Performance Check

GeneMapper® *ID-X* Version 1.5

The following report verifies the performance of the Applied Biosystems GeneMapper ID-X Version 1.5 Software.

GMID-X v1.5 is approved for use on 03307.

Performance check reviewed by:

Susan E Welti

Susan Welti, Forensic Biology Unit Technical Leader

Tests were performed, written, concluded and reviewed by:

Andrew Feiter, Forensic Scientist I

I. Introduction

This report describes a performance check of the Applied Biosystems GeneMapper® *ID-X* Version 1.5 Software. It demonstrates the laboratory's adherence to Standard 8.7 of the FBI Quality Assurance Standards for DNA Testing Laboratories which states:

"Modifications to software, such as an upgrade, shall require a performance check prior to implementation. New software or significant software changes that may impact interpretation or the analytical process shall require a validation prior to implementation."

It also demonstrates the laboratory's adherence to the SWGDAM Validation Guidelines, Section 7.2, which states:

"A software upgrade that would not impact interpretation, the analytical process, or sizing algorithms shall require a performance check."

II. Performance Check

a. Objective

Samples will be analyzed in GeneMapper® *ID-X* Version 1.5 on three host computers: DFS-3081XB2, DFS-D0NKD82, and DFS-7W32382. Allele calls, peak heights and base pair sizes will be evaluated to confirm concordance for two different analysis methods. In addition, all panels, bin sets and stutter files will be compared to verify concordance.

b. Materials and Methods

GeneMapper® *ID-X* Version 1.5

Analysis Method: Globalfiler

Panel:	Globalfiler_Panel_DFS
Bin Set:	Globalfiler_Panel_DFS_Globalfiler_Bins_DFS_bins
Stutter File:	Globalfiler_Panel_DFS_stutter
Size Standard:	GS600_LIZ_(60-460)

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Analysis Method: Globalfiler_STRmix

Panel:	Globalfiler_Panel_DFS_strmix
Bin Set:	Globalfiler_Panel_DFS_strmix_Globalfiler_Bins_DFS_strmix_bins
Stutter File:	Globalfiler_Panel_DFS_strmix_stutter
Size Standard:	GS600_LIZ_(60-460)

Runs used for analysis:

Plate Name:	060616JS-RUN1-3500A
Samples:	GG-0.75_01_B03_3500 Instrument.hid
	Ladder_01_A01_3500 Instrument.hid
	POS_03_A09_3500 Instrument.hid
Plate Name:	082516AF-RUN1
Samples:	081916JS-POS1_04_E11_3500A.hid
	Ladder_01_A01_3500A.hid
	MIX1_1_01_0_3_01_B01_3500A.hid
Plate Name:	082916AF-RUN1
Samples:	082416YP-POS1_04_G12_3500A.hid

	LADDER_03_G08_3500A.hid
	MIX10_10_5_1_0_2R1_03_A08_3500A.hid
Plate Name:	MIX_4P_1b
Samples:	091216YP-POS1_03_C08_3500A.hid
	Ladder_01_E03_3500A.hid
	MIX17_1_2_3_4_0_1R1_01_G02_3500A.hid
Plate Name:	Mix_5P_1
Samples:	091416YP-POS1_06_A09_3500A.hid
	Ladder_04_E02_3500A.hid
	MIX20_10_5_2_1_1_0_3R1_04_C02_3500A.hid

c. Experimental Setup/Data Analysis

The above listed samples were analyzed in GeneMapper® *ID-X* Version 1.5 using the parameters listed above. Each electropherogram was reviewed and a combined table was exported. All allele calls, base pair sizes and peak heights were evaluated by two separate individuals to confirm concordance.

The different panels, bin sets and stutter files were also reviewed. Each value was compared and evaluated by two separate individuals to confirm concordance.

d. Results

See electropherograms and data tables.

All allele calls, peak heights and base pair sizes were verified by Forensic Scientist I Andrew Feiter and Forensic Biology Unit Technical Lead Susan Welti. All values were determined to be concordant.

All values in the panels, bin sets and stutter files were verified by Forensic Scientist I Andrew Feiter and Forensic Biology Unit Technical Lead Susan Welti. All values were determined to be concordant.

e. Conclusions

The GeneMapper® *ID-X* Version 1.5 software produced concordant results among the different Host computers. The GeneMapper® *ID-X* Version 1.5 software is recommended for use in casework analysis for the purpose of analyzing samples and printing electropherograms for interpretation.

III. Appendix

a. Electropherograms
b. Data tables (maintained electronically)