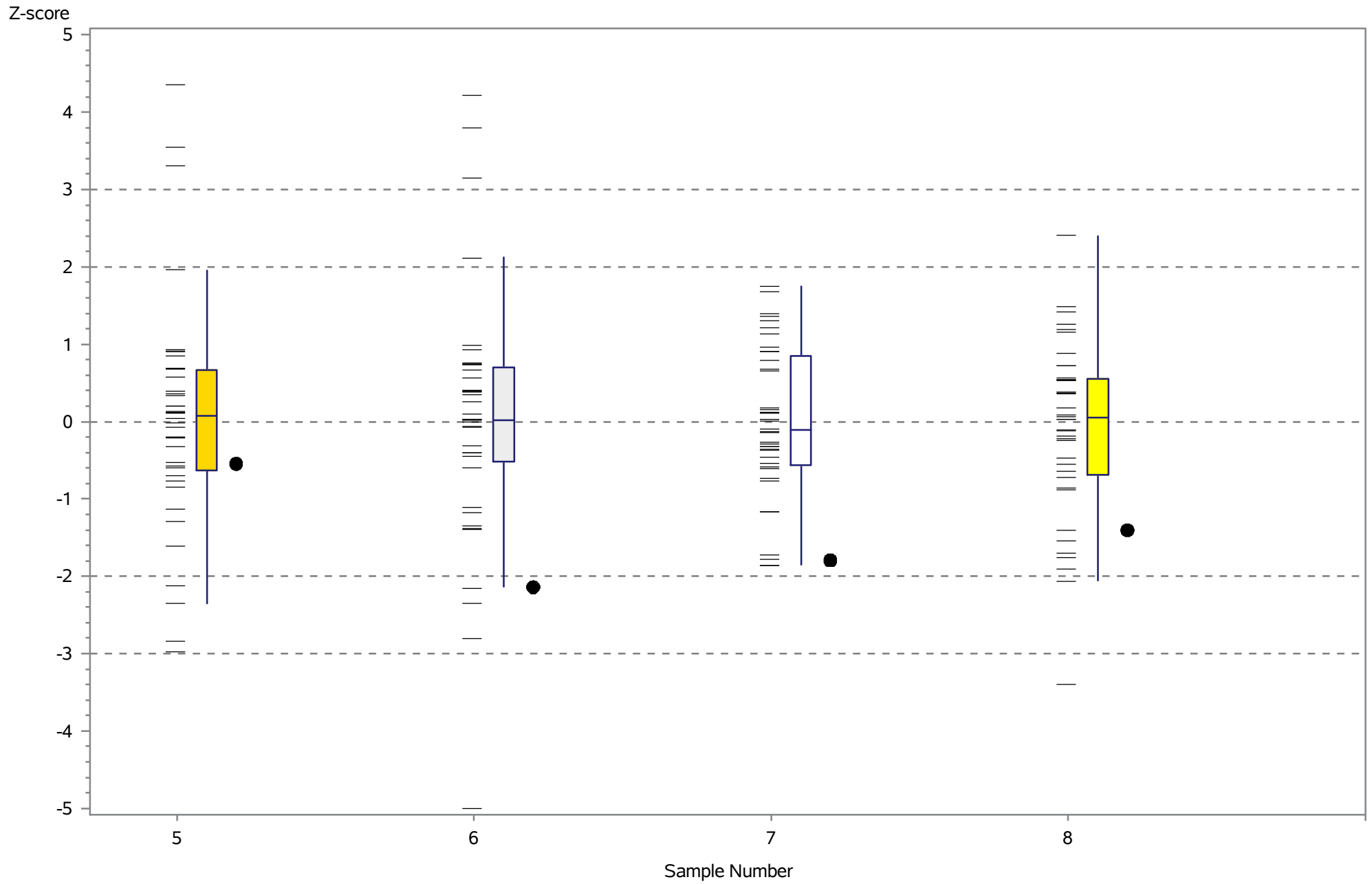
05/28/2019 12:46:58

Quantitative Results: M09 Site ID xxxxx - Set A

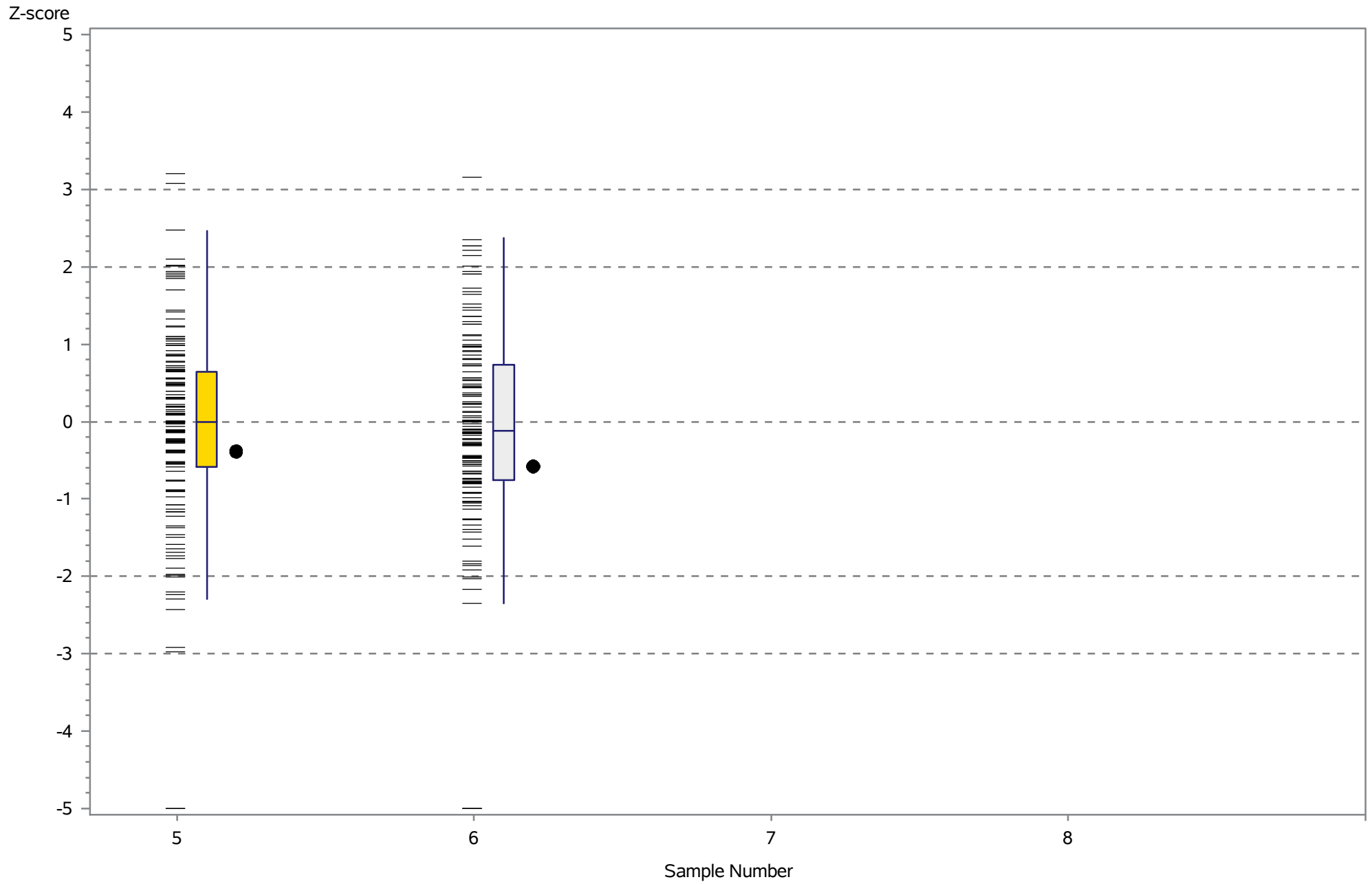
Test	Sample	Method	Number of reported results	Reported result	log10 of reported result	Min result	Lower quartile	Upper quartile	Max result	Median	Geometric mean	Assigned value (Mean log10)	Std dev	Z-score	Standard uncertainty of the assigned value	Notes
MPN <i>Bacillus cereus</i>	7	R	37	43500	4.638	3.892	4.155	4.415	4.672	4.261	19050	4.280	0.189	1.90	0.039	
	8	R	37	32500	4.512	3.833	4.033	4.284	4.512	4.176	14862	4.172	0.188	1.80	0.039	
	5		6	Not tested	.	4.061	4.191	4.446	4.477	Z not computed
	6		5	Not tested	.	4.176	4.176	4.371	4.371	Z not computed
	7		5	Not tested	.	0.000	0.000	0.000	0.000	Z not computed
<i>Bacillus cereus</i> Plate Count	8		5	Not tested	.	0.000	0.000	0.000	0.000	Z not computed
	5		49	Not tested	.	3.279	4.041	4.230	4.919	4.116	12997	4.114	0.168	.	0.030	
	6		49	Not tested	.	3.255	3.903	4.204	4.875	4.079	12146	4.084	0.233	.	0.042	
	7		48	Not tested	.	0.000	0.000	0.000	4.932	Negative sample
MPN Enterobacteriaceae	8		48	Not tested	.	0.000	0.000	0.000	1.875	Negative sample
	5		8	Not tested	.	3.959	3.968	4.380	4.602	Z not computed
	6		8	Not tested	.	3.362	4.041	4.663	4.875	Z not computed
	7		8	Not tested	.	3.462	3.633	3.756	3.968	Z not computed
Enterobacteriaceae Plate Count	8		8	Not tested	.	3.491	3.591	3.968	3.968	Z not computed
	5		121	12000	4.079	0.000	4.079	4.431	5.155	4.301	18682	4.271	0.239	-0.81	0.027	
	6		121	9300	3.968	0.000	3.996	4.398	5.114	4.176	15492	4.190	0.287	-0.77	0.033	
	7		121	1745	3.242	2.000	3.415	3.763	4.114	3.613	3951	3.597	0.251	-1.41	0.029	
	8		121	2800	3.447	2.000	3.431	3.778	4.504	3.643	4166	3.620	0.279	-0.62	0.032	

Z-score distribution analysis M0189 April 2019 - Set A

Site ID=xxxxx Test=APC Method=A



Z-score distribution analysis M0189 April 2019 -
Set A Site ID= xxxxx Test=E. coli plate count Method=' '



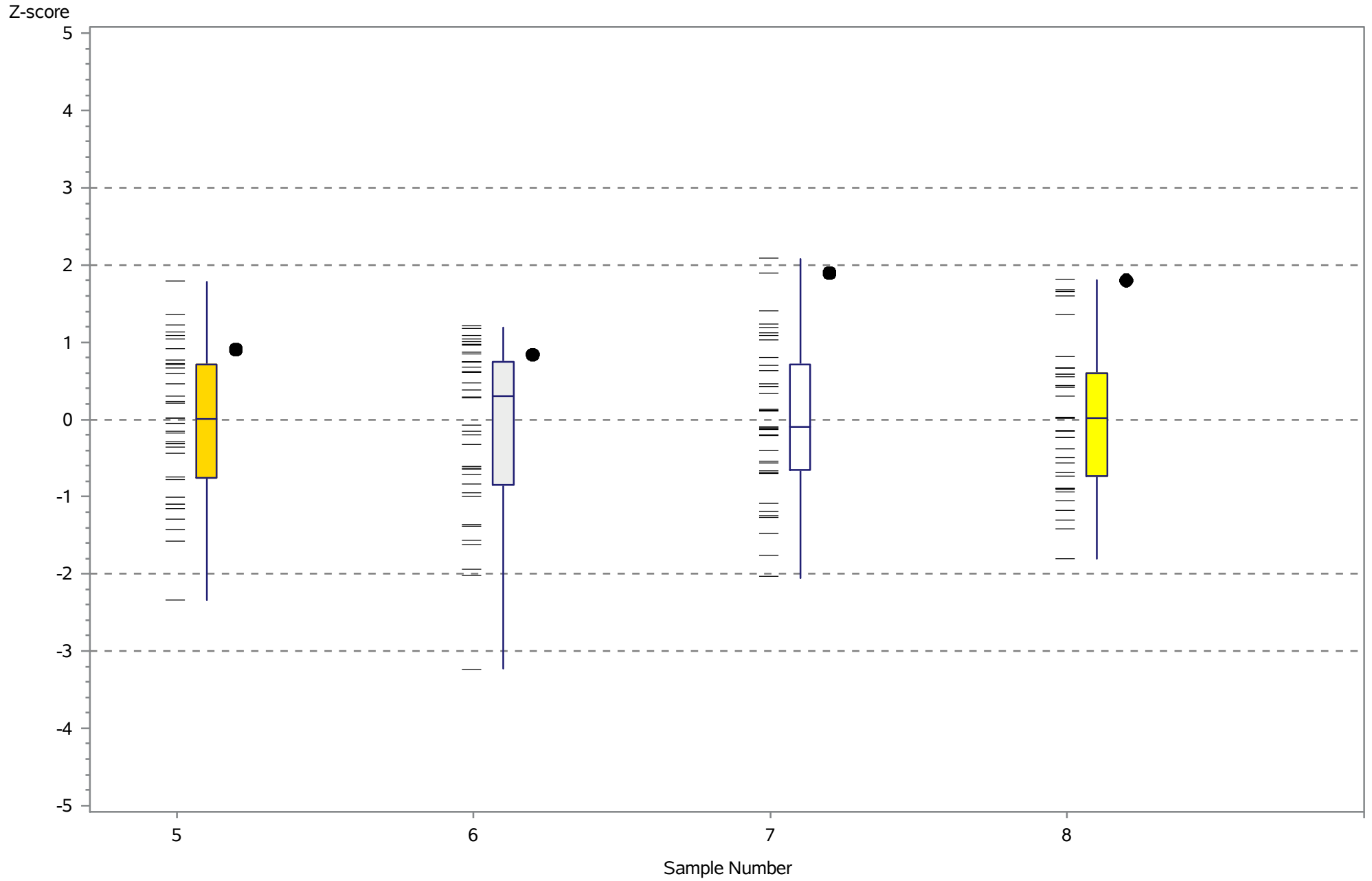
Your results (dot) compared with all reported results

04/15/2019

05/28/2019 12:46:58

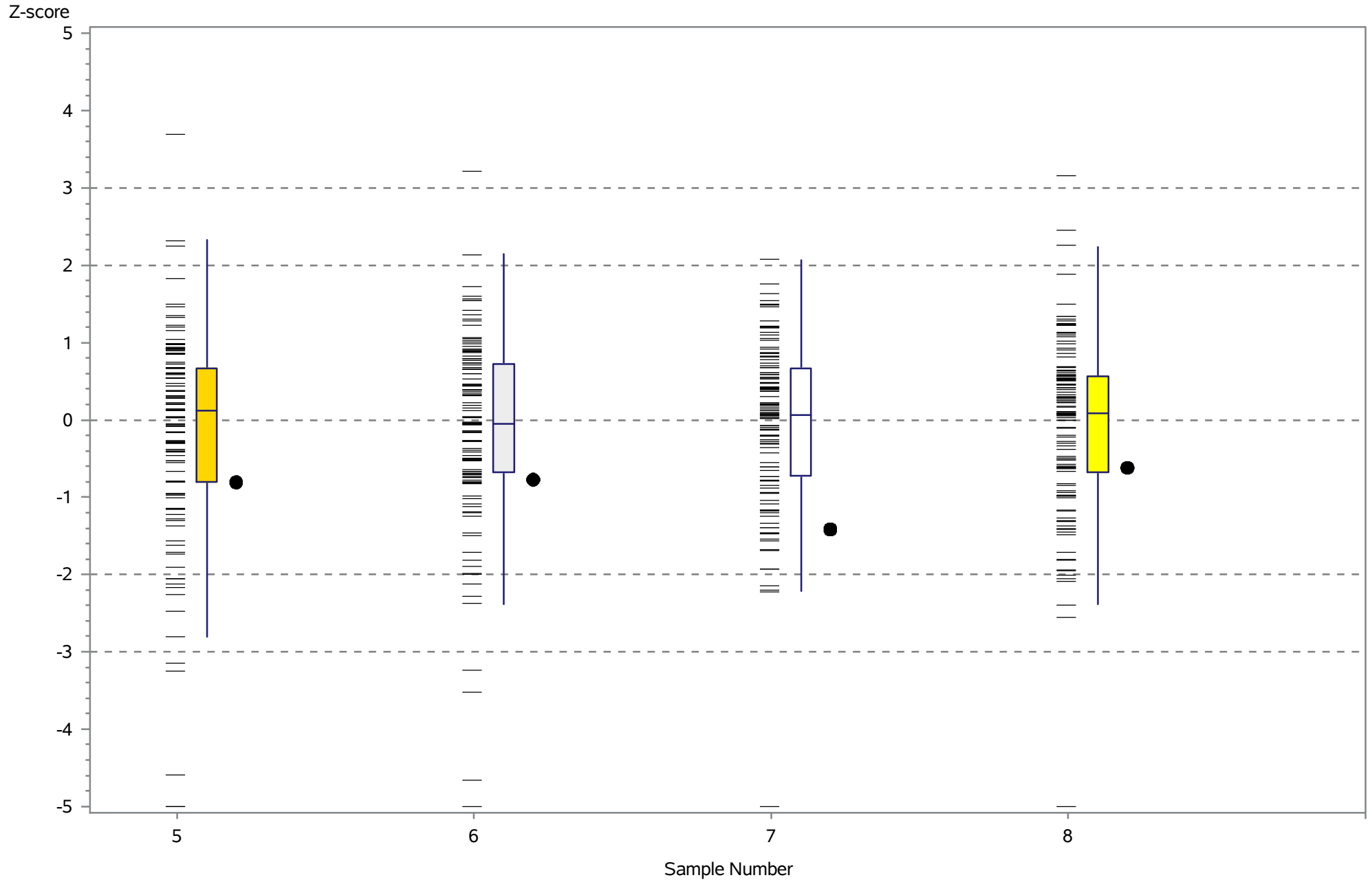
Z-score distribution analysis M0189 April 2019 - Set A

Site ID=xxxxx Test=Yeast/Mold Method=R



Your results (dot) compared with all reported results

Z-score distribution analysis M0189 April 2019 - Set A
Site ID= xxxxxx Test=Enterobacteriaceae Plate Count Method=' '



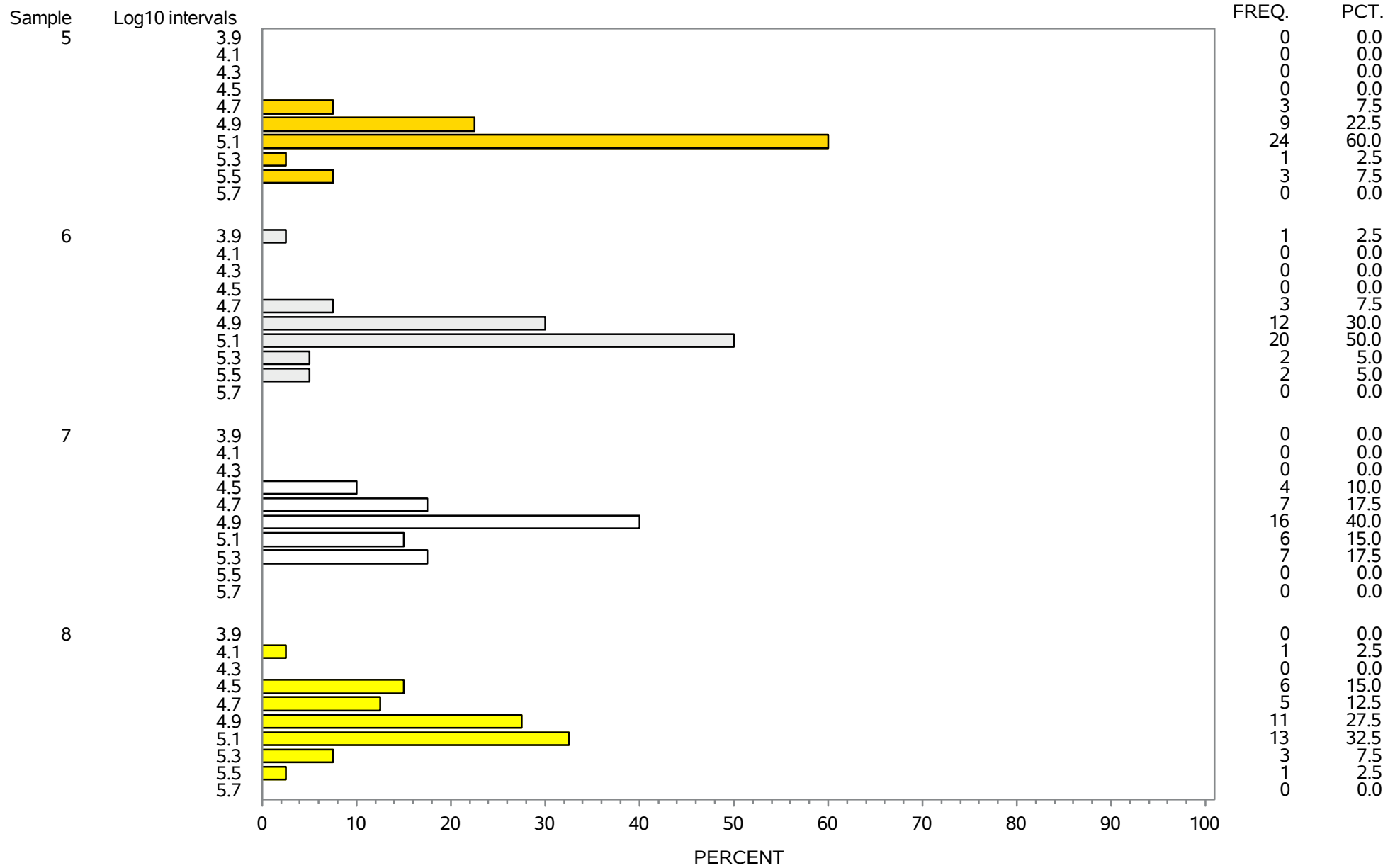
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04/15/2019

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Distribution of Results Converted to log10 - Set A

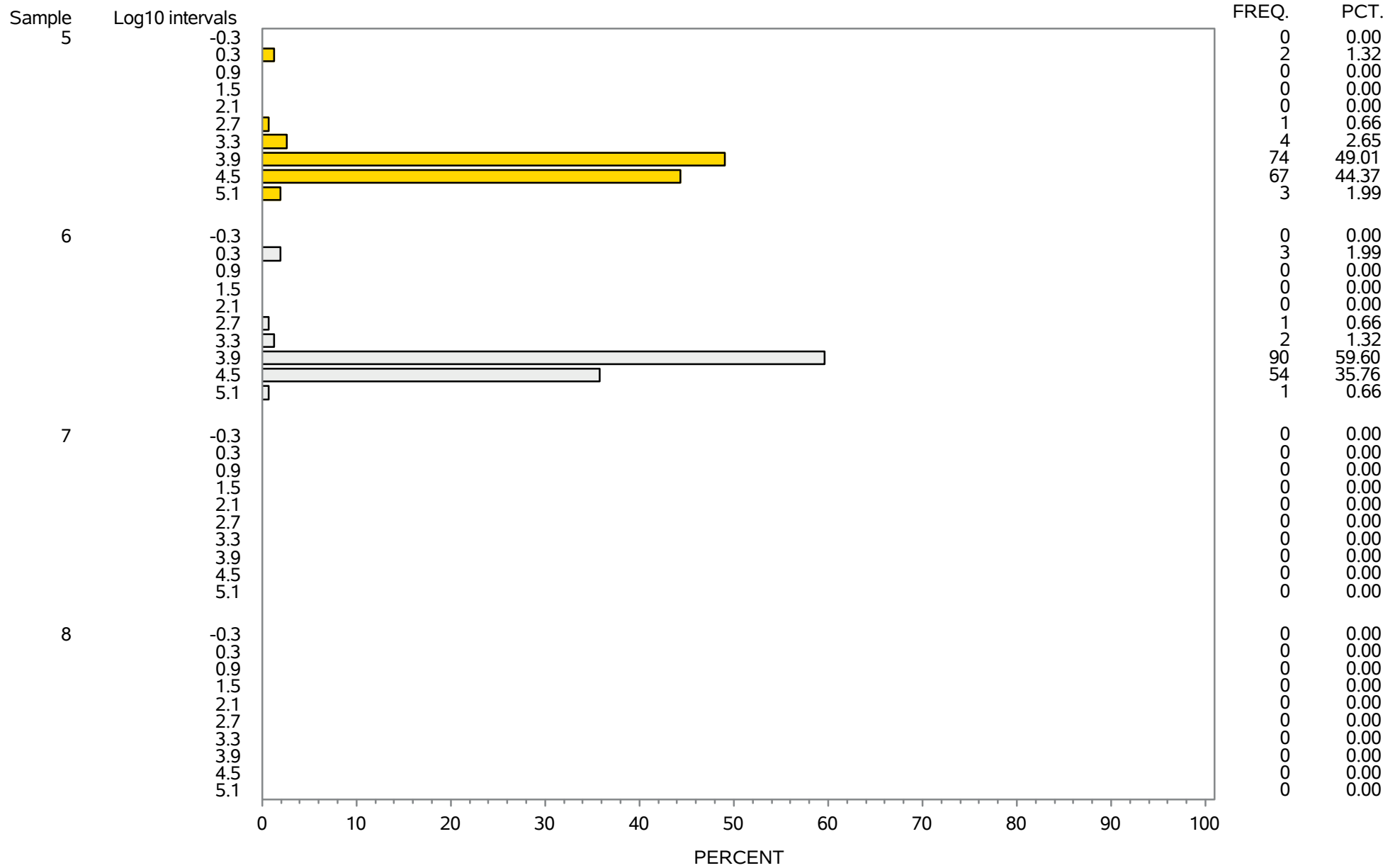
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04/15/2019

05/28/2019 12:46:58

Distribution of Results Converted to log10 - Set
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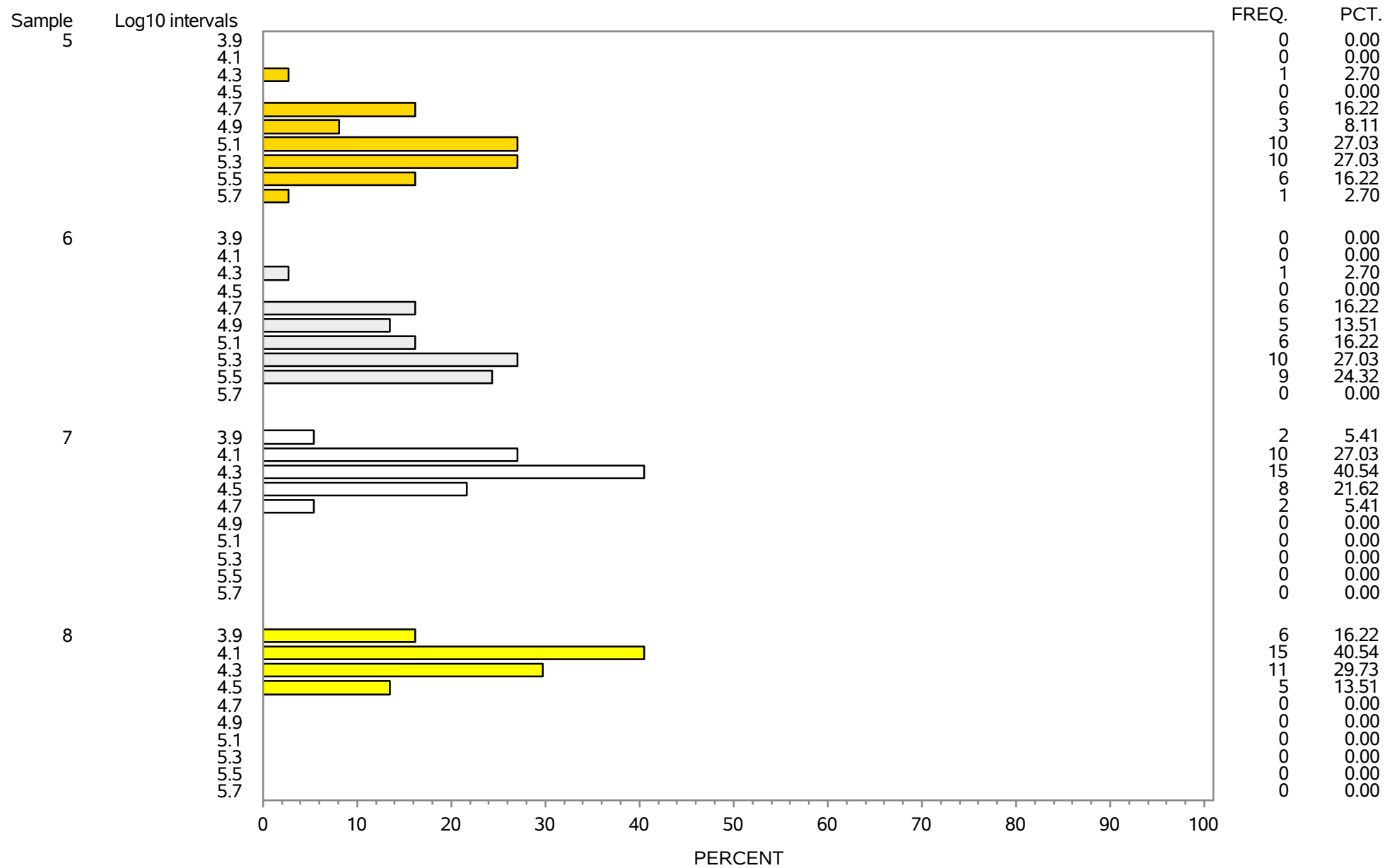
Distribution of results converted to log10

04/15/2019

05/28/2019 12:46:58

Distribution of Results Converted to log10 - Set

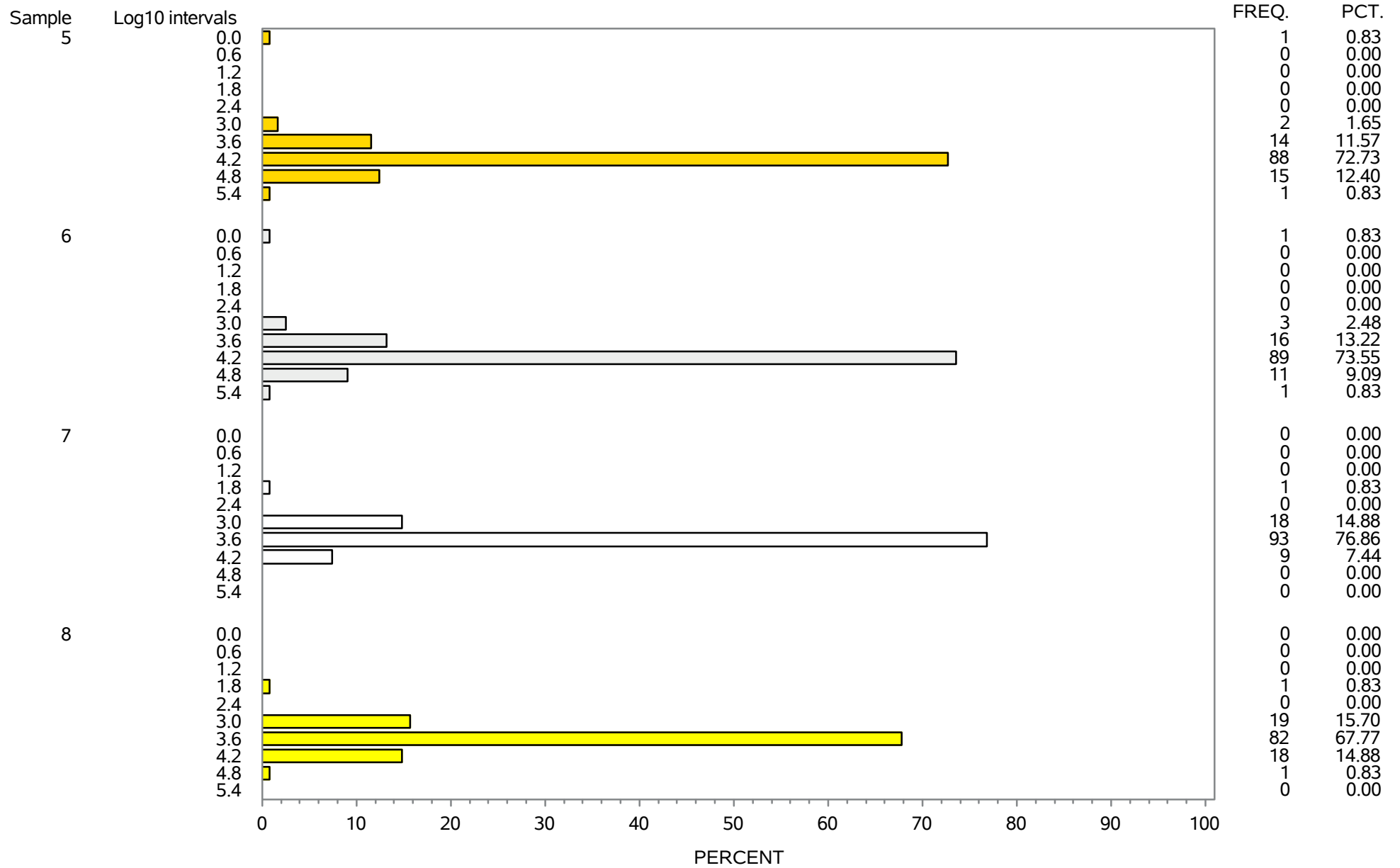
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04/15/2019

05/28/2019 12:46:58

Distribution of Results Converted to log10 - Set A
 Site ID=xxxxx Test=Enterobacteriaceae Plate Count Method=' '



Distribution of results converted to log10