M08

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

04-15-19 (Shipment Date)

06-04-19 (Report Issue Date)

Proficiency Testing Provider
Certificate 1782.01

AOAC INTERNATIONAL
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Report Authorization

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

Arlene Fox

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 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, Listeria* 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 April 30, 2019. 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**	*Salmonella*	Indicate Positive/Negative If positive, report presence/absence of O and H antigens, and antigen identification if applicable.
	Listeria	Indicate Positive/Negative If positive, report *Listeria* species.
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}
	E. coli MPN	Dilution 10^{-2} – 10^{-5}
	E. coli Plate Count	Dilution 10^{-1} – 10^{-3}
	Coagulase Positive *Staphylococcus* MPN	Dilution 10^{-2} – 10^{-6}
	Coagulase Positive *Staphylococcus* Plate Count	Dilution 10^{-1} – 10^{-3}
	Yeast & Mold MPN	Dilution 10^{-1} – 10^{-4}
	Yeast & Mold	Dilution 10^{-1} – 10^{-4}
	Bacillus cereus MPN	Dilution 10^{-1} – 10^{-3}
	Bacillus cereus Plate Count	Dilution 10^{-1} – 10^{-3}
	Enterobacteriaceae MPN	Dilution 10^{-1} – 10^{-3}
	Enterobacteriaceae 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 $\log_{10}$ transformation, by a factor of 100. These results have been labeled as "pre-screened as an outlier."

The data was $\log_{10}$ 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**
IzI ≤ 2	Satisfactory
2 < IzI < 3	Questionable
IzI ≥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, Listeria, 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

Listeria

Results were submitted by as many as 146 participants for the *Listeria* qualitative analyses. Greater than ninety eight percent of the results submitted correctly detected the presence or absence of *Listeria.* Participants should compare their individual results to the expected results. Reports of false positives and false negatives were tabulated for methods that were specified as the method chosen by greater than 10 participating laboratories. Participants are reminded that AOAC Official Method 993.09 is to be used for *Listeria* determination in dairy products, seafood, and meats. Participants are encouraged to investigate their false positive and false negative results. Participants are encouraged to be aware of transcription errors as well as proper sample identification.

Listeria Methods

Method	# of Participants	False Negatives	False Positives
AOAC Official Method 999.06, Vidas	17	0	0

APC

The table below indicates which methods where 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 where 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 where 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 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 log10 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 -M08 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 (-20ºC) until analysis date. Thaw quickly when ready to analyze. Place the samples into a plastic bag in a 45 ºC 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 ºC water bath for longer than 15 minutes. If the samples are still not adequately thawed, refrigerate the samples at 4 ºC 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**.

Listeria species -Specify the method. Report as POSITIVE or NEGATIVE or NOT TESTED. If positive, report the *Listeria* species.

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
	PASSED	**PASSED**	**PASSED**	**PASSED**

Results of Homogeneity Testing - *Listeria* spp. 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	negative
Rep 2	negative	positive	positive	negative

Species	NA	*L. monocytogenes*	*L. monocytogenes*	NA

Expected	negative	*L. monocytogenes*	*L. monocytogenes*	negative
	PASSED	**PASSED**	**PASSED**	**PASSED**

NA = Not applicable.

Appendix D
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

Appendix D
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

04/15/2019

Qualitative Results: M08 Site ID xxxxx- Set A

Test	Method (Reported)	Corresponding Method	sample	Your reported result	% labs agreeing w/ your reported result*	Expected result
Salmonella	MFHPB-20+MFLP-06	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
Listeria	AOAC PTM 051401+MFHPB-30+MFLP-05	Other	1	-	98.5	-
			2	-	98.5	-
			3	+	98.6	+
			4	+	99.3	+
Listeria species ID			1		.	Not tested
			2		.	Not tested
			3	L. monocytogenes	.	L. monocytogenes
			4	L. monocytogenes	.	L. monocytogenes

* % based on labs reporting results

Quantitative Results: M08 Site ID xxxxx Set A

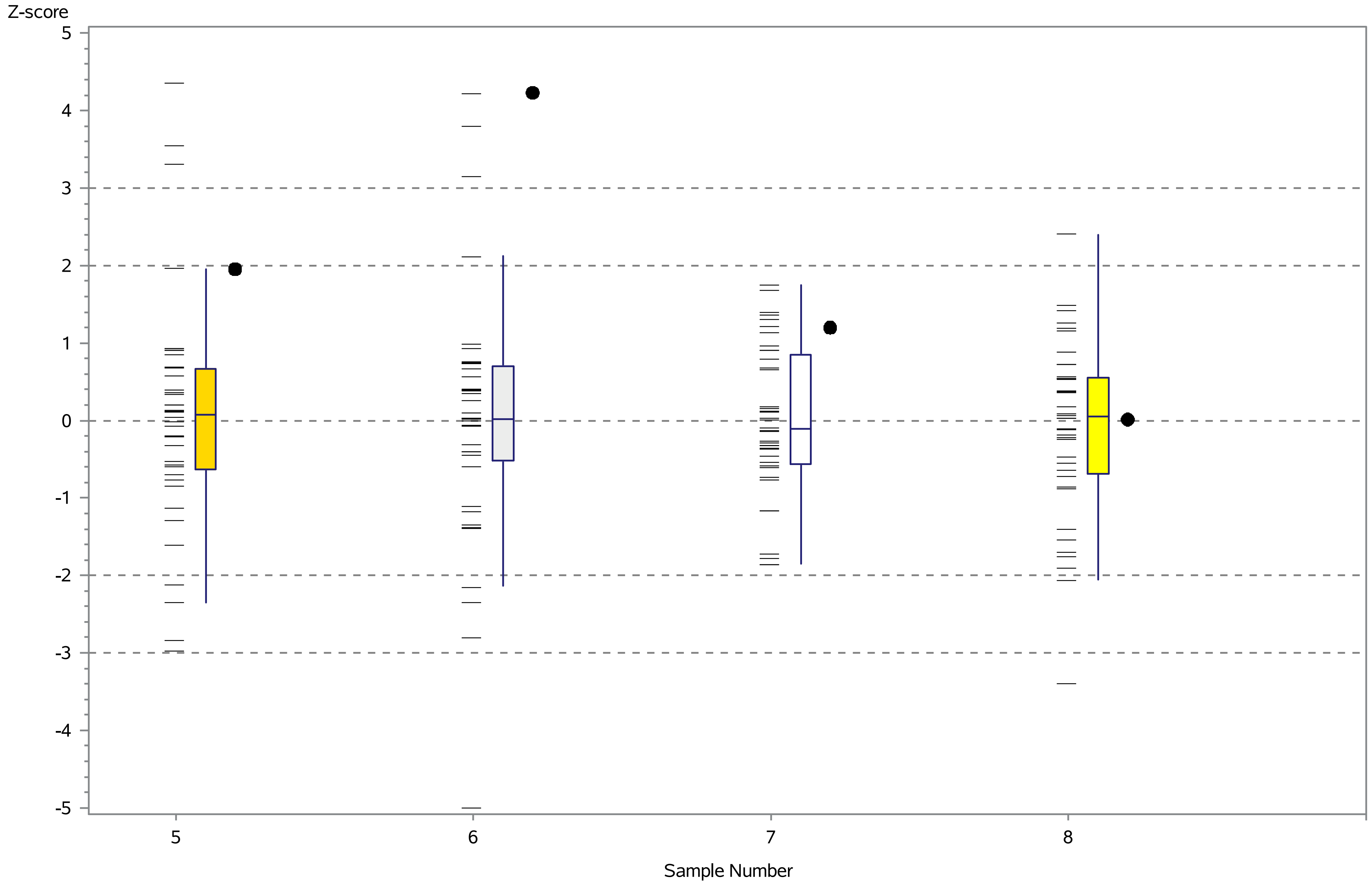
Test	Sample	Method	Number of reported results	Reported result	log10 of reported result	Min result	Lower quartile	Upper quartile	Max result	Median	Geometric mean	Assigned value (Mean log10)	Std dev	Z-score	Standard uncertainty of the assigned value	Notes
MPN APC	5		12	Not tested	.	4.833	4.999	5.224	5.322	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	200000	5.301	4.708	4.989	5.146	5.591	5.074	116274	5.065	0.120	***1.96***	0.024	
	6	A	40	290000	5.462	3.959	4.942	5.076	5.462	5.000	99570	4.998	0.110	***4.23***	0.022	Outlier: Z beyond 3
	7	A	40	179000	5.253	4.447	4.787	5.161	5.398	4.906	86254	4.936	0.264	***1.20***	0.052	
	8	A	40	83000	4.919	4.146	4.760	5.041	5.462	4.927	82406	4.916	0.228	***0.01***	0.045	
MPN Coliform	5		69	21000	4.322	2.826	4.097	4.544	5.041	4.380	21025	4.323	0.303	***-0.00***	0.046	
	6		68	4900	3.690	2.643	3.968	4.380	5.041	4.322	17413	4.241	0.349	***-1.58***	0.053	
	7		68	2400	3.380	1.756	3.380	3.663	4.380	3.633	3916	3.593	0.315	***-0.68***	0.048	
	8		68	1500	3.176	1.845	3.380	3.875	4.886	3.633	4080	3.611	0.337	***-1.29***	0.051	
Coliform plate count	5		156	9600	3.982	0.000	4.035	4.342	4.968	4.194	15649	4.194	0.250	***-0.85***	0.025	
	6		156	4200	3.623	0.000	3.949	4.301	4.806	4.114	13327	4.125	0.254	***-1.97***	0.025	
	7		155	1900	3.279	2.431	3.362	3.708	4.315	3.544	3506	3.545	0.255	***-1.04***	0.026	
	8		155	1140	3.057	2.230	3.380	3.740	4.447	3.602	3707	3.569	0.254	***-2.02***	0.025	
MPN E. coli	5		73	21000	4.322	2.833	4.176	4.544	5.041	4.380	22117	4.345	0.299	***-0.08***	0.044	
	6		72	4900	3.690	3.322	3.968	4.380	5.041	4.342	18120	4.258	0.354	***-1.60***	0.052	
	7		72	< 18	.	0.000	0.000	0.000	0.000	.	.	.	.	**.**	.	Negative sample
	8		72	< 18	.	0.000	0.000	0.000	0.000	.	.	.	.	**.**	.	Negative sample
E. coli plate count	5		151	9600	3.982	0.000	4.029	4.342	4.991	4.176	15055	4.178	0.255	***-0.76***	0.026	
	6		151	4200	3.623	0.000	3.924	4.301	4.919	4.086	13039	4.115	0.254	***-1.94***	0.026	
	7		149	< 5	.	0.000	0.000	0.000	3.934	.	.	.	.	**.**	.	Negative sample
	8		149	< 5	.	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	K	39	< 10	.	0.000	0.000	0.000	5.230	.	.	.	.	**.**	.	Negative sample
	6	K	39	< 10	.	0.000	0.000	0.000	4.342	.	.	.	.	**.**	.	Negative sample
	7	K	39	130000	5.114	0.000	4.826	5.146	5.342	5.013	104033	5.017	0.196	***0.49***	0.039	
	8	K	39	64000	4.806	0.000	4.763	5.164	5.362	5.029	102867	5.012	0.209	***-0.99***	0.042	
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	V	156	210000	5.322	0.000	5.079	5.362	5.699	5.230	164774	5.217	0.226	***0.47***	0.023	
	6	V	156	320000	5.505	0.000	5.083	5.398	5.914	5.255	172081	5.236	0.216	***1.25***	0.022	

Quantitative Results: M08 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
	7	V	155	41000	4.613	0.000	4.176	4.462	4.991	4.301	20101	4.303	0.196	***1.58***	0.020	
	8	V	155	13000	4.114	0.000	4.079	4.362	5.322	4.230	16692	4.223	0.197	***-0.55***	0.020	
MPN Bacillus cereus	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
	8		5	Not tested	.	0.000	0.000	0.000	0.000	.	.	.	.	.	.	Z not computed
Bacillus cereus Plate Count	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
	8		48	Not tested	.	0.000	0.000	0.000	1.875	.	.	.	.	.	.	Negative sample
MPN Enterobacteriaceae	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
	8		8	Not tested	.	3.491	3.591	3.968	3.968	.	.	.	.	.	.	Z not computed
Enterobacteriaceae Plate Count	5		121	27000	4.431	0.000	4.079	4.431	5.155	4.301	18682	4.271	0.239	***0.67***	0.027	
	6		121	6800	3.833	0.000	3.996	4.398	5.114	4.176	15492	4.190	0.287	***-1.24***	0.033	
	7		121	3300	3.519	2.000	3.415	3.763	4.114	3.613	3951	3.597	0.251	***-0.31***	0.029	
	8		121	3400	3.531	2.000	3.431	3.778	4.504	3.643	4166	3.620	0.279	***-0.32***	0.032	

Z-score distribution analysis M0189 April 2019 - Set A

Site ID= xxxxx Test=APC Method=A

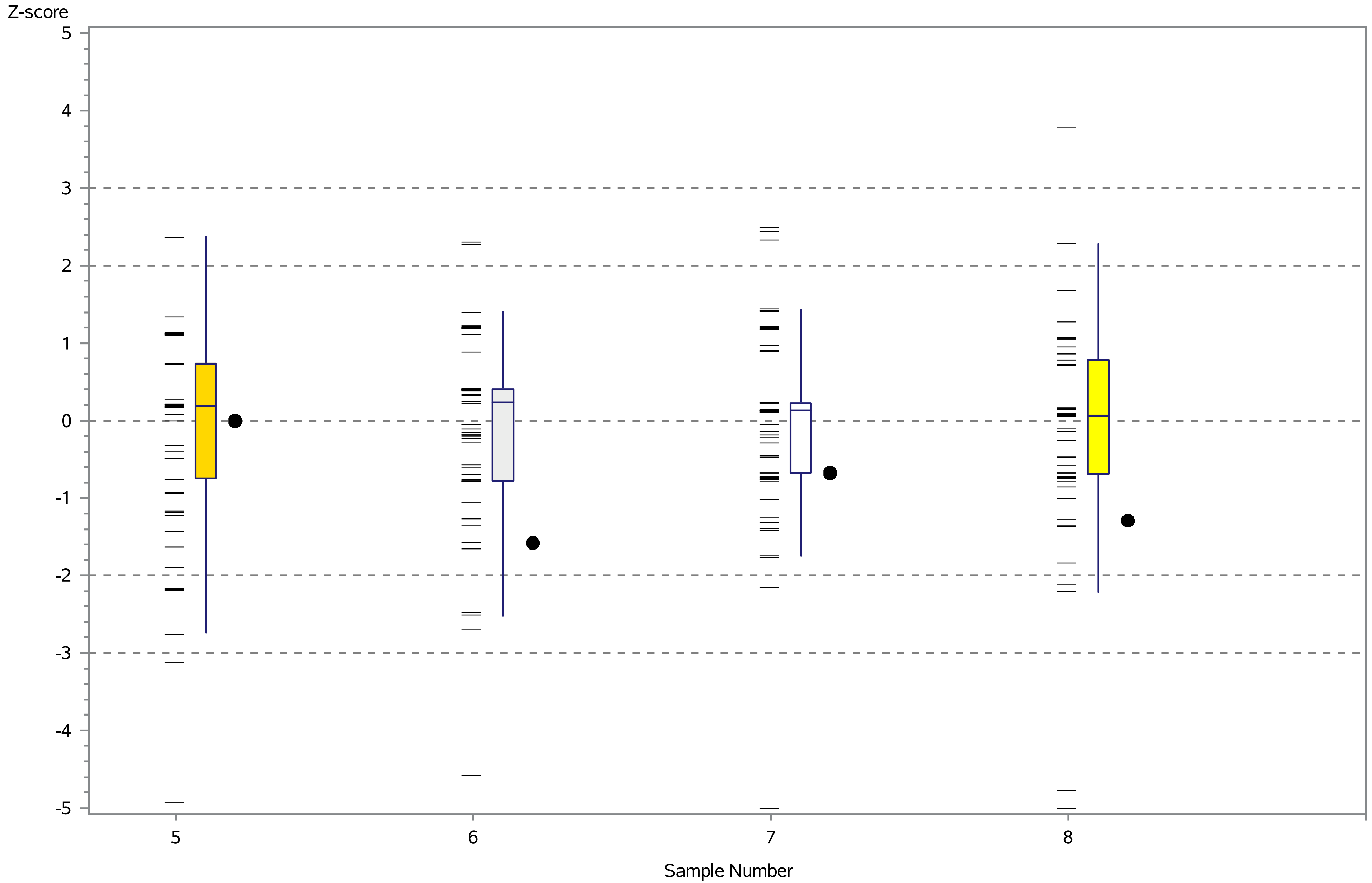


Your results (dot) compared with all reported results

04/15/2019

Z-score distribution analysis M0189 April 2019 - Set A

Site ID= xxxxx Test=MPN Coliform Method=' '

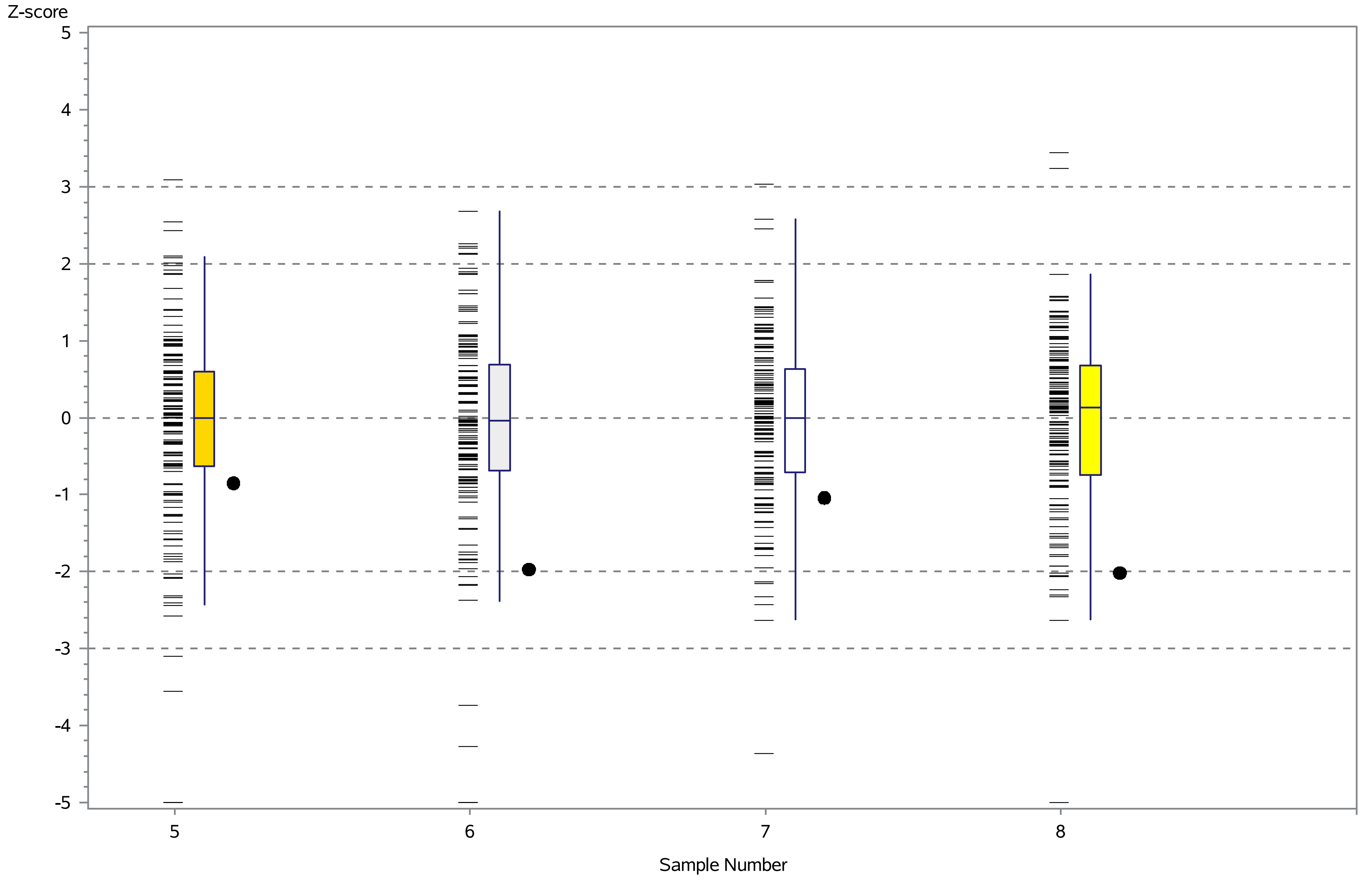


Your results (dot) compared with all reported results

04/15/2019

Z-score distribution analysis M0189 April 2019 - Set A

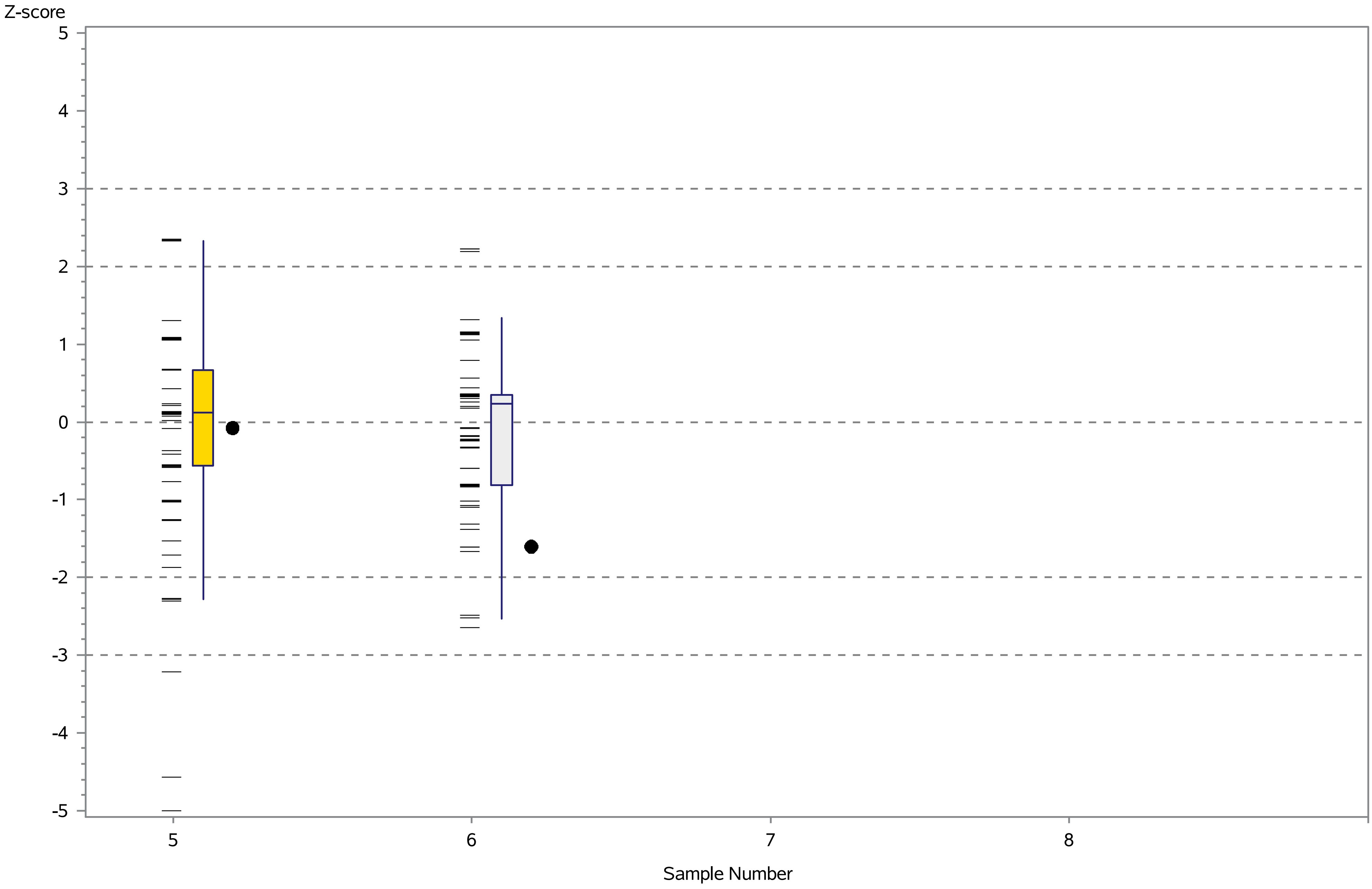
Site ID= xxxxx Test=Coliform plate count Method=' '



Your results (dot) compared with all reported results

Z-score distribution analysis M0189 April 2019 - Set A

Site ID= xxxxx Test=MPN E. coli Method=' '



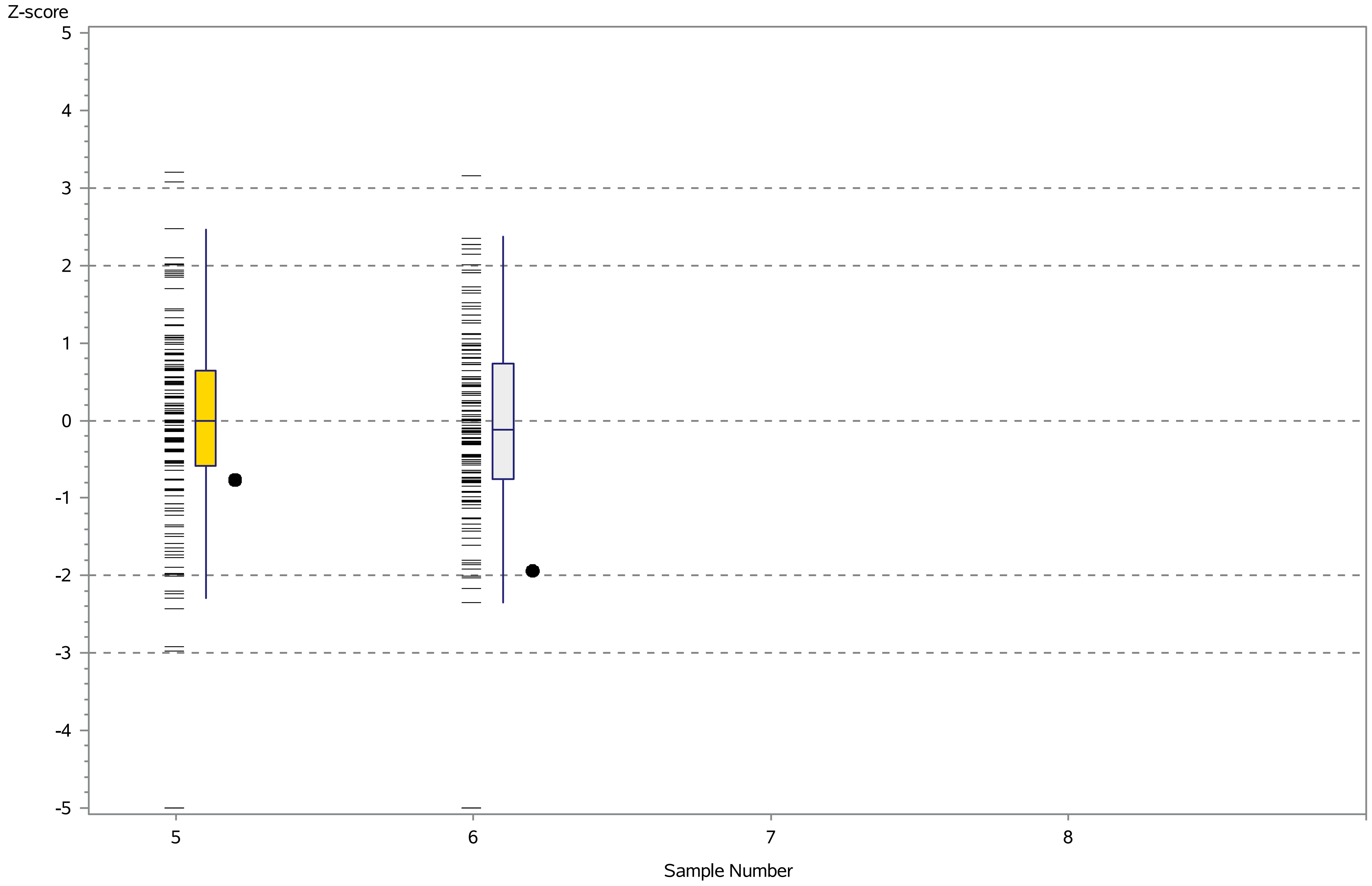
Your results (dot) compared with all reported results

04/15/2019

05/28/2019 12:46:58

Z-score distribution analysis M0189 April 2019 -

Set A Site ID= xxxxx Test=E. coli plate count Method=' '



Your results (dot) compared with all reported results

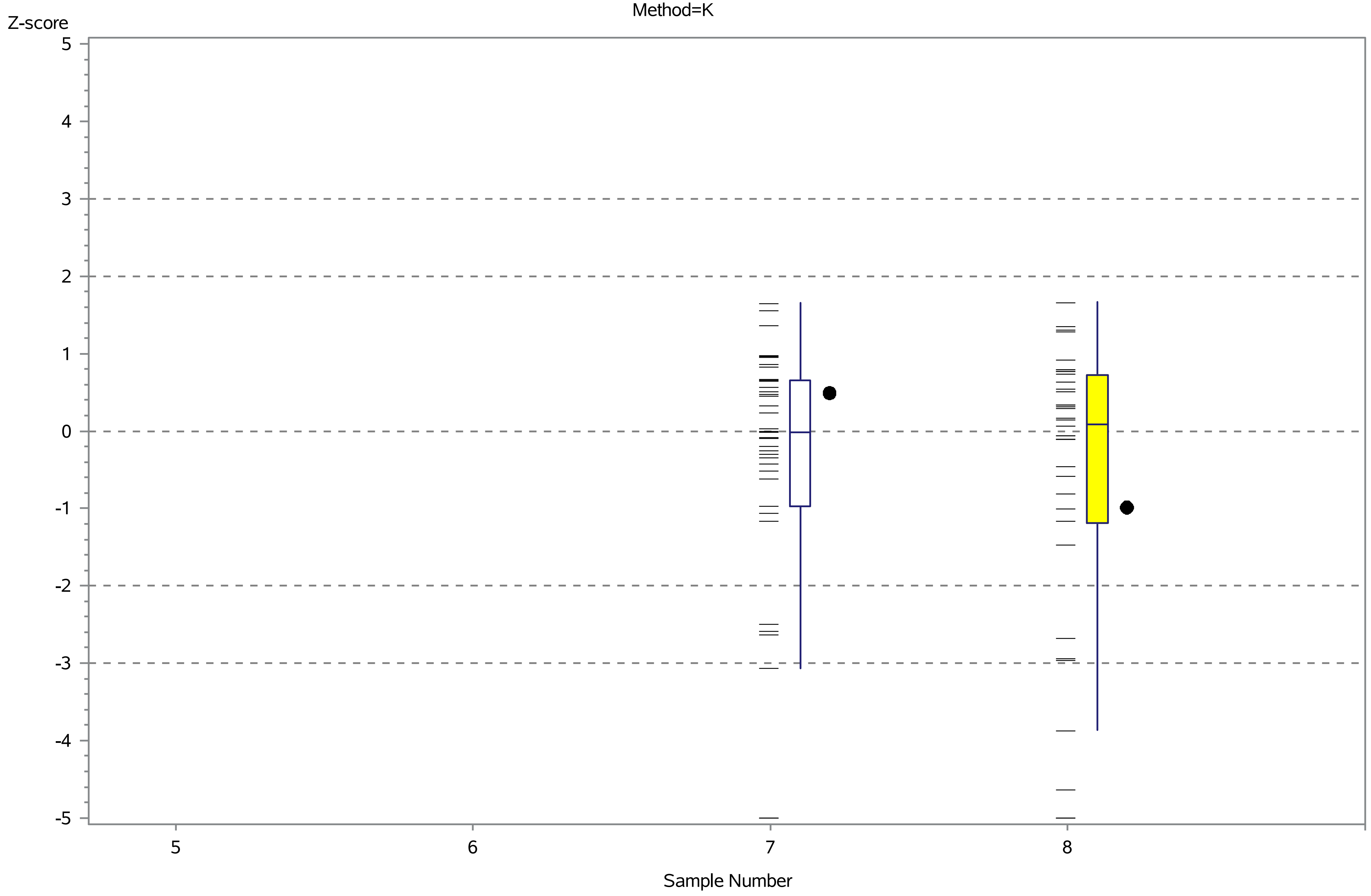
04/15/2019

05/28/2019 12:46:58

Z-score distribution analysis M0189 April 2019 - Set

A Site ID= xxxxx Test=Coagulase Positive Staph

Method=K

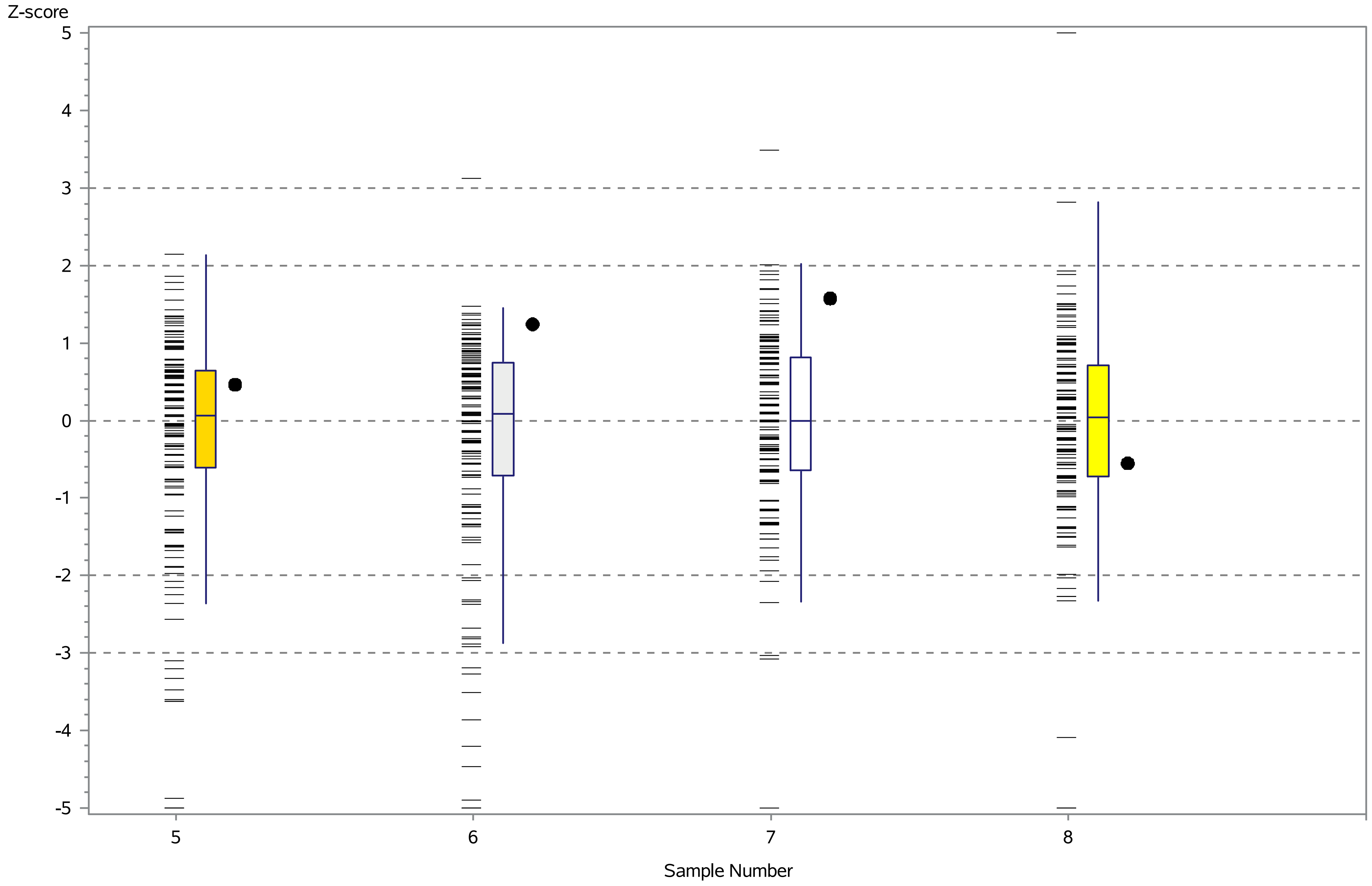


Your results (dot) compared with all reported results

04/15/2019

Z-score distribution analysis M0189 April 2019 - Set A

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

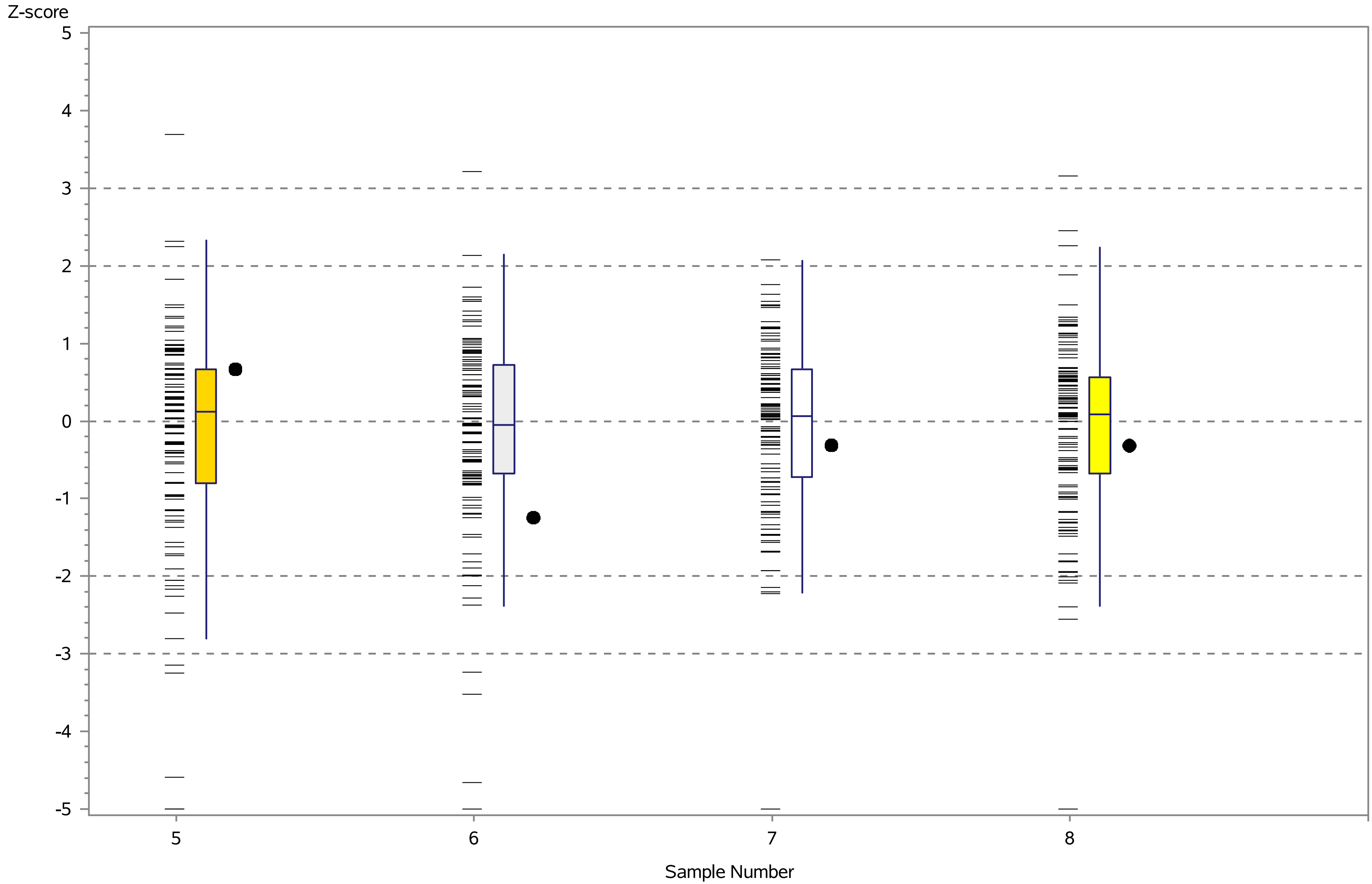


Your results (dot) compared with all reported results

04/15/2019

Z-score distribution analysis M0189 April 2019 - Set A

Site ID= xxxxx Test=Enterobacteriaceae Plate Count Method='
'

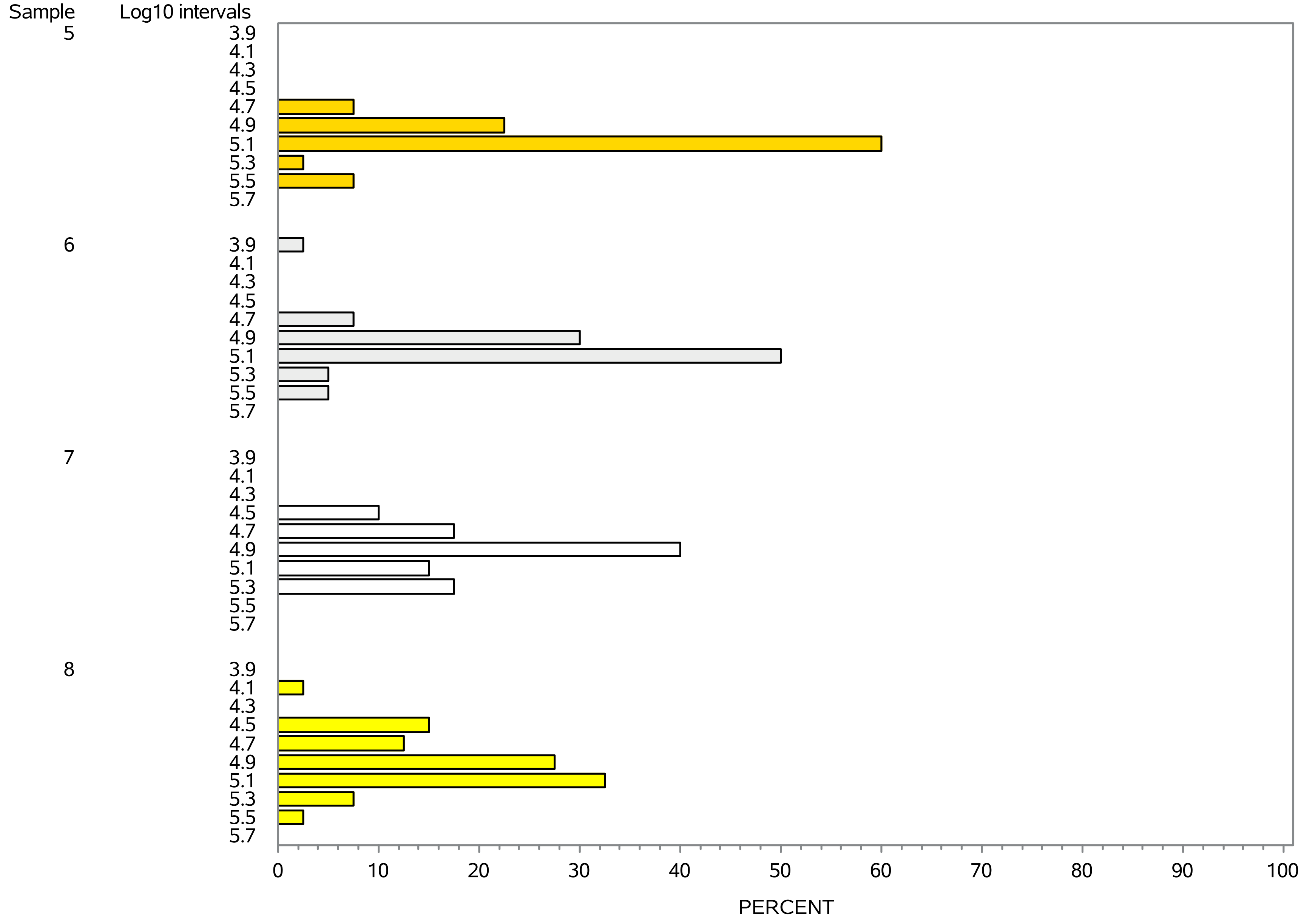


Your results (dot) compared with all reported results

04/15/2019 **05/28/2019 12:46:58**

Distribution of Results Converted to log10 - Set A

Site ID= xxxxx Test=APC Method=A



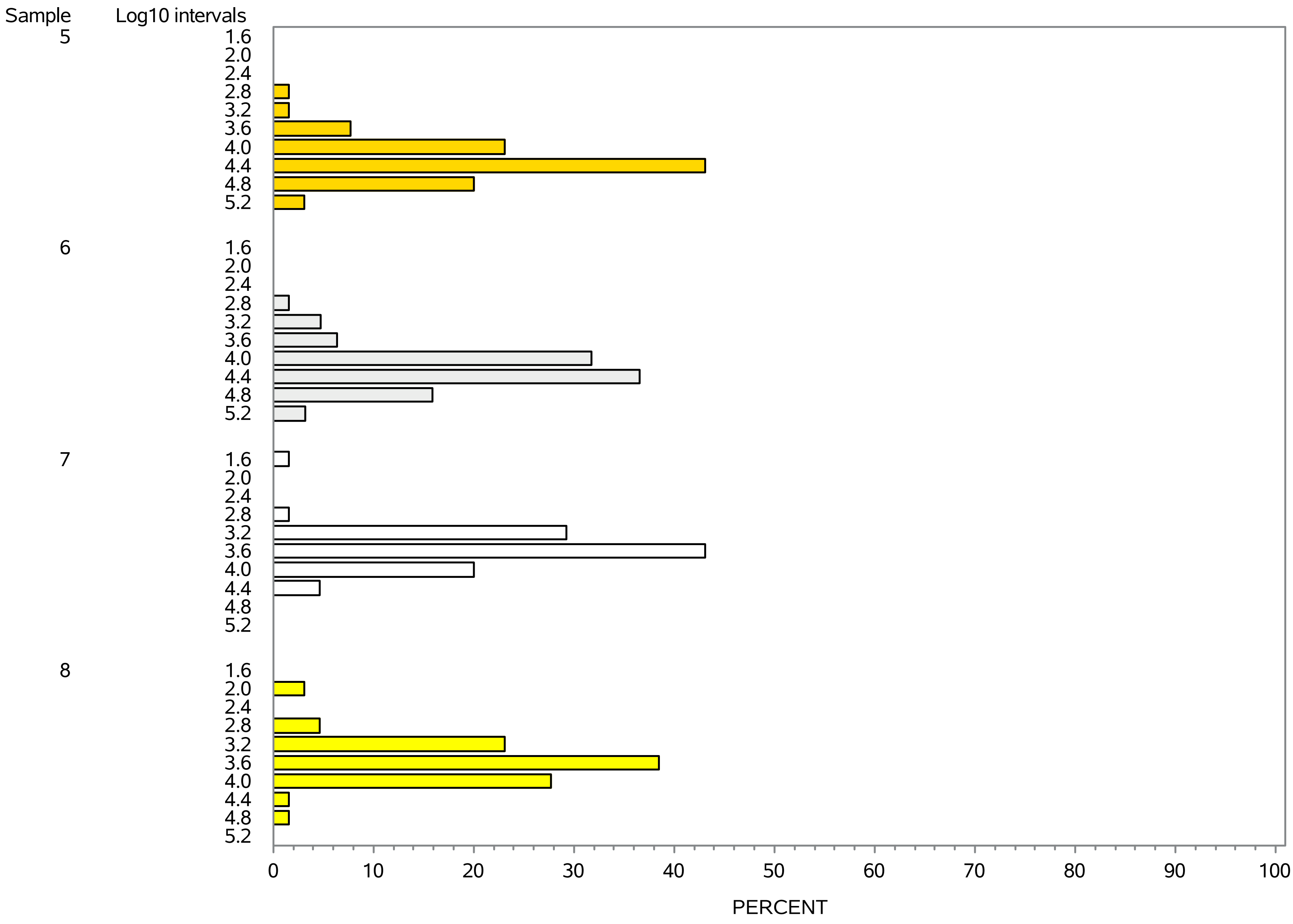
Sample	Log10 intervals	FREQ.	PCT.
5	3.9	0	0.0
	4.1	0	0.0
	4.3	0	0.0
	4.5	0	0.0
	4.7	3	7.5
	4.9	9	22.5
	5.1	24	60.0
	5.3	1	2.5
	5.5	3	7.5
	5.7	0	0.0
6	3.9	1	2.5
	4.1	0	0.0
	4.3	0	0.0
	4.5	0	0.0
	4.7	3	7.5
	4.9	12	30.0
	5.1	20	50.0
	5.3	2	5.0
	5.5	2	5.0
	5.7	0	0.0
7	3.9	0	0.0
	4.1	0	0.0
	4.3	0	0.0
	4.5	4	10.0
	4.7	7	17.5
	4.9	16	40.0
	5.1	6	15.0
	5.3	7	17.5
	5.5	0	0.0
	5.7	0	0.0
8	3.9	0	0.0
	4.1	1	2.5
	4.3	0	0.0
	4.5	6	15.0
	4.7	5	12.5
	4.9	11	27.5
	5.1	13	32.5
	5.3	3	7.5
	5.5	1	2.5
	5.7	0	0.0

Distribution of results converted to log10

04/15/2019

Distribution of Results Converted to log10 - Set

A Site ID= xxxxx Test=MPN Coliform Method=' '



Sample	Log10 intervals	FREQ.	PCT.
5	1.6	0	0.00
	2.0	0	0.00
	2.4	0	0.00
	2.8	1	1.54
	3.2	1	1.54
	3.6	5	7.69
	4.0	15	23.08
	4.4	28	43.08
	4.8	13	20.00
	5.2	2	3.08
6	1.6	0	0.00
	2.0	0	0.00
	2.4	0	0.00
	2.8	1	1.59
	3.2	3	4.76
	3.6	4	6.35
	4.0	20	31.75
	4.4	23	36.51
	4.8	10	15.87
	5.2	2	3.17
7	1.6	1	1.54
	2.0	0	0.00
	2.4	0	0.00
	2.8	1	1.54
	3.2	19	29.23
	3.6	28	43.08
	4.0	13	20.00
	4.4	3	4.62
	4.8	0	0.00
	5.2	0	0.00
8	1.6	0	0.00
	2.0	2	3.08
	2.4	0	0.00
	2.8	3	4.62
	3.2	15	23.08
	3.6	25	38.46
	4.0	18	27.69
	4.4	1	1.54
	4.8	1	1.54
	5.2	0	0.00

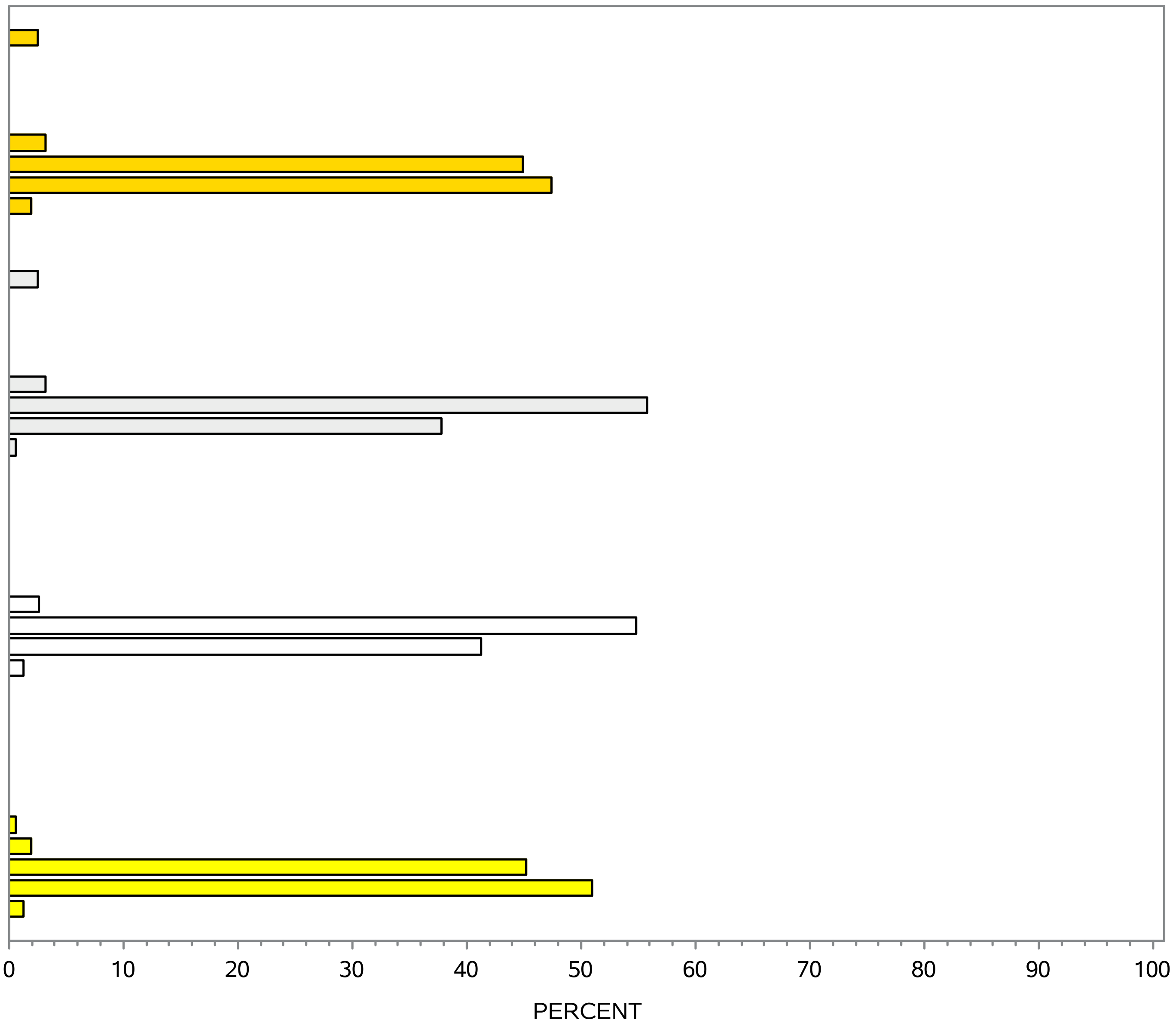
Distribution of results converted to log10

04/15/2019

Distribution of Results Converted to log10 - Set A

Site ID= xxxxx Test=Coliform plate count Method=' '

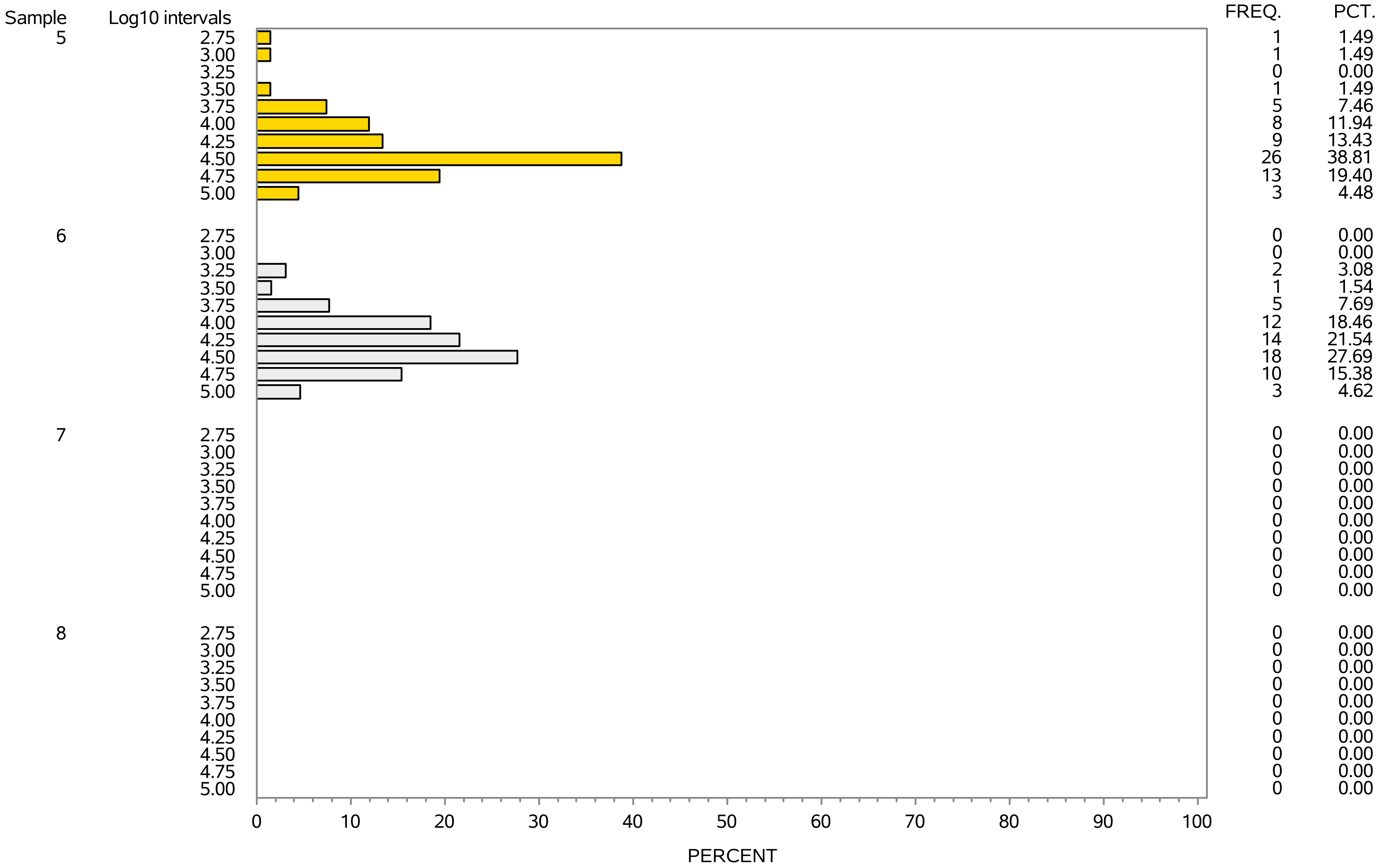
Sample	Log10 intervals	FREQ.	PCT.
5	-0.3	0	0.00
	0.3	4	2.56
	0.9	0	0.00
	1.5	0	0.00
	2.1	0	0.00
	2.7	0	0.00
	3.3	5	3.21
	3.9	70	44.87
	4.5	74	47.44
	5.1	3	1.92
6	-0.3	0	0.00
	0.3	4	2.56
	0.9	0	0.00
	1.5	0	0.00
	2.1	0	0.00
	2.7	0	0.00
	3.3	5	3.21
	3.9	87	55.77
	4.5	59	37.82
	5.1	1	0.64
7	-0.3	0	0.00
	0.3	0	0.00
	0.9	0	0.00
	1.5	0	0.00
	2.1	0	0.00
	2.7	4	2.58
	3.3	85	54.84
	3.9	64	41.29
	4.5	2	1.29
	5.1	0	0.00
8	-0.3	0	0.00
	0.3	0	0.00
	0.9	0	0.00
	1.5	0	0.00
	2.1	1	0.65
	2.7	3	1.94
	3.3	70	45.16
	3.9	79	50.97
	4.5	2	1.29
	5.1	0	0.00



Distribution of results converted to log10

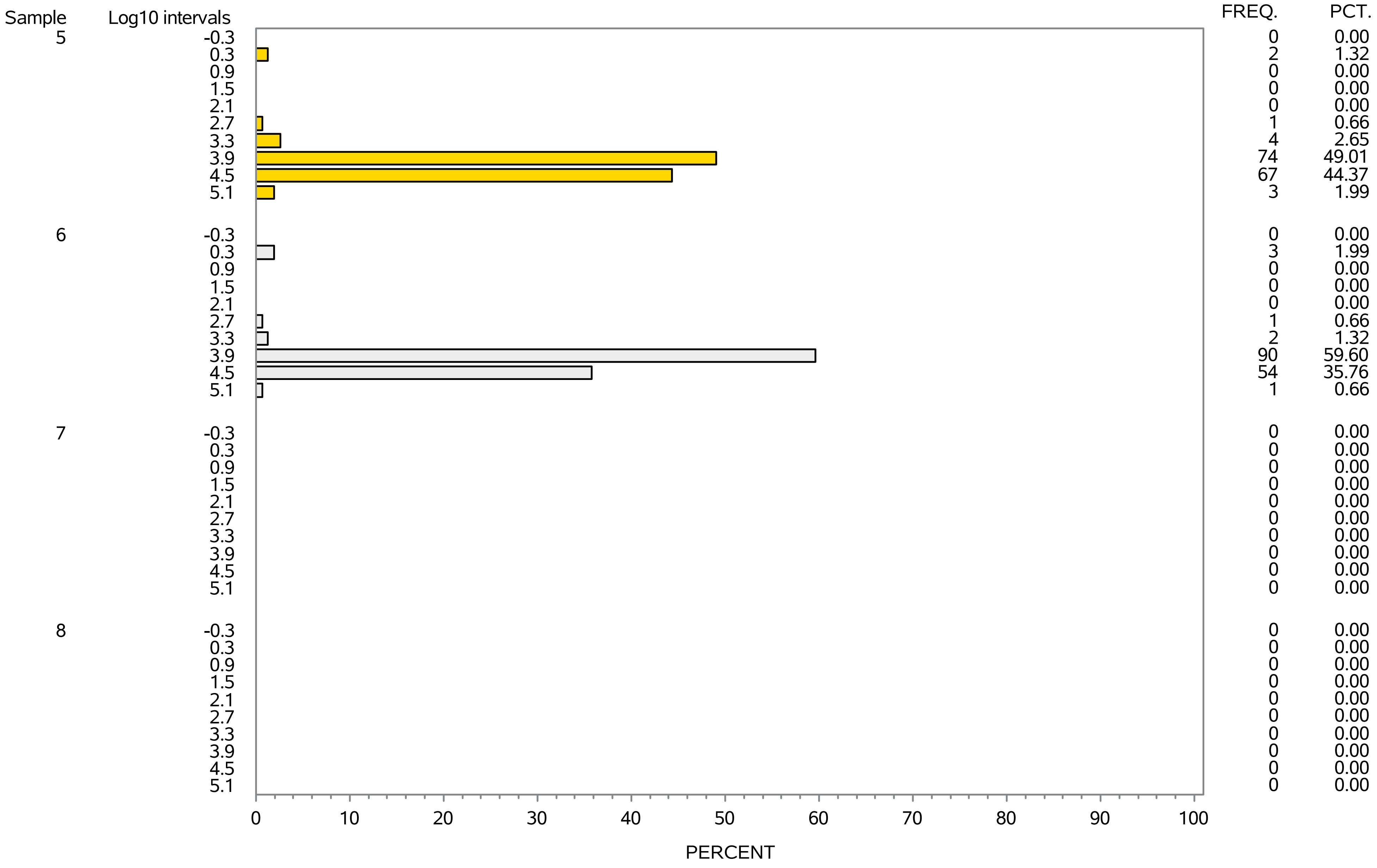
04/15/2019

Distribution of Results Converted to log10 - Set A Site ID=xxxxx Test=MPN E. coli Method=' '



Distribution of results converted to log10

Distribution of Results Converted to log10 - Set A Site ID= xxxxx Test=E. coli plate count Method=' '



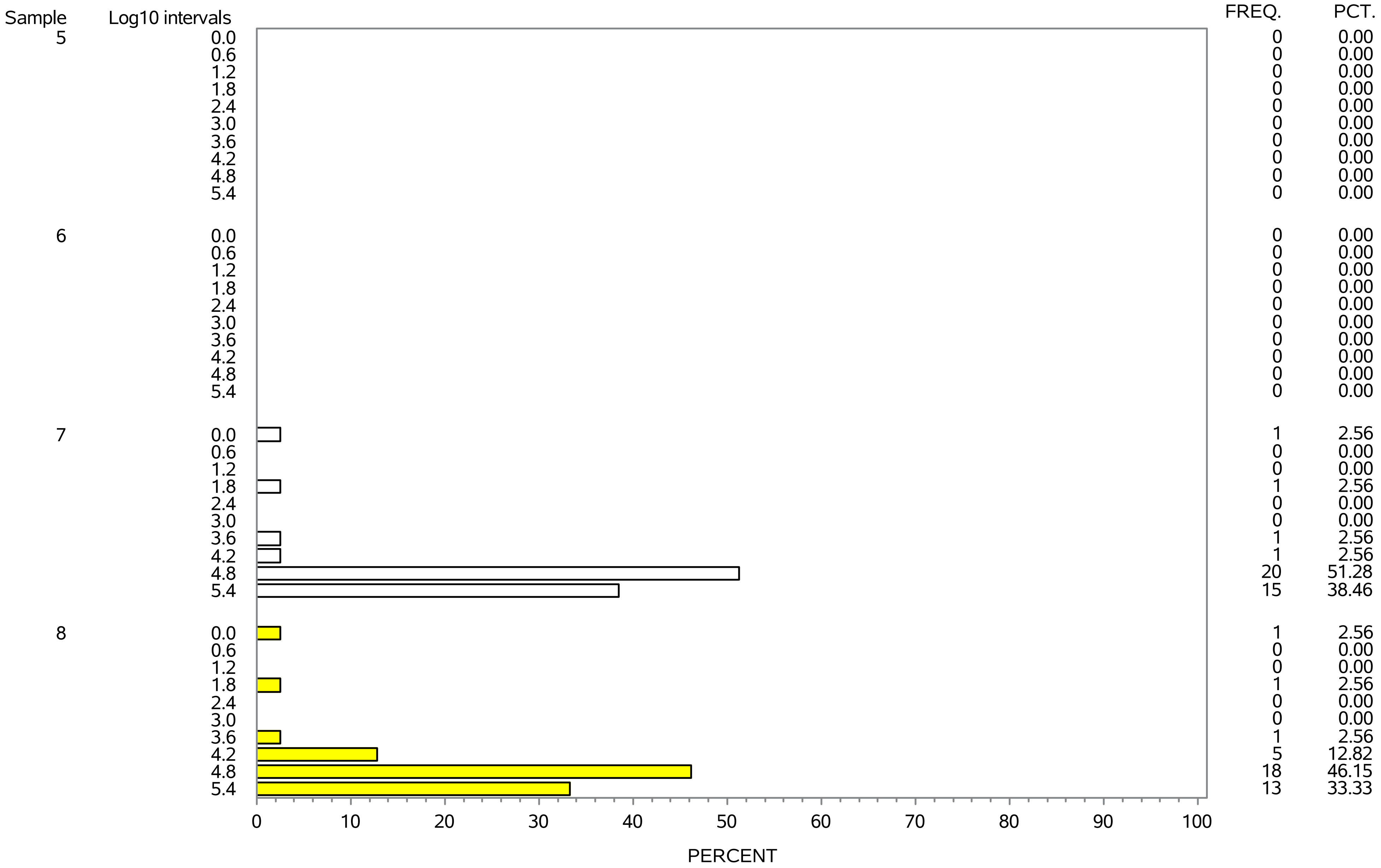
Distribution of results converted to log10

04/15/2019

05/28/2019 12:46:58

Distribution of Results Converted to log10 - Set A Site

ID=xxxxx Test=Coagulase Positive Staph Method=K

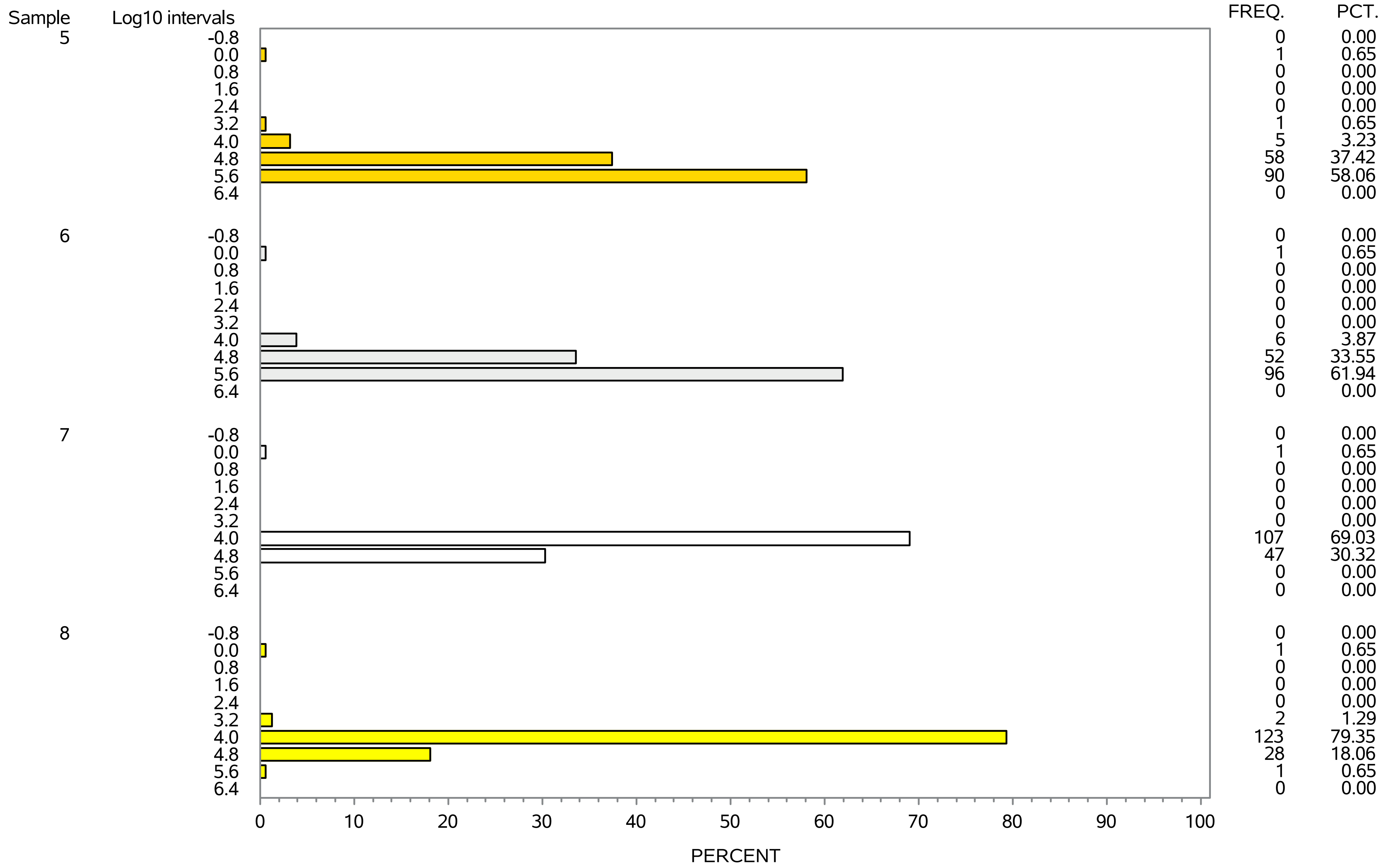


Sample	Log10 intervals	FREQ.	PCT.
5	0.0	0	0.00
	0.6	0	0.00
	1.2	0	0.00
	1.8	0	0.00
	2.4	0	0.00
	3.0	0	0.00
	3.6	0	0.00
	4.2	0	0.00
	4.8	0	0.00
	5.4	0	0.00
6	0.0	0	0.00
	0.6	0	0.00
	1.2	0	0.00
	1.8	0	0.00
	2.4	0	0.00
	3.0	0	0.00
	3.6	0	0.00
	4.2	0	0.00
	4.8	0	0.00
	5.4	0	0.00
7	0.0	1	2.56
	0.6	0	0.00
	1.2	0	0.00
	1.8	1	2.56
	2.4	0	0.00
	3.0	0	0.00
	3.6	1	2.56
	4.2	1	2.56
	4.8	20	51.28
	5.4	15	38.46
8	0.0	1	2.56
	0.6	0	0.00
	1.2	0	0.00
	1.8	1	2.56
	2.4	0	0.00
	3.0	0	0.00
	3.6	1	2.56
	4.2	5	12.82
	4.8	18	46.15
	5.4	13	33.33

Distribution of results converted to log10

Distribution of Results Converted to log10 - Set

A Site ID= xxxxx Test=Yeast/Mold Method=V



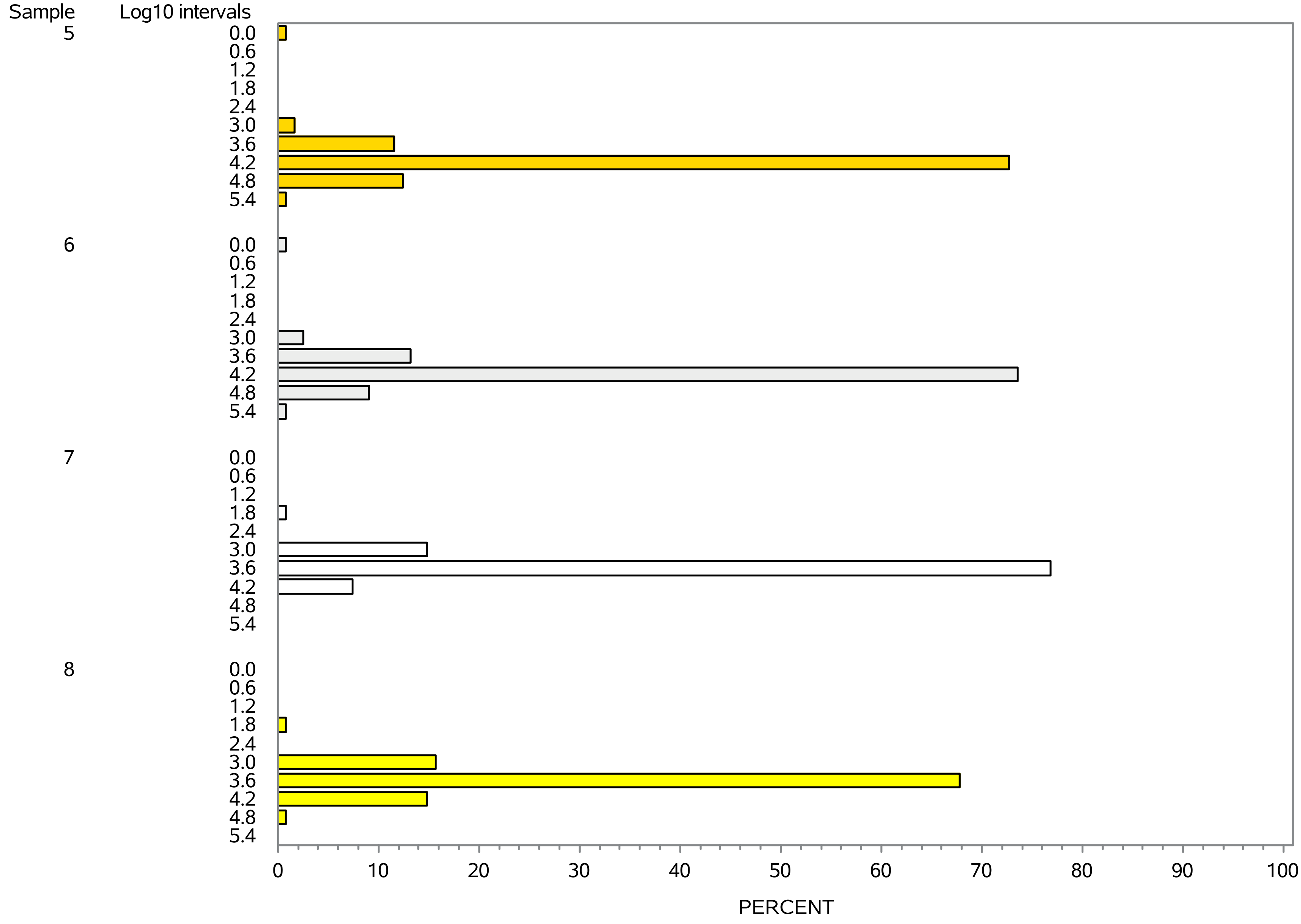
Sample	Log10 intervals	FREQ.	PCT.
5	-0.8	0	0.00
	0.0	1	0.65
	0.8	0	0.00
	1.6	0	0.00
	2.4	0	0.00
	3.2	1	0.65
	4.0	5	3.23
	4.8	58	37.42
	5.6	90	58.06
	6.4	0	0.00
6	-0.8	0	0.00
	0.0	1	0.65
	0.8	0	0.00
	1.6	0	0.00
	2.4	0	0.00
	3.2	0	0.00
	4.0	6	3.87
	4.8	52	33.55
	5.6	96	61.94
	6.4	0	0.00
7	-0.8	0	0.00
	0.0	1	0.65
	0.8	0	0.00
	1.6	0	0.00
	2.4	0	0.00
	3.2	0	0.00
	4.0	107	69.03
	4.8	47	30.32
	5.6	0	0.00
	6.4	0	0.00
8	-0.8	0	0.00
	0.0	1	0.65
	0.8	0	0.00
	1.6	0	0.00
	2.4	0	0.00
	3.2	2	1.29
	4.0	123	79.35
	4.8	28	18.06
	5.6	1	0.65
	6.4	0	0.00

Distribution of results converted to log10

04/15/2019

Distribution of Results Converted to log10 - Set A

Site ID= xxxxx Test=Enterobacteriaceae Plate Count Method='
'



Sample	Log10 intervals	FREQ.	PCT.
5	0.0	1	0.83
	0.6	0	0.00
	1.2	0	0.00
	1.8	0	0.00
	2.4	0	0.00
	3.0	2	1.65
	3.6	14	11.57
	4.2	88	72.73
	4.8	15	12.40
	5.4	1	0.83
6	0.0	1	0.83
	0.6	0	0.00
	1.2	0	0.00
	1.8	0	0.00
	2.4	0	0.00
	3.0	3	2.48
	3.6	16	13.22
	4.2	89	73.55
	4.8	11	9.09
	5.4	1	0.83
7	0.0	0	0.00
	0.6	0	0.00
	1.2	0	0.00
	1.8	1	0.83
	2.4	0	0.00
	3.0	18	14.88
	3.6	93	76.86
	4.2	9	7.44
	4.8	0	0.00
	5.4	0	0.00
8	0.0	0	0.00
	0.6	0	0.00
	1.2	0	0.00
	1.8	1	0.83
	2.4	0	0.00
	3.0	19	15.70
	3.6	82	67.77
	4.2	18	14.88
	4.8	1	0.83
	5.4	0	0.00

Distribution of results converted to log10