

GeneMapper[®] *ID-X* Software Version 1.4

Pub. No. 4477684 Rev. B

SUBJECT: New Features, Installation Procedures, and Software Verification Testing

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Purpose of this user bulletin

This user bulletin:

- Describes the new features of the GeneMapper[®] *ID-X* Software Version 1.4.
- Provides instructions for installing GeneMapper[®] *ID-X* Software Version 1.4.
- Provides troubleshooting information for the installation.
- Contains software verification testing information.



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New features and changes in GeneMapper[®] *ID-X* Software Version 1.4

Overview of new features

GeneMapper[®] *ID-X* Software Version 1.4 expands upon the functionality provided in Version 1.3 as described below.

- Support for the GlobalFilerTM or GlobalFilerTM Express PCR Amplification Kits:
 - Data generated with the GlobalFiler[™] Express Kit and the J6 dye set can be analyzed in GeneMapper[®] *ID*-X Software. See "New features" on page 6.
 - The following analysis files are provided:

Files automatically installed and imported into the software	Comments
GeneScan [™] 600 LIZ [®]	GS600_LIZ+Normalization_(60-460)
size standards	• GS600_LIZ_(60-460)
Panels, bins, table settings	Updated for the GlobalFiler [™] Express Kit
Plot settings	Updated for the GlobalFiler [™] Express Kit IMPORTANT! The 6-dye plot setting starts at 75 bp. However, the smallest markers in the GlobalFiler [™] Express Kit and low molecular weight microvariant alleles may fall below 75 bp. Therefore, you may want to decrease the starting size range (for example, to 60 bp) to ensure all alleles are displayed in plots.

Files automatically installed	Comments
Stutter settings	Updated for the GlobalFiler [™] Express Kit
	Stutter files must be imported into the software before use.

Y-marker analysis. In addition to the ability to analyze autosomal STR and Y-STR data separately, GeneMapper[®] *ID-X* Software Version 1.4 can analyze autosomal and Y-STR markers in one multiplexed sample. A new marker-level PQV, Amelogenin Cross Check (ACC), has been added and the Allele Number (AN) PQV has been enhanced to evaluate the quality of Y markers

designated for analysis in the Panel Manager. Y markers designated in the Panel Manager are excluded from the Mixture Analysis and Statistical Calculations performed in the Mixture Analysis Tool. See "Y-marker analysis overview" on page 6.

By default, the software designates two loci in the GlobalFiler[™] panel, DYS391 and the Y Indel, as Y markers, and processes all other loci as autosomal.

• **Spike detection disable/enable**. Spike detection functionality has been enhanced to allow you to disable spike detection for samples and controls. The disable/ enable spike detection for allelic ladders functionality introduced in v1.1.1 remains unchanged. See "Disable spike detection for samples and controls" on page 6.

Issues addressed in GeneMapper[®] *ID-X* Software v1.4

- Oracle installation errors: The issues with installation of GeneMapper[®] *ID-X* Software v1.3 that caused ORA-12528 and ORA-12541 Oracle errors have been mitigated. If you observe these errors, see "Troubleshooting" on page 36.
- Define New Sample Path function: The Edit > Define New Sample Path function in the Sample Info view is used if sample files are moved from their original location. This function now supports .hid files.
- JFS Population Database update: An update was made to the STR_JFS_Database and the STR_JFS_D2_D19 Database. The first allele designation for the D8S1179 marker was updated in the African American population from >9 to <9.

Compatibility with earlier versions of software

GeneMapper[®] *ID-X* Software

All data objects listed below can be imported from any earlier version of GeneMapper[®] *ID-X* Software or from GeneMapper[®] *ID* Software v3.2.x. All original values are retained. Values for new functions are set to defaults (for example, Sample Spike Detection is enabled).

Project	Report settings
Analysis method	Panel, bins, and stutter
Size standard	Genotype profiles for profile comparison [†]
Table settings	Mixture Analysis analysis Method [†]
Plot settings	Known reference profiles for Mixture Analysis [†]
Matrix	Audit map configuration [†]

⁺ Not applicable for GeneMapper[®] *ID-X* Software v1.0.1 or GeneMapper[®] *ID* Software v3.2.x.

Table sort order: Data in tables is sorted based on dye color, then fragment size. If you analyze data using overlapping loci that are configured differently in different panel and bin files (as you may when comparing exported results between 5-dye and 6-dye data, for example), the sort order may vary.

Data Collection Software GeneMapper[®] *ID-X* Software v1.4 can process data from:

- .fsa data files generated on 31xx Series and 310 Genetic Analyzers or 37xx Series DNA Analyzers
- .hid data files generated on 3500 Series Genetic Analyzers

Documentation and support

Related • For more information on features, updates, and known issues for GeneMapper[®] *ID-X* Software v1.4, see the following: documentation _ GeneMapper[®] ID-X Software Version 1.4 Release Notes (Part no. 4477874) located in <drive>:\AppliedBiosystems\GeneMapperID-X\Docs, where <drive> is the drive on which you installed the GeneMapper® ID-X Software. *GeneMapper*[®] *ID-X Software Help* – Start the GeneMapper[®] *ID-X* Software _ and press F1 or select Help > Contents and Index. To access contextsensitive help in the software application, click **(7)** or **Help**, located on selected windows and dialog boxes. • Related product documentation is also available in Adobe[®] Acrobat[®] format (.pdf), including: - GeneMapper[®] ID-X Software v1.0 Administrator's Guide (Pub. no. 4376327) *GeneMapper® ID-X Software v1.0 Getting Started Guide* (Pub. no. 4375574) _ GeneMapper[®] ID-X Software v1.1 Getting Started Guide: Mixture Analysis Tool _ (Pub. no. 4396773) GeneMapper[®] ID-X Software v1.1 Quick Reference Card: Mixture Analysis Tool _ (Pub. no. 4402094) *GeneMapper[®] ID-X Software v1.2 Installation Guide* (Pub. no. 4425023) *GeneMapper*[®] *ID-X Software v1.2 Reference Guide* (Pub. no. 4426481)

	– GeneMapper [®] ID-X Software v1.2 Quick Reference Card (Pub. no. 4426482)
	– GeneMapper [®] ID-X Software v1.3 User Bulletin (Pub. no. 4470483)
	 Applied Biosystems[®] 3500 Series Genetic Analyzer Data Collection Software v2 User Guide (Pub. no. 4476988)
	 Applied Biosystems[®] 3130 Series Genetic Analyzer Data Collection Software v4 Getting Started Guide (Pub. no. 4477796)
	 Applied Biosystems[®] 3730 Series DNA Analyzer Data Collection Software v4 Getting Started Guide (Pub. no. 4478016)
	To open the documentation, use the Adobe [®] Acrobat [®] Reader [®] software available from:
	www.adobe.com
	• For details on analysis method settings to use, refer to the user guide provided with the STR kit you are using.
Obtaining support	For HID support:
	 In the United States and Canada – send an email to HIDTechSupport@lifetech.com, or call 888-821-4443 option 1.
	• Outside the United States and Canada – contact your local support office.
	For the latest services and support information for all locations, go to:
	www.lifetechnologies.com/support
	At the web site, you can:
	 Access worldwide telephone and fax numbers to contact Technical Support and Sales facilities.
	• Search through frequently asked questions (FAQs).
	Submit a question directly to Technical Support.
	• Search for user documents, Safety Data Sheets (SDSs), vector maps and sequences, application notes, formulations, handbooks, certificates of analysis, citations, and other product support documents.
	Download .pdf documents.
	Obtain information about customer training.

New features

Six-dye fragment analysis

GlobalFiler[™] Kit Series use the J6 dye set listed in the following table. All software fields that display genotypes include the purple dye (P).

Note: Six-dye fragment analysis is not supported on 3100 Series or 310 genetic analyzers.

Dye	Color
6-FAM [™]	Blue
VIC®	Green
NED™	Yellow
TAZ TM	Red
SID™	Purple
LIZ®	Orange (reserved for size standard)

Disable spike detection for samples and controls

Spike detection functionality has been enhanced to allow you to disable spike detection for samples and controls. The disable/enable spike detection for allelic ladders functionality introduced in GeneMapper[®] *ID-X* Software v1.1.1 remains unchanged.

If enabled, the software examines samples and controls and updates the SSPK and SPK PQVs according to the table below.

If disabled, SSPK (Sample Spike) and SPK (Marker Spike) PQVs are set to N/A for sample, positive control, and negative control samples.

Flag Indicator	Description
Pass 📕	No spikes are detected within the range.
Check 📥	One or more spikes are detected within the range.
NA	PQV does not apply.
🔳 or 🔔	At least one label in the marker was edited or the GQ was overridden.

Y-marker analysis overview

The following functionality was added or modified in GeneMapper[®] *ID-X* Software v1.4 to support the analysis of samples that contain both Y and autosomal STRs:

- Y-marker check box added to the Panel Manager
- New Amelogenin Cross Check PQV (ACC)
- Modified Allele Number PQV (AN)
- Modified Mixture Analysis functionality
- Modified Duplicate Homozygous Allele Label functionality

Y-marker check box added to the Panel Manager

Panel Manager

The Panel Manager (**Tools > Panel Manager**) includes a Y-Marker check box for each locus, which allows you to specify any marker as a Y-marker.

This checkbox is used by the software to apply Y-marker handling rules for the ACC PQV, AN PQV, Mixture Analysis tool, and the Duplicate Homozygous Allele Label functions (described in more detail in sections that follow).

By default, the panel for the GlobalFiler[™] Kits includes DYS391 and the Y Indel selected as Y markers, and processes all other loci as autosomal. However, any locus in any AmpFℓSTR[®] kit can be designated as a Y marker.

Figure 1 Panel for the GlobalFiler[™] Express Kit with DYS391 and Y Indel selected as Y markers

🧬 Panel Manager										
File Edit Bins View Help	File Edit Bins View Help									
🚔 🗙 📄 🖬 📓 📖 🛤 🛛 Bir	Set:	AmpFLSTR_Bins	5_V3X			Image: Contract of the second seco		2 🔳 🛛 🔳		
🖃 🚠 Panel Manager 📃 🔺		Marker Name	Dye Color	Min Size	Max Size	Control Alleles	Marker	Comments	Y Marker	Ladder Alleles
AmpFLSTR_Panels_v3X	1	D351358	Blue	90.5	146.5	15,16	4	none		9,10,11,12,13,14,15,16,17,18,19,20
Profiler_v1.2X	2	VWA .	Blue	151.0	215.0	14,16	4	none		11,12,13,14,15,16,17,18,19,20,21,22,23,24
Conter_v1.2X	3	D165539	Blue	221.5	273.5	9,10	4	none		5,8,9,10,11,12,13,14,15
	4	CSF1PO	Blue	277.0	325.0	11,12	4	none		6,7,8,9,10,11,12,13,14,15
😥 - 🧰 SEfiler_Plus_v1.2X	5	TPOX	Blue	332.5	384.5	8	4	none		5,6,7,8,9,10,11,12,13,14,15
i Clentifiler_v1.2X	6	Yindel	Green	79.5	87.5	2	5	none		1,2
Cofiler_Plus_CODIS_v1.2X	7	AMEL	Green	97.0	107.5	x,y	9	none	Y	Х, Ү
Identifiler CODIS_V1.2X	8	D851179	Green	108.5	176.5	12,13	4	none		5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
🛓 🛅 MiniFiler_v1.2X	9	D21511	Green	179.5	246.5	28,31	4	none		24,24.2,25,26,27,28,28.2,29,29.2,30,30.2,31,3
	10	D18551	Green	255.5	347.5	12,15	4	none		7,9,10,10.2,11,12,13,13.2,14,14.2,15,16,17,18
🕢 🧰 Identifiler_Plus_v1.2X	11	DYS391	Green	359.5	395.5	11	4	none		7,8,9,10,11,12,13
Gentinier_Direct_v1.2x	12	D25441	Yellow	75.0	113.5	14,15	4	none	Y	8,9,10,11,11.3,12,13,14,15,16,17
GlobalFiler_Express_v1.1X	13	D195433	Yellow	115.5	173.5	14,15	4	none		6,7,8,9,10,11,12,12.2,13,13.2,14,14.2,15,15.2
	14	TH01	Yellow	174.0	219.5	7,9.3	4	none		4,5,6,7,8,9,9.3,10,11,13.3
B B NGM_SElect_Express_v1.1X ▼	15	FGA	Yellow	221.0	380.0	24,26	4	none		13,14,15,16,17,18,19,20,21,22,23,24,25,26,26
	16	D2251045	Red	83.5	126.5	11,16	3	none		8,9,10,11,12,13,14,15,16,17,18,19
	17	D55818	Red	133.5	189.5	11	4	none		7,8,9,10,11,12,13,14,15,16,17,18
	18	D135317	Red	197.0	249.0	11	4	none		5,6,7,8,9,10,11,12,13,14,15,16
	19	D75820	Red	256.5	304.5	7,12	4	none		6,7,8,9,10,11,12,13,14,15
	20	SE33	Red	306.0	444.0	17,25.2	4	none		4.2,6.3,8,9,11,12,13,14,15,16,17,18,19,20,20.
	21	D1051248	Purple	80.0	132.0	12,15	4	none		8,9,10,11,12,13,14,15,16,17,18,19
	22	D151656	Purple	154.0	209.5	13,16	4	none		9,10,11,12,13,14,14,3,15,15,3,16,16,3,17,17,3
	23	D125391	Purple	211.0	270.5	18,19	4	none		14,15,16,17,18,19,19.3,20,21,22,23,24,25,26,
	24	D251338	Purple	275.5	355.5	20,23	4	none		11,12,13,14,15,16,17,18,19,20,21,22,23,24,25
		<	· · ·				·		-	
						ОК	Cance	el Apply	Help]

Using the new Y marker functions with the AmpF $\ell\!STR^{\circledast}$ Yfiler $^{\circledast}$ PCR Amplification Kit

The Y marker checkbox in the Panel Manager is unselected by default in the Yfiler panel provided with the software. To use the new Y marker functions, select the Y marker checkbox for each Yfiler[®] Kit locus in the Panel Manager.

The ACC PQV is applied only to samples that contain both the Amelogenin marker and 1 or more Y markers and designated in the Panel Manager. For example, Yfiler[®] Kit samples do not contain the Amelogenin marker, and therefore will not be subject to the ACC PQV.

New Amelogenin Cross Check PQV (ACC)

The new Amelogenin Cross Check PQV (ACC) is a marker-level PQV that is applied to samples containing the Amelogenin marker and Y markers that have been designated in the Panel Manager as described above. It indicates if Amelogenin and Y marker results are concordant. The same flag is displayed for Amelogenin and all designated Y markers. When viewing a sample, the Quality Value Details (QVD) panel in the Genotypes plot displays a description for a ACC value.

Flag Indicator	Description					
Pass 🧧	Sample or positive control contains the amelogenin marker and one or more Y markers, and amelogenin and all Y marker results are concordant.					
Check 🝐	Amelogenin and one or more Y marker results are not concordant:					
	 Amelogenin genotype is not X, X or X,Y (for example it is X,OL, OL,OL, or Y only - no X allele detected). 					
	• Amelogenin genotype is X or X,X but one or more Y markers contain called alleles.					
	• Amelogenin genotype is X,Y and one or more Y markers do not contain called alleles.					
	Note: Peaks identified and labeled by the software as spikes are not considered in the ACC PQV.					
NA	Negative control.					
	Allelic Ladder.					
	• Sample or positive control that does not contain both the Amelogenin marker and at least one Y marker selected in the Panel Manager (for example, samples generated with the AmpFlSTR® Yfiler® PCR Amplification Kit, which does not contain Amelogenin).					
📄 or 🔺	At least one label in either the amelogenin or Y marker(s) was edited or the GQ was overridden.					

The ACC result is a composite result that begins with the analysis of the Amelogenin marker, before considering Y-marker results. Therefore, the ACC PQV will be flagged as (for both Amelogenin and any Y markers that have been selected in the Panel Manager) if:

- The Amelogenin marker contains more than two alleles.
- The Amelogenin marker contains one or more OL alleles.

Table 1 on page 9 shows the possible ACC results for the GlobalFiler[™] Express Kit. The ACC is marked as only if both Y markers also contain at least one called allele.

Nun	nber of alleles dete Amelogenin† X, Y	cted	Number of alleles detected Amelogenin X, X			
DYS391 result	Y-Indel result	ACC result	DYS391 result	Y-Indel result	ACC result	
1 or more	1 or more	Pass 🔛	1 or more	1 or more	Check 📥	
1 or more	Not present	Check 📥	1 or more	Not present	Check 📥	
Not present	1 or more	Check 📥	Not present	1 or more	Check 📥	
Not present	Not present	Check 📥	Not present	Not present	Pass 📕	

Table 1 ACC results for the GlobalFiler[™] Express Kit

† Spikes in the Amelogenin marker are not considered.

The ACC can be used to determine a sample Genotype Quality (GQ) value by setting weighting in the Analysis Method SQ & GQ Settings tab.

Note: The values shown in the figure are for example only. Perform internal validation studies to determine the appropriate setting to use for your analysis.

Analysis Method Editor	R.					X
General Allele Peak Dete	ctor Peak (Quality	5Q & 😡 Settir	igs		
Quality weights are betwe Sample and Control GQ Wi	en 0 and 1. eighting					
Broad Peak (BD)	0.8		Allele Numb	er (AN)	1.0	
Out of Bin Allele (BIN)	0.8		Low Peak He	eight (LPH)	0.3	
Overlap (OVL)	0.8		Max Peak H	eight (MPH)	0.3	
Marker Spike (SPK)	0.3	6	Off-scale (C	·S)	0.8	
AMEL Cross Check (ACC)	0.5		Peak Height	Ratio (PHR)	0.3	
SQ Weighting Broad Peak (BD) Allelic Ladder GQ Weightin Spike (SSPK/SPK)	0.5		Off-scale (C	5)	1 💌	
SQ & GQ Ranges	Pass Range 0.75	to 1.0	Low Qual From 0.0 to From 0.0 to	0.25		
Sav	/e As	Save	Cancel	Reset D	efaults	

Modified Allele Number PQV (AN)

The Allele Number PQV (AN) is a marker-level PQV that indicates if the software detects the expected number of alleles within a marker size range. The functionality of this PQV has been enhanced to define a separate threshold for Y markers (designated in the Panel Manager) in addition to autosomal markers:

Flag Indicator	Description					
Pass 🧧	At least one allele and not more than the Max Expected Alleles are detected for the marker, or the X allele is detected for the Amelogenin marker.					
Check 🝐	• More than the Max Expected Alleles are detected for any markers specified as Y markers in the Panel Manager.					
	 More than the Max Expected Alleles are detected for Autosomal/ Amelogenin markers. 					
	No alleles are detected for autosomal or amelogenin markers.					
	No X allele is detected in Amelogenin.					
📄 or 📥	At least one label in the marker was edited or the GQ was overridden.					

In the Analysis Method Peak Quality tab, the AN threshold can be set separately for autosomal markers/Amelogenin and Y markers (designated in the Panel Manager).

Note: The values shown in the figure are for example only. Perform internal validation studies to determine the appropriate setting to use for your analysis.

Analysis Method Editor	×
General Allele Peak Detector Peak Quality	SQ & GQ Settings
Min/Max Peak Height (LPH/MPH)	
Homozygous min peak height	200.0
Heterozygous min peak height	100.0
Max Peak Height (MPH)	5000.0
Peak Height Ratio (PHR)	
Min peak height ratio	0.7
Broad Peak (BD)	
Max peak width (basepairs)	1.5
Allele Number (AN)	
Max expected alleles:	
For autosomal markers & AMEL	2
For Y markers	1
Allelic Ladder Spike	
Spike Detection	Enable 🗸
Cut-off Value	0.2
Sample Spike Detection	
Spike Detection	Enable 💌
	Factory Defaults
Save	ncel Help

Note: The DYS385 marker in the Yfiler[®] Kit may include two alleles. If this marker is designated as a Y marker in the Panel Manager and the default Y marker AN threshold of 1 is used, AN will be \bigwedge if two alleles are detected.

The AN threshold can be used to determine a sample Genotype Quality (GQ) value by setting weighting in the Analysis Method Peak Quality tab.

Note: The values shown in the figure are for example only. Perform internal validation studies to determine the appropriate setting to use for your analysis.

	0		
uality weights are between ample and Control GQ Weig	u and 1. Inting		
Broad Peak (BD)	0.8	Allele Number (AN)	1.0
Dut of Bin Allele (BIN)	0.8	Low Peak Height (LPH)	0.3
Overlap (OVL)	0.8	Max Peak Height (MPH)	0.3
Marker Spike (SPK)	0.3	Off-scale (OS)	0.8
AMEL Cross Check (ACC)	0.5	Peak Height Ratio (PHR)	0.3
Control Concordance (CC) \	Weight = 1.0 (Only	applicable to controls)	
	and the second second second second		
Q Weighting	·		
Q Weighting 3road Peak (BD)	0.5		
Q Weighting 3road Peak (BD) Ilelic Ladder GQ Weighting-	0.5		
Q Weighting 3road Peak (BD) Ilelic Ladder GQ Weighting- spike (SSPK/SPK)	0.5	Off-scale (OS)	1 👻
Q Weighting Broad Peak (BD) Ilelic Ladder GQ Weighting- Spike (SSPK/SPK) Q & GQ Ranges	0.5	Off-scale (OS)	1 💌
Q Weighting 3road Peak (BD) Ilelic Ladder GQ Weighting- 5pike (SSPK/SPK) Q & GQ Ranges	0.5	Off-scale (OS)	1
Q Weighting Broad Peak (BD) Ilelic Ladder GQ Weighting- Spike (SSPK/SPK) Q & GQ Ranges	0.5	Off-scale (OS)	1 💌
Q Weighting Broad Peak (BD) Ilelic Ladder GQ Weighting- Spike (SSPK/SPK) Q & GQ Ranges Ileling Quality: From	0.5 1 • Pass Range: 0.75 to 1.0	Off-scale (OS)	1 💌
Q Weighting Broad Peak (BD) Ilelic Ladder GQ Weighting- Spike (SSPK/SPK) Q & GQ Ranges Q & GQ Ranges Izing Quality: From ienotype Quality: From	0.5 1 •• Pass Range: 0.75 to 1.0 0.75 to 1.0	Off-scale (OS)	1 💌
Q Weighting Sroad Peak (BD) Ilelic Ladder GQ Weighting- Spike (SSPK/SPK) Q & GQ Ranges Q & GQ Ranges izing Quality: From ienotype Quality: From	0.5 1 •• Pass Range: 0.75 to 1.0 0.75 to 1.0	Off-scale (OS) Low Quality Renge: From 0.0 to 0.25 From 0.0 to 0.25	1
Q Weighting Broad Peak (BD) Ilelic Ladder GQ Weighting- Spike (SSPK/SPK) Q & GQ Ranges Q & GQ Ranges izing Quality: From Senotype Quality: From	0.5 1 •• Pass Range: 0.75 to 1.0 0.75 to 1.0	Off-scale (OS) Low Quality Range: From 0.0 to 0.25 From 0.0 to 0.25	1

Modified Mixture Analysis functionality

Y markers that have been designated in the Panel Manager are displayed in the Mixture Analysis Plot Viewer along with the autosomal markers, but are not considered in the Mixture Analysis calculations.

If you select a sample that contains only Y markers (designated in the Panel Manager), the software displays a message and excludes the entire sample from processing.

If you select a sample that contains autosomal and Y markers (as designated in the Panel Manager), the Mixture Analysis software displays a message indicating that Y marker data is excluded from calculations. In the Mixture Analysis Plot Viewer, Y marker alleles (designated in the Panel Manager) will be displayed in gray to indicate that the Mixture Interpretation Threshold and Mixture Analysis calculations are not applied to the Y marker data.

When you export data from the Mixture Analysis Tool:

- Loci designated as Y markers are not included in the calculated data and are not included in the list of Missing Markers (the Missing Markers list contains loci that do not produce interpretable results).
- Loci designated as Y markers in the Panel Manager are listed as excluded from mixture analysis. If a sample does not contain Y markers, the excluded marker field is shown as N/A.

Modified Duplicate Homozygous Allele Label functionality

The Duplicate Homozygous Allele Label functionality in Project Options has been modified to accommodate Y markers (designated in the Panel Manager) in addition to autosomal markers. When enabled:

- Autosomal markers Single alleles are displayed in the Genotypes table with two labels to indicate presumed homozygotes.
- **Y-markers** Single alleles in Y markers (designated in the Panel Manager) are displayed with a single label.

Computer requirements

Recommended configuration (for optimal performance)	Minimum requirements
Core 2 Duo 3 GHz or newer	Core 2 Duo 2.2 GHz or compatible
4 GB RAM	2 GB RAM
200 MB available on boot drive	200 MB available on boot drive
10 GB available on install drive (full install)	10 GB available on install drive (full install)
450 MB available on install drive (client install)	450 MB available on install drive (client install)
DVD-ROM drive	DVD-ROM drive
10/100 NIC with RWU (internal) or above installed	10/100 NIC with RWU (internal) or above installed
TCP/IP installed	TCP/IP installed
$Microsoft^{\circledast}$.NET Framework 2.0 or later	$Microsoft^{\textcircled{R}}$.NET Framework 2.0 or later

IMPORTANT! Ensure that the computer name does not contain spaces, special characters, or non-alphanumeric characters (! % in particular). Special characters in the computer name may interfere with installation of the Oracle[®] software.

TCPIP

TCP Internet Protocol (TCP/IP) is integral to the communication between the user interface of the GeneMapper[®] *ID-X* Software and the Oracle[®] database in which data is stored. TCP/IP is also the protocol your computer uses to access the internet and local intranets within a local network. Any disruption in the TCP/IP connection will disconnect the GeneMapper[®] *ID-X* Software from the Oracle[®] database.

Network recommendation To minimize disconnection issues between the GeneMapper[®] *ID-X* Software and the Oracle[®] database, use a cable-based network system, such as a CAT5e network, with plug-in Network Interface Controller (NIC) cards rather than wireless NIC cards. The GeneMapper[®] *ID-X* Software uses TCP Internet Protocol (TCP/IP) to communicate between the user interface and the Oracle[®] database. Any disruption in the TCP/IP connection will disconnect the GeneMapper[®] *ID-X* Software from the Oracle[®] database. For more information, see "Troubleshooting" on page 36.

Procedures to perform before installation: Windows[®] XP Operating System (OS)

You must perform all procedures in this section before installing the software:

- "Check user access" on page 13
- "Modify antivirus, firewall, and network computer settings" on page 14
- "Export data objects and settings from the current version of GeneMapper[®] ID-X Software" on page 15
- "Uninstall GeneMapper[®] ID-X Software or Oracle[®] software" on page 15
- "Check virtual memory settings" on page 15
- "Clear Windows[®] XP application and system logs" on page 17
- "Check Microsoft .NET Framework version" on page 18
- "Restart the computer and recheck virtual memory settings" on page 19

Check user access You must log on to the local computer using a local account with administrator privileges (read, write, and execute [rwx] permissions). The local computer is typically identified in the log in dialog box by the text "(this computer)" after the computer name.

A local computer account may be different from the account you normally use to log in to the computer. The local account:

- Can not include network domain policies that restrict access to the install drive of the local computer account.
- Can not restrict access to the operating system by firewall or other security configurations.

To check user access:

1. Select **Control Panel > User Accounts**.

2. In the Users tab, verify that your user account belongs to the Administrators group and that the domain name is the same as the computer name. (The ora_dba group will be added to your account after you install the software.)



Modify antivirus, firewall, and network computer settings

- 1. Disable Antivirus software (including anti-malware software) before the installation.
- 2. Disable Firewalls before the installation.
- **3.** Ensure that your network access meets the following conditions:
 - Do not use a wireless network. Use a cable-based network system, such as a CAT5e network, with plug-in Network Interface Controller (NIC) cards rather than wireless NIC cards. The GeneMapper[®] *ID-X* Software uses TCP Internet Protocol (TCP/IP) to communicate between the user interface and the Oracle[®] database. Any disruption in the TCP/IP connection will disconnect the GeneMapper[®] *ID-X* Software from the Oracle[®] database.
 - Only one network should be connected. Go to Settings > Network connections. If more than one network is connected, right-click then select Disable until only one network connection is listed.
 - All virtual network adapters are disabled (refer to manufacturer documentation for instructions).
 - Laptop computers Wireless network connections are disabled.

Solutions Sections			
File Edit View Favorites Ti	ols Advanced Help		A
🚱 Back 🝷 🕥 🕤 🏂 🚺	🛛 🗸 🔎 Search 🛛 🦻 Folder	s 🕼 🎯 🗙 🍤	
Address 🔇 Network Connections			💌 🔁 Go
Name	Туре	Status	Device Name
Dial-up			
LAN or High-Speed Internet	Dial-up	Disconnected	Standard 336
🕹 Local Area Connection 3	LAN or High-Speed	Inter Connected	Intel(R) 8256
🕹 1394 Connection	LAN or High-Speed	Inter Connected	1394 Net Ada
^{((P)} Wireless Network Connection	LAN or High-Speed	Inter Disabled	Intel(R) WiFi I

 Export data objects and settings from the current version of GeneMapper[®] *ID-X* Software
 Computers running a full version of GeneMapper[®] *ID-X* Software (contains the database): Export the data objects or settings you would like to restore after upgrade (analyzed projects, analysis methods, plot settings, etc.). For information, refer to the GeneMapper[®] *ID-X* Software online help.
 Computers running a client version of GeneMapper[®] *ID-X* Software: Export is not required.
 Computers running GeneMapper[®] *ID* Software v3.2: Do not export at this time.

• **Computers running GeneMapper**[®] *ID* **Software v3.2:** Do not export at this time. You will be prompted to export during the installation.

Uninstall GeneMapper[®] *ID-X* Software or Oracle[®] software Uninstall GeneMapper[®] *ID-X* Software, any other programs that use Oracle databases, and any existing versions of Oracle databases, whether Life Technologies products or products from other companies. Go to **Start > Control Panel > Add or Remove Programs**.

After uninstallation, Ensure that the GeneMapper[®] *ID-X* Software is uninstalled (go to **Start** > **Control Panel** > **Add or Remove Programs** and make sure it is not listed.

If it is still listed, manually uninstall the software (see "If the GeneMapper[®] ID-X Software is still listed after uninstalling (tested on Windows[®] XP only)" on page 38).

Check virtual memory settings

1. On the desktop, right-click **My computer**, select **Properties** > **Advanced**, then click **Settings** in the Performance section.

System Proper	ties			? 🛽
System Res	tore	Automa	tic Updates	Remote
General	Compute	r Name	Hardware	Advanced
You must be lo Performance Visual effects	gged on as ar , processor sc	n Administrat heduling, me	cor to make most of	these changes.
User Profiles Desktop setti	ngs related to	your logon		
Startup and F System startu	lecovery p, system failu	ire, and debi	ugging information	Settings
				Settings
	Envir	onment Varia	ables Erro	r Reporting

2. In the Performance Options dialog box, click the **Advanced** tab, then click **Change** in the Virtual Memory section.

rformance Opt	ions	? 🛛
isual Effects Advi	anced Data Execution Prevention	
Processor schedu	uling	
By default, the c	omputer is set to use a greater share a	of
Adjust for best p	erformance of:	
Programs	O Background services	
-Memory usage		
By default, the c memory to run y	omputer is set to use a greater share o our programs.	of
Adjust for best p	erformance of:	
Programs	O System cache	
Virtual memory -		
A paging file is an if it were RAM.	n area on the hard disk that Windows (uses as
Total paging file	size for all drives: 2046 MB	
	Char	nge
		Arrely
	OK Cancel	Apply

3. In the Virtual Memory dialog box, select the **C:** drive. Click the **Custom size** radio button. Specify **2046** MB for initial and **4092** for maximum size.

IMPORTANT! The exact Maximum Size necessary may depend on your computer configuration. If installation still fails when using these values, or if Oracle[®] ORA-12528 and ORA-12541 errors are displayed, increase the Maximum size to at least 2X the physical memory (the minimum required for the installation of Oracle[®] software) up to the value shown for Space Available, then repeat the

installation. To determine the physical memory for your computer, right-click **My Computer** on the desktop, select **Properties**, then look for the RAM value on the General tab. Example: If the physical memory is 3.0 GB RAM, set the Maximum Size to 6000.

Virtual Memory	? 🛛
Drive [Volume Label]	Paging File Size (MB)
C:	2046 - 12000
Paging file size for sel	ected drive
Drive:	C:
Space available:	155803 MB
 Custom size: 	
Initial size (MB):	2046
Maximum size (MB):	4092
O System managed s	size
○ No paging file	Set
Total paging file size f	or all drives
Minimum allowed:	2 MB
Recommended:	5302 MB
Currently allocated:	2046 MB
	OK Cancel

4. Click Set, then click OK.

These settings are not activated until you restart the computer.

- 1. Select Start > Settings > Control Panel > Administrative Tools > Event Viewer.
- 2. Right-click **Applications**, then select **Properties**.



Clear Windows[®] XP application and system logs **3.** In the Application Properties dialog box, set the Maximum Log Size to **10048**, then click **Clear Log**.

And Kanadian David	
Application Pro	pernes [[
General Filter	
Display name:	Application
Log name:	C:\WINDOWS\system32\config\AppEvent.Evt
Size:	512.0 KB (524,288 bytes)
Created:	Tuesday, February 03, 2004 11:06:42 AM
Modified:	Monday, August 06, 2012 12:21:59 PM
Accessed:	Monday, August 06, 2012 12:21:59 PM
Log size	
Maximum log :	size: 10048 🤤 KB
When maximu	ım log size is reached:
🔿 O verwrite i	events as needed
💿 Overwrite	events older than 🛛 🗧 days
O Do not ove (clear log r	erwrite events nanually) Restore Defaults
Using a low-s	peed connection Clear Log
	OK Cancel Apply

- 4. Click OK.
- 5. Right-click System, then select Properties.
- **6.** In the System Properties dialog box, set the Maximum Log Size to **10048**, then click **Clear Log**.
- 7. Click OK.

Ensure that a version of 2.0 or later is installed on the computer:

1. Select Start > Settings > Control Panel > Add or Remove Programs.

2. Scroll down and determine if a version of 2.0 or later is installed. (There may be multiple versions installed. Do not remove any versions of the software.)



3. If a version of 2.0 or later is not installed, insert the v1.4 Full installation or Full Upgrade DVD in the DVD drive. Navigate to the DotNet directory, then double-click **NETFx20SP2_x86.exe** to launch the Microsoft .NET Framework 2.0 Service Pack 2 (SP2) installer.

Check Microsoft .NET Framework version 4. Read and accept the end user licensing agreement, then click **Install**.



After installation completes, verify the Microsoft .NET Framework 2.0 SP2 was successfully installed (select Start > Settings > Control Panel > Add or Remove Programs).

🐻 Add or Re	move Programs				
	Currently installed programs:	Show up <u>d</u> ates	Sort by: Name		~
Change or	S 225 Kanane Environment 3.0 opdate 17	. 0052	Size	154,00008	~
Programs	👙 J2SE Runtime Environment 5.0 Update 6		Size	152.00MB	
1201	🛃 Java(TM) 6 Update 22		Size	191.00MB	8
	🛃 Java(TM) 6 Update 5		Size	228.00MB	8
Add New Programs	A Microsoft .NET Framework 1.1				
	🗗 Microsoft .NET Framework 2.0 Service Pack 2		Size	184.00MB	
6	Click here for support information.		Used	<u>rarely</u>	
Add/Remove Windows	To change this program or remove it from your computer, click Cha	ange or Remove.	Change	Remove	
Components	📴 Microsoft Office Professional Edition 2003		Size	246.00MB	
	🛃 Microsoft Visual C++ 2005 Redistributable		Size	5.21MB	8 2
Set Program	🥮 Mozilla Firefox (3.6.20)		Size	27.21MB	8
Access and	MSXML 6.0 Parser (KB933579)		Size	1.31MB	a l
Derdales	🥝 Mycoplasma Assay Software Module		Size	1,12MB	-
	NVIDIA Drivers				
	RowerDVD		Size	33,51MB	8
	😁 Roxio Creator Audio				
	🚷 Roxio Creator BDAV Plugin				
	🚷 Roxio Creator Copy				*
	Toxio Creator Copy				

Restart the computer and recheck virtual memory settings To activate the changes made in the previous sections, restart the computer before installing the software.

After the computer restarts, follow the procedure in "Check virtual memory settings" on page 15 and ensure that the new settings are activated.

Procedures to perform before installation: Windows[®] 7 Operating System (OS)

You must perform all procedures in this section before installing the software.

- "Check user access" on page 20
- "Modify antivirus, firewall, and network computer settings" on page 22
- "Export data objects and settings from the current version of GeneMapper[®] ID-X Software" on page 22
- "Uninstall GeneMapper[®] ID-X Software or Oracle[®] software" on page 22
- "Check virtual memory settings" on page 23
- "Check notification settings" on page 26
- "Check Microsoft .NET Framework version" on page 26
- "Restart the computer and recheck virtual memory settings" on page 27

Check user access You must log on to the local computer using a local account with administrator privileges (read, write, and execute [rwx] permissions). The local computer is typically identified in the log in dialog box by the text "(this computer)" after the computer name

A local computer account may be different from the account you normally use to log in to the computer. The local account:

- Can not include network domain policies that restrict access to the install drive of the local computer account.
- Can not restrict access to operating system firewall or other security configurations.

Check Local status



2. Select your local user account and ensure that the Type is Local.



Check Administrator privileges

- 1. Right-click My Computer, then select Manage.
- **2.** In the Computer Management dialog box, click **Local Users and Groups**, then double-click **Groups**.

🎥 Computer Management	- • •
File Action View Help	
🗢 🔿 🖄 🖬 🔛 🖬	
Somputer Management (Local Name	Actions
A 👫 System Tools	Local User 🔺
Description of the second s	More 🕨
Shared Folders	
🕟 🌺 Local Users and Groups	
Performance	
🚔 Device Manager	
🔺 🔄 Storage	
🔤 Disk Management	
Services and Applications	

3. Double-click **Administrators**. Ensure that your local account is listed in the Administrators group.

Administrators Pro	operties	? 🔀
General		
Admin	istrators	
Description:	Administrators to the compute	nave complete and unrestricted access #/domain
Members:		
ABService Administrato INSTR-ADI vijaucsn MyLocalAc	or MIN count	
Add	Remove	Changes to a user's group membership are not effective until the next time the user logs on.

Modify antivirus, firewall, and network computer settings

- 1. Disable Antivirus software (including anti-malware software) before the installation.
- 2. Disable Firewalls before the installation.
- 3. Ensure that your network access meets the following conditions:
 - Do not use a wireless network. Use a cable-based network system, such as a CAT5e network, with plug-in Network Interface Controller (NIC) cards rather than wireless NIC cards. The GeneMapper[®] *ID-X* Software uses TCP Internet Protocol (TCP/IP) to communicate between the user interface and the Oracle[®] database. Any disruption in the TCP/IP connection will disconnect the GeneMapper[®] *ID-X* Software from the Oracle[®] database.
 - Only one network should be connected. Go to **Control Panel Network and Sharing center**. If more than one network is connected, double-click a connection, then select **Disable** until only one network connection is listed.
 - All virtual network adapters are disabled (refer to manufacturer documentation for instructions).
 - Laptop computers Wireless network connections are disabled.



Export data objects and settings from the current version of GeneMapper[®] *ID-X* Software

- Computers running a full version of GeneMapper[®] *ID-X* Software (contains the database): Export the data objects or settings you would like to restore after upgrade (analyzed projects, analysis methods, plot settings, etc.). For information, refer to the GeneMapper[®] *ID-X* Software online help.
- Computers running a client version of GeneMapper[®] *ID-X* Software: Export is not required.
- **Computers running GeneMapper** *ID* **Software v3.2:** Do not export at this time. You will be prompted to export during the installation.

Uninstall GeneMapper[®] *ID-X* Software or Oracle[®] software

Uninstall GeneMapper[®] *ID-X* Software, any other programs that use Oracle databases, and any existing versions of Oracle databases, whether Life Technologies products or products from other companies. Go to Start ➤ Control Panel ➤ Add or Remove Programs.

After uninstallation, ensure that the GeneMapper[®] *ID-X* Software is uninstalled (go to **Start > Control Panel > Add or Remove Programs** and make sure it is not listed.

If it is still listed, manually uninstall the software (see "If the GeneMapper[®] ID-X Software is still listed after uninstalling (tested on Windows[®] XP only)" on page 38).

1. On the desktop, right-click **My Computer**, then click **Advanced System Settings**.

Check virtual memory settings

🕖 🗢 🛃 🕨 Control Panel 🕨	All Control Panel Items 🔸 Systen	n	-	Search Control Panel
Control Panel Home	View basic information	about your computer		
Device Manager	Windows edition			
Remote settings	Windows 7 Professional			
System protection	Copyright © 2009 Microso	ft Corporation. All rights reserved.		
Advanced system settings	Service Pack 1 Get more features with a n	ew edition of Windows 7		
	System			
	Manufacturer:	Dell		
	Model:	Optiplex XE		
	Rating:	5.1 Windows Experience Index		Dél
	Processor:	Intel(R) Core(TM)2 Duo CPU E8400 @ 3.00GHz 3.00 GHz		
	Installed memory (RAM):	4.00 GB (3.25 GB usable)		
	System type:	32-bit Operating System		
	Pen and Touch:	No Pen or Touch Input is available for this Display		
	Dell support			
	Website:	Online support		
See also	Computer name, domain, and	workgroup settings		
Action Center	Computer name:	OPTIPLEX-XE-SV		🚱 Change settings
Windows Update	Full computer name:	OPTIPLEX-XE-SV		
Performance Information and	Computer description:	Optiplex XE Series Instrument & Application Computer		
10015	Workgroup:	WORKGROUP		

2. In the System Properties dialog box, click Settings in the Performance section.

System Properties				
Computer Name Hardware Advanced System Protection Remote				
You must be logged on as an Administrator to make most of these changes.				
Performance				
Visual effects, processor scheduling, memory usage, and virtual memory				
Settings				
User Profiles				
Desktop settings related to your logon				
Settings				
Startup and Recovery				
System startup, system failure, and debugging information				
Settings				
Environment Variables				
OK Cancel Apply				

3. Click the **Advanced** tab, then click **Change** in the Virtual Memory section.

6
Performance Options
Visual Effects Advanced Data Execution Prevention
Processor scheduling Choose how to allocate processor resources.
Adjust for best performance of:
Programs O Background services
Virtual memory
A paging file is an area on the hard disk that Windows uses as if it were RAM.
Total paging file size for all drives: 3325 MB
Change
OK Cancel Apply

4. In the Virtual Memory dialog box, deselect the Automatically Manage paging file size for all drives check box. Select the **C:** drive. Click the **Custom size** radio button. Specify **2046** MB for initial and **4092** for maximum size.

IMPORTANT! The exact Maximum Size necessary may depend on your computer configuration. If installation still fails when using these values, or if Oracle[®] ORA-12528 and ORA-12541 errors are displayed, increase the Maximum size to at least 2X the physical memory (the minimum required for the installation of Oracle[®] software) up to the value shown for Space Available, then repeat the

installation. To determine the physical memory for your computer, right-click **My Computer** on the desktop, select **Properties**, then look for the RAM value on the General tab. Example: If the physical memory is 3.0 GB RAM, set the Maximum Size to 6000.

Virtual Memory	×
Automatically manage paging file size for all drives)
Drive [Volume Label] Paging File Size (MB)	
C: [OS] System managed	
S: [AB Service] None	
Selected drive: C: [OS] Space available: 41217 MB	
Custom size:	
Initial size (MB): 2046	
Maximum size (MB): 4092	
System managed size	_
No paging file	
Total paging file size for all drives	_
Minimum allowed: 16 MB	
Recommended: 4987 MB	
Currently allocated: 3325 MB	
ОК Са	ncel

5. Click Set, then click OK.

These settings are not activated until you restart the computer.

Check notification settings

- 2. In the User Account Control Settings, drag the slider to the bottom position Never Notify.



Check Microsoft .NET Framework version Ensure that a version of 2.0 or later is installed on the computer:

- 1. Select 🚳 🕨 Control Panel 🕨 User Programs and Features.
- **2.** Scroll down and determine if a version of 2.0 or later is installed. (There may be multiple versions installed. Do not remove any versions of the software.)



- **3.** If a version of 2.0 or later is not installed, insert the v1.4 Full installation or Full Upgrade DVD in the DVD drive. Navigate to the \DotNet directory, then double-click **NETFx20SP2_x86.exe** to launch the Microsoft .NET Framework 2.0 Service Pack 2 (SP2) installer.
- 4. Read and accept the end user licensing agreement, then click Install.



Restart the computer and recheck virtual memory settings To activate the changes made in the previous sections, restart the computer before installing the software.

After the computer restarts, follow the procedure in "Check virtual memory settings" on page 23 and ensure that the new settings are activated.

Installing GeneMapper[®] *ID-X* Software v1.4

General installation instructions **IMPORTANT!** If you use a computer platform that does not meet the requirements listed in "Computer requirements" on page 12, you may experience difficulties during installation (new or upgrade) of GeneMapper[®] *ID-X* Software, or the software may not function properly, even if the installation proceeded successfully. Review the list of recommended software operating systems included in the GeneMapper[®] *ID-X* Software *v1.4 Release Notes* (see page 4) before beginning installation, and report any issues encountered during installation to HID Technical Support (see page 5).

Before installing the GeneMapper[®] *ID-X* Software:

- Review "Computer requirements" on page 12, the GeneMapper[®] *ID-X* Software *v1.4 Release Notes* (see page 4), the *GeneMapper*[®] *ID-X Software Version 1.2 Installation Guide*, and any supplemental documentation (see page 4).
- Log in to the local computer and have Administrator privileges when installing, un-installing, or upgrading the GeneMapper[®] *ID-X* Software. Logging in to a network domain with administrative privileges is not sufficient.
- During installation (new or upgrade) of GeneMapper[®] *ID-X* Software:
 - Install the Full version first, then install all Client versions which will connect to the Full version database.
 - Allow the installation DVD to Autostart, or double-click the **Setup.exe** file to launch the installer.
- When un-installing the GeneMapper[®] *ID-X* Software, log in using the same local user account as the one used when installing the software and follow the un-installation message prompts during the un-installation process to ensure clean un-installation.

Perform a
GeneMapper® /D-X
SoftwareUse the GeneMapper® ID-X Software v1.4 Full or Client installation DVD for new installations or installations to
computers installed with GeneMapper® ID Software v3.2. A detailed description of different installation scenarios and
steps performed by the user is summarized in Table 2 and Table 3.

Table 2 Full installation scenarios and steps

Installation Type	5	Scenario	Choose DVD	Steps
GeneMapper [®] <i>ID</i> - <i>X</i> Software Full Full installation Stand Alone Computer without any version of		GeneMapper [®] <i>ID-X</i> Software	 Log in to the local computer (not a network domain) using an account with Administrator privileges. 	
installation		GeneMapper [®] <i>ID-X</i> Software or Data Collection	v1.4 Full Part no 4479707	2. Insert the GeneMapper [®] <i>ID-X</i> Software v1.4 Full DVD and follow the instructions.
		Software installed		Installation may take up to 1 hour to complete.
				3. Enter the Registration Code to launch the software.
	Full installation to a computer installed	Stand Alone Computer with GeneMapper $^{\textcircled{B}}$ <i>ID</i>	GeneMapper [®] <i>ID-X</i> Software	 Log in to the local computer (not a network domain) using an account with Administrator privileges.
	with GeneMapper [®] Software v3.2.x installed ID Software v3.2	v1.4 Full Part no. 4479707	2. Insert the GeneMapper [®] <i>ID-X</i> Software v1.4 Full DVD and follow the instructions.	
		The software detects the GeneMapper $^{\circledast}$ /D Software v3.X.		
		3. When prompted, export the GeneMapper [®] <i>ID</i> Software v3.2 data objects or settings you would like to restore after installation (analyzed projects, analysis methods, etc.) using the export utility located on the Full or Full Upgrade DVD.		
			 Un-install the GeneMapper[®] ID Software v3.2 (go to the Windows[®] Control Panel, then select Add or Remove Programs). 	
			 Restart the computer, then log in to the local computer using an account with Administrator privileges. 	
			6. Install the GeneMapper [®] <i>ID-X</i> Software v1.4 Full version from the Full DVD.	
				Installation may take up to 1 hour to complete.
				7. Enter the Registration Code to launch the software.

Table 3 Client installation scenarios and steps

Installation Type		Scenario	Choose DVD	Steps
GeneMapper [®] <i>ID-X</i> Software Client installation	Client installation	Stand Alone Computer without any version of GeneMapper [®] <i>ID-X</i> Software installed	GeneMapper® <i>ID-X</i> Software v1.4 1-Client Part no. 4479711 5-Client Part no. 4479708 10-Client Part no. 4479709	 Before installing, perform the procedures in the section appropriate for the computer: "Procedures to perform before installation: Windows® XP Operating System (OS)" on page 13. "Procedures to perform before installation: Windows® 7 Operating System (OS)" on page 20. Install a full version of the software before the client version (see Table 2 on page 29). Log in to the local computer (not a network domain) using an account with Administrator privileges. Insert the GeneMapper[®] <i>ID-X</i> Software v1.4 Client DVD and follow the instructions. Installation takes about 15 minutes to complete.
				b. Enter the Registration Code to launch the software.

ЗО

Installation Type		Scenario	Choose DVD	Steps
GeneMapper [®] ID- X Software Client installation	Client installation to a computer with GeneMapper [®] <i>ID</i> Software v3.2	Stand Alone Computer with GeneMapper [®] ID Software v3.2.x installed	Choose DVDGeneMapper®ID-X Softwarev1.41-ClientPart no. 44797085-ClientPart no. 447970810-ClientPart no. 4479709	 Steps Before installing, perform the procedures in the section appropriate for the computer: "Procedures to perform before installation: Windows® XP Operating System (OS)" on page 13. "Procedures to perform before installation: Windows® 7 Operating System (OS)" on page 20. Log in to the local computer (not a network domain) using an account with Administrator privileges. Insert the GeneMapper® <i>ID-X</i> Software v1.4 Full DVD and export the GeneMapper® <i>ID</i> Software v3.2 data objects or settings you would like to restore after installation (analyzed projects, analysis methods, plot settings, etc.) using the export utility located on the Full DVD. Un-install the GeneMapper® <i>ID</i> Software v3.2 (go to the Windows® Control Panel, then select Add or Remove Programs). Restart the computer, then log in to the local computer using an account with Administrator privileges. Insert the GeneMapper[®] <i>ID-X</i> Software v1.4 Client DVD and follow the instructions.
				Installation takes about 15 minutes to complete.
				7. Enter the Registration Code to launch the software.

<u>3</u>

Upgrade from a previous version of GeneMapper[®] *ID-X* Software

Note the following:

- Before upgrading the software, close all instances of previous versions of GeneMapper[®] *ID-X* Software (on both Client and Full computers), and close all other software programs and open windows.
- You need two registration codes:
 - During the upgrade, the installer will prompt for the registration code for the previously installed version of GeneMapper[®] *ID*-X Software.
 - After upgrading to v1.4 and launching the software for the first time, enter the new registration code provided with version 1.4.
- The data exported from previous versions of the GeneMapper[®] *ID-X* Software can be imported and viewed in GeneMapper[®] *ID-X* Software v1.4.

A detailed description of different upgrade scenarios and steps performed by the user is summarized in Table 4 and Table 5.

Table 4 Full upgrad	e scenarios and	steps
---------------------	-----------------	-------

Installation Type	Scenario	Choose DVD	Steps
Upgrade to GeneMapper® ID-X Software Full installationUpgrade GeneMapper® ID-X Software v1.0.1 or later Full install on a stand-alone computerGeneMapper® ID-X Software Version 1.4 Full Upgrade Part no. 4479715	 Before installing, perform the procedures in the section appropriate for the computer: "Procedures to perform before installation: Windows[®] XP Operating System (OS)" on page 13. "Procedures to perform before installation: Windows[®] 7 Operating System (OS)" on page 20. 		
		2. Log in to the local computer using an account with Administrator privileges.	
		3. Insert the GeneMapper [®] <i>ID-X</i> Software Full Upgrade DVD and follow the instructions.	
			 Enter the Registration Code from the <i>previous</i> version of software. (The software will prompt you to enter the Registration Code from the new version when you launch the software for the first time.)

Installation Type	Scenario	Choose DVD	Steps
Upgrade to GeneMapper [®] <i>ID-X</i> Software Client	Upgrade GeneMapper® <i>ID-X</i> Software v1.0.1 or later Client installed on a stand-alone computer	GeneMapper [®] <i>ID-X</i> Software Version 1.4 Client Upgrade Part no. 4479710	 Before installing, perform the procedures in the section appropriate for the computer: "Procedures to perform before installation: Windows[®] XP Operating System (OS)" on page 13. "Procedures to perform before installation: Windows[®] 7 Operating System (OS)" on page 20. Upgrade a full version of the software before the client version (see Table 4 on page 33). Log in to the local computer using an account with Administrator privileges. Insert the GeneMapper[®] <i>ID-X</i> Software Client Upgrade DVD and follow the instructions. The software detects the previous version of GeneMapper[®] <i>ID-X</i> Software. Enter the Registration Code from the <i>previous</i> version of software. (The software will prompt you to enter the Registration Code from the new version when you launch the software for the first time.)

Procedures to perform after installation

Reset file and
folder permissions
after installation
(Client installation)The client installer specifies folder privileges at the time of the GeneMapper® ID-X Software installation.
However, the NTFS permissions set by the system administrator may not allow the GeneMapper® ID-X Software to
access the GeneMapper folder following installation. Before you run the software, check the permissions to make sure
that the GeneMapper® ID-X Software can access the GeneMapper folder.If you do not have the required permissions, you may see a "can't access file" or "..\GeneMapper_Preferences (Access is
denied)" error message when using the software. To set the privileges manually, either before running the software or in
the event of an error message:

- 1. Right-click the **AppliedBiosystems** folder.
- 2. Select **Properties**, then click the **Security** tab.
- **3.** In the top pane, select **Users**.

<u></u>

4. Windows 7 OS only: Click Edit.

5. In the bottom pane, select Full Control. Windows[®] XP 0S

Local Disk (C:) Properties	🐌 Applied Biosystems Properties 🛛 💽
General Tools Hardware Sharing Security Quota	General Sharing Security Previous Versions Customize
Group or user names:	Object name: C:\Applied Biosystems
Administrators (FRMVREELAMML06\Administrators)	Group or user names:
🕵 CREATOR OWNER	
G Everyone	Authenticated Users
SYSTEM	A device the CODTIDE EX VE CV6 & device the text
	Administrators (UPTIPLEA:AE-SV Administrators)
Add Remove	To change permissions, click Edit. Edit
Permissions for Users Allow Deny	Permissions for Users Allow Deny
Full Control	Full control
Modifu 🔽 🗖	Modify
Bead & Execute	Read & execute 🗸 🗉
List Folder Contents	List folder contents
Bead	Read
Write	Write 🗸 👻
	For special permissions or advanced settings
For special permissions or for advanced settings	click Advanced.
click Advanced.	
	Learn about access control and permissions
OK Cancel Apply	OK Cancel Apply

Windows[®] 7 0S

Reset the antivirus, firewall, and network settings you changed for installation.

Import the stutter files provided with the software into the GeneMapper® ID-X Software database. See the GeneMapper[®] *ID-X* Software online help for information. Obtain and run the You can run 6-dye samples on 3500 Data Collection Software v1 or v2. Before running on either system for the first time, run the HID Updater 3500 DC v2.0 (Part no. 4480670). The HID Updater installs the plate templates, assays, and instrument protocols needed to run GlobalFiler[™] Kit samples. For more information, refer to the release notes provided with the Updater. Note: If you have a new instrument installed by a Life Technologies representative, the updater may have been run during installation. 1. Obtain the HID Updater 3500 DC v2.0 from www.lifetechnologies.com/ support > Software, Patches & Updates > 3500 Series Genetic Analyzers for Human Identification. 2. Exit the 3500/3500xL Data Collection Software. 3. Load the HID Updater Installer CD on the instrument computer. 4. Double click the HID_Updater_3500_DC_SW_2.0.exe file on the CD. 5. When installation is complete, restart the computer.

Reset antivirus. firewall, and network computer settings

Import GlobalFiler[™] stutter files

HID Updater on 3500 Series instruments

Troubleshooting

Symptoms and

causes

Symptom	Possible cause	Action
ORA-12528 and ORA-12541 Oracle $^{\textcircled{B}}$ errors displayed during installation	Problem with Oracle [®] software installation.	Contact Life Technologies.

C:\WINDOWS\system32\cmd.exe	_ _ X		
SQL*Plus: Release 11.2.0.1.0 Production on Thu May 17 14:19:19 2012 Copyright (c) 1982, 2010, Oracle. All rights reserved. ERROR: ORA-12528: TNS:listener: all appropriate instances are blocking new connections Enter user-name: SQL*Plus: Release 11.2.0.1.0 Production on Wed May 2 12:01:16 2012 Copyright (c) 1982, 2010, Oracle. All rights reserved. ERROR: ORA-12541: TNS:no listener Enter user-name:			
"GeneMapper [®] ID-X software requires Microsoft .NET Framework 2.0 or greater. You can download from Microsoft or run the .NET setup included in the DVD to install it."	Incorrect Microsoft [®] .NET Framework version	 Cancel the installation. Install the required version. See "Check Microsoft .NET Framework version" on page 18. Start the installation again. 	
GeneMapper [®] <i>ID-X</i> Software will not start after installation	Uninstallation of the previous version of GeneMapper [®] <i>ID-X</i> Software failed. Note: In most cases, uninstallation should succeed. However, third-party software, firewall interference, and other situations may interfere with successful uninstallation.	Uninstall the software. See "Uninstall the GeneMapper [®] ID-X Software" on page 38. If the problem persists, contact Life Technologies.	
"No databases found" message	Network security settings are preventing communication between the user interface and the Oracle [®] database. Virtual network adapters are enabled.	Modify network security settings. See "Enable communication with port 1521 Windows [®] XP OS" on page 39 or "Enable communication with port 1521 Windows [®] 7 OS" on page 39. Disable virtual network adapters.	
	Virtual network adapters are enabled.	Disable virtual network adapters. If the problem persists, contact Life Technologies.	

Symptom	Possible cause	Action	
"The database connection has been	Network communication is	Restart the software.	
lost. Please restart the application. This message may appear multiple times." message	interrupted.	Restart Oracle services (see "Restart Oracle services" on page 43).	
J	Wireless network in use.	Use a cable-based network system, such as a CAT5e network, with plug-in Network Interface Controller (NIC) cards.	
Full installation regularly loses	Anti-virus software is interfering with	Use less restrictive anti-virus settings.	
connection with the database	communication.	Disable, replace, or remove the anti- virus software.	
		Use a cable-based network system, such as a CAT5e network, with plug-in Network Interface Controller (NIC) cards.	
	Unstable network connections.	Contact your network administrator.	
		Use a cable-based network system, such as a CAT5e network, with plug-in Network Interface Controller (NIC) cards.	
Client installation "cannot access file" or "\GeneMapper_Preferences (Access is denied)" message	File and folder permissions are not set correctly on the client computer.	Set permissions. See "Reset file and folder permissions after installation (Client installation)" on page 34.	
Client installation regularly loses connection with the database, but full installation does not lose connection	Unstable network connections.	Contact your network administrator.	
Disk space message is displayed when you start the software	The computer has limited available disk space.	If possible, archive then delete data from the database.	
		Use the Database Dashboard utility to compress the database.	
		Note: You may see a discrepancy between the space used in the Database Dashboard → GeneMapper IDX → Projects Statistics and the available free space. This discrepancy is caused when you delete projects from the GeneMapper [®] <i>ID-X</i> Software.	
Version error displayed when you import a panel file (this message differs from the message displayed in earlier versions of the software) GeneMapper® ID-X Error Version' incorrect or missing. Offending line #1	The version text in the panel .txt file is not present. AmpFLSTR_Panels_v3X.txt - Notepad File Edit Format View Help Version GMID-X v 1.4 Kit type. MICROSATELLITE Chemistry Kit AmpFLSTR_Panels_v3X Panel Profiler_v1.2X null	Edit the panel .txt file to include the text shown in the figure.	

Symptom		Possible cause	Action			
Cannot access deleted audit records		Restore the audit records.	 In the Project window, select Admin ▶ Audit Manager ▶ Report. Log in to the Audit Manager 			
			 2. Eog in to the Addit Manager. 3. In the Audit History Viewer, File ▶ Edit Query, leave the default settings, then click OK. 			
			4. Select File ▶ Execute Query.			
Small markers and low m weight microvariant alleles displayed in plots when us default 6-dye plot setting	olecular s are not ing the	The 6-dye plot setting starts at 75 bp. However, the smallest markers in the GlobalFiler™ Express Kit and low molecular weight microvariant alleles may fall below 75 bp.	Edit plot settings to decrease the starting size range (for example, to 60 bp) to ensure all alleles are displayed in plots.			
Uninstall the GeneMapper [®] ID-X	1. Restar (see "C	t the computer and log on using a loca Check user access" on page 13 or page	al computer administrator account 20).			
Software	2. Ensure	e that no programs or applications are	running.			
	3. Disabl	le any antivirus software (including ar	timalware software).			
	4. Select Softw	 Select Select				
	5. Restart the computer and log on using a local computer administrator account					
	6. Confir Panel "If the Windo	Confirm that the software has been uninstalled: select Software is still listed, go "If the GeneMapper [®] ID-X Software is still listed on Windows [®] XP only)" below.				
If the	1. Ensure	e antivirus/antimalware software is disabled.				
GeneMapper [®] <i>ID-X</i> Software is still	Note: enable	Note: In some instances, the antivirus/antimalware software is automatically enabled, so you must ensure it is disabled more than one time in the procedure.				
listed after uninstalling (tested	2. Confir setting	nfirm the Virtual Memory settings are correct ("Check virtual memory tings" on page 15).				
only)	3. Run th	ne Remove Oracle utility:				
	a. Ir D E	nsert the GeneMapper [®] <i>ID-X</i> Software VD in the computer DVD drive, right xplore .	Full or Full Upgrade Installation -click on the drive icon, then select			
	b. N	Javigate to Utilities > RemoveOracle.	exe.			
	c. C	c. Copy RemoveOracle.exe to the desktop.				
	d . C d	Oouble-click RemoveOracle.exe (a blac isappears).	k box appears for a few seconds and			
	4. Navig	Navigate to and delete the entire x:\AppliedBiosystems folder.				
	5. Restar	art the computer and log on using a local computer administrator accour				

Enable communication with port 1521 Windows[®] XP OS The GeneMapper[®] *ID-X* Software uses port 1521 to communicate between the user interface and the Oracle database via the TCP Internet Protocol and TNS Names. On most computers, this port is enabled automatically during installation.

However, if the software does not start or a "No databases found" message is displayed after installation, modify settings to enable communication with port 1521.

IMPORTANT! In addition to Windows security settings, some third-party anti-virus or firewall applications may affect port 1521. If you are running, third-party anti-virus or firewall applications, modify settings for those applications to enable communication with port 1521.

- 1. Log on to the computer using a local computer administrator account (see "Check user access" on page 13).
- 2. Select Start > Network connections. Right-click Local Area Connection, select Properties, click Advanced, then click Settings.
- **3.** If the Windows Firewall is on, click **Exceptions**, click **Add Program**, then select **GeneMapper**[®] *ID-X* **Software**.

Enable communication with port 1521 Windows[®] 7 0S The GeneMapper[®] *ID-X* Software uses port 1521 to communicate between the user interface and the Oracle database via the TCP Internet Protocol and TNS Names. On most computers, this port is enabled automatically during installation.

However, if the software does not start or a "No databases found" message is displayed after installation, modify settings to enable communication with port 1521.

IMPORTANT! In addition to Windows security settings, some third-party anti-virus or firewall applications may affect port 1521. If you are running, third-party anti-virus or firewall applications, modify settings for those applications to enable communication with port 1521.



2. In the Windows Firewall with Advanced Security window, click Inbound Rules.



3. Click New Rule.

🔐 Windows Firewall with	Advanced Security		
File Action View H	lelp		
🗢 🄿 🖄 🖬 🗟	? 🗊		
💮 Windows Firewall witł	Inbound Rules	Actions	
Inbound Rules	Name	Inhound Rules	•
Connection Secur	🕜 Akamai NetSession Interface —	🕻 🗽 New Rule)	
Monitoring	🕑 Akamai NetSession Interface	Y Filter by Profile	•
	🕑 Akamai NetSession Interface	V Eilter by State	
	🕜 Akamai NetSession Interface	Pricer by state	•
	 CyberLink PowerDVD DX CyberLink PowerDVD DX Resident Progra DCOM 	🛛 🍸 Filter by Group	•
		View	•
		Refresh	
	🜑 GeneMapper IDX	Neiresti	
	🕑 HP BPT Remote Agent	Export List	
	🕑 HP BPT Remote Agent	🛛 📝 Help	
	🕑 Microsoft Office Outlook		
	BranchCache Content Retrieval (HTTP-In)		
	BranchCache Hosted Cache Server (HTT		

4. Select **Port**, then click **Next**.

🔗 New Inbound Rule Wizard	
Rule Type	
Select the type of firewall rule to o	rreate.
Steps:	
a Rule Type	What type of rule would you like to create?
Protocol and Ports	
 Action 	🔘 Program
Profile	Rule that controls connections for a program.
Name	Port
	Rule that controls connections for a TCP or UDP port.
	Predetined.
	BranchCache - Content Retrieval (Uses HTTP)
	Rule that controls connections for a Windows experience.
	O Custom
	Custom rule.

5. Select **TCP**, then type **1521** in the Specific Local Ports, then click **Next**.

🔗 New Inbound Rule Wizard .	
Protocol and Ports	
Specify the protocols and ports to	which this rule applies.
Steps:	
Rule Type	Does this rule apply to TCP or UDP?
Protocol and Ports	(• TCP)
Action	O UDP
Profile	
Name	Does this rule apply to all local ports or specific local ports?
	O All local ports
	Specific local ports: 1521
	Example: 80, 443, 5000-5010
	Back Next > Cancel

6. In the Action page, select Allow the connection, then click Next.



7. In the Profile page, leave the default settings selected, then click Next.

🔐 New Inbound Rule Wizard			
Profile			
Specify the profiles for which this ru	ile applies.		
Steps:			
Bule Type	When does this rule apply?		
Protocol and Ports			
Action	🔽 Domain		
Profile	Applies when a computer is connected to its corporate domain.		
Name	✓ Private		
	Applies when a computer is connected to a private network location.		
	Public		
	Applies when a computer is connected to a public network location.		
	< Back Next > Cancel		

8. In the Name page, type GeneMapper IDX, then click Finish.

🔐 New Inbound Rule Wiza	rd	X
Name		
Specify the name and descrip	tion of this rule.	
Steps:		
Rule Type		
Protocol and Ports		
Action	\frown	
Profile		
Name	Genemapper IDX	
	Description (optional):	
	l .	
	< <u>B</u> ack <u>Finish</u> Cancel	

The Inbound Rules List is displayed with GeneMapper IDX added as a rule. The rule should be enabled by default (indicated by the presence of the Disable Rule command).

🔐 Windows Firewall with /	Advanced Security					
File Action View H	File Action View Help					
🗢 🄿 🖄 🔜 🗟	? 🖬					
Windows Firewall with	Inbound Rules		Actions			
Inbound Rules	Name	-	Inbound Rules			
🚡 Connection Secur	🖉 GeneMapper IDX		🚉 New Rule			
Monitoring	Akamai NetSession Interface Akamai NetSession Interface		V Filter by Profile			
	Akamai NetSession Interface		🕎 Filter by State			
	Akamai NetSession Interface		🐨 Filter by Group			
	OcyberLink PowerDVD DX		View			
	CyberLink PowerDVD DX Resident Progra		🖸 Refresh			
	GeneMapper IDX		📑 Export List			
	🕑 HP BPT Remote Agent		? Help			
	🔮 HP BPT Remote Agent		Const Manuau TDV			
	🥑 Microsoft Office Outlook	(Genemapper IDA			
	🎯 BranchCache Content Retrieval (HTTP-In)	-	🕒 Disable Rule			
۰ III ک			2 Cut			

9. If Enable Rule is displayed instead of Disable Rule, click Enable Rule.

Restart OracleIf a "The database connection has been lost" message is displayed, restart Oracleservicesservices using a .bat file or manually.

Restarting with a .bat file

- 1. On the v1.4 Full, Demo, or Full Upgrade installer DVD, navigate to the **Utilities** folder.
- **2.** Double-click **ServicesRestart.bat**. (You can also copy the file to your hard disk and start the .bat file from your hard drive.)

The following window is displayed for ~2 minutes as the services restart.



3. When the window closes, start the GeneMapper[®] *ID-X* Software.

Restarting manually

- 1. Go to Start > Control > Panel > Administrative Services > Services.
- 2. In the Services screen, right-click the following services, then select **Restart**:
 - OracleIFAGMIDXTNSListener
 - OracleMTSRecoveryService
 - OracleServiceIFA

🌯 Services (Local)							
OracleIFAGMIDXTNSListener	Name 🛆		Description	Status	Startup Type	Log On As	
	Network Access Protei	ction Agent	Allows win		Manual	Local System	
Stop the service	Network Connections		Manages o	Started	Manual	Local System	
Restart the service	Network DDE		Provides n		Disabled	Local System	
	🏶 Network DDE DSDM		Manages D		Disabled	Local System	
	🏶 Network Location Awa	reness (NLA)	Collects an	Started	Manual	Local System	
	Network Provisioning S	Service	Manages X		Manual	Local System	
	NT LM Security Suppor	rt Provider	Provides s		Manual	Local System	
	🖏 O2FLASH			Started	Automatic	Local System	
	🍓 Office Source Engine		Saves inst		Manual	Local System	
	CradeIFAGMIDXCI A	ent			Manual	Local System	
	OradeIFAGMIDXTNSI			Started	Automatic	Local System	
	Cracle JobScheduler IF	Start			Disabled	Local System	
	CracleMTSRecoveryS	Stop		Started	Automatic	Local System	
	CracleServiceIFA	Pause		Started	Automatic	Local System	
	Resultie Restart Restart		Collects pe		Manual	Network S	
			Enables a c	Started	Automatic	Local System	
	Pml Driver HPZ12	All Tasks 🔹 🕨		Started	Automatic	Local Service	
	Portable Media Serial		Retrieves t		Manual	Local System	
	Print Spooler	Kerresn	Loads files	Started	Automatic	Local System	
	Protected Storage	Properties	Provides pr	Started	Automatic	Local System	
	QoS RSVP		Provides n		Manual	Local System	
	Remote Access Auto	Help	Creates a		Manual	Local System	
	Remote Access Conne	ction Manager	Creates a	Started	Manual	Local System	
	Remote Desktop Help	Session Manager	Manages a		Manual	Local System	
	Remote Procedure Call (RPC)		Provides th	Started	Automatic	Network S	
	Remote Procedure Cal	ll (RPC) Locator	Manages t		Manual	Network S	
	Remote Registry		Enables re	Started	Automatic	Local Service	
	Removable Storage				Manual	Local System	

3. Ensure the Startup Type is set to Automatic for each service. If it is not, right-click a service, then select **Automatic** for Startup Type.

OracleIFAGMIDX	TNSListener Properties (Local Comput ? 🗙
General Log On	Recovery Dependencies
Service name:	OracleIFAGMIDXTNSListener
Display name:	OracleIFAGMIDXTNSListener
Description:	
Path to executabl C:\AppliedBiosyst	e: ems\OracleGMIDX\BIN\TNSLSNR
Startup type:	Automatic Automatic
Service status:	Manual Disabled Started
Start	Stop Pause Resume
You can specify t from here.	he start parameters that apply when you start the service
Start parameters:	
	OK Cancel Apply

4. Start the GeneMapper[®] *ID-X* Software.

Software verification testing

Test cases performed 45
Computers used 47
Samples used for concordance testing 48
Samples used for GlobalFiler TM Kit Express genotyping testing 51
Samples used for Spike enable/disable testing 51
Samples used for ACC and AN testing 51
Legacy samples used for Mixture analysis testing 51
GlobalFiler [™] Express samples used for Mixture Analysis
Data Collection Software settings used to run GlobalFiler [™] Express samples. 52
GeneMapper [®] ID-X Software v1.4 analysis settings for GlobalFiler [™] Express data
Results
Testing observations
Conclusions

Test cases performed

 Table 6
 Data collection software verification testing

Testing Categories	Subcategories	Test Description
3130/3730 Data Collection software v4 3500 Data Collection Software v2 2500 Data Collection	Run setup, instrument control, and data collection of 5-dye and 6-dye samples.	Activate 6-dye license (not required for 3500), perform spatial calibration, perform a spectral calibration with DS-33 and DS-36 Matrix standards, run samples processed with existing AmpF <i>t</i> STR [®] PCR Amplification Kit and the GlobalFiler [™] Express Kit.
Software v1	Genotyping	Evaluate genotyping concordance between new and earlier versions of Data Collection Software.
	Sizing precision	Calculate sizing precision and size range per run for each instrument using GlobalFiler [™] Express Kit allelic ladder data.
	Sensitivity	Evaluate GlobalFiler [™] Express Kit sample peak heights and allelic dropout with 125 pg total DNA input.

Testing Categories	Subcategories	Test Description
GeneMapper [®] <i>ID-X</i> Software v1.4	Allelic ladder genotyping	• Compare the allelic ladder run sizing, genotyping, and PQV scoring between v1.3 and v1.4 (without ACC).
GlobalFiler [™]		 Visually inspect 20 allelic ladders from each instrument for proper allele calling, PQV scoring, and PQV flagging.
	Sample genotyping	 Compare the single-source (population) and positive control sample allele calls: To corresponding allele calls generated with Identifiler[®] NGM
		SElect [™] , and Yfiler [®] Kits.
		 Between instruments. Compare the single-source (population), positive control sample, and sensitivity sample: sizing, genotyping, and PQV scoring between v1.3 and v1.4 (without ACC).
GeneMapper [®] ID-X	Mixture Analysis	Evaluate for accurate results:
Software v1.4 testing GlobalFiler™		MIT pruning and sample segregation.
Express Kit		• Pattern extraction, PHR, residual, Mx and Avg Mx calculation, and flags and values.
		 Individual data files for RMP, CPI, LR, and multiple-kit merging calculations.
Concordance testing of legacy kit data	Sizing and genotyping	 Export Genotype and Sizing tables and compare peak heights, areas, data points, sizes, allele names, and PQV scores.
with GeneMapper [®]		Compare the 310 matrix results.
	Mixture analysis	Compare mixture analysis calculations and flags using the same analysis methods and thresholds.
Verification of new v1.4 software	ACC and AN PQVs, Y Marker check	 Process GlobalFiler[™] Express Kit data with the GlobalFiler panel and bins.
features and updates	box in Panel Manager (new)	• Visually verify the accuracy of the ACC and AN flag results.
	Spike Detection disable/enable function for samples (new)	Disable/enable sample spike detection and visually verify accuracy of SPK and GC flag results.
	SPK PQV results (updates to N/A and Check Flag	 Confirm SPK flag is Check for any sample type where spike detection is enabled and a spike is present (including samples that contain a spike, but do not contain true alleles).
	rules)	 Confirm SPK flag is N/A for any sample type where spike detection is disabled.
	Define New Sample Path function	Define New Sample Path function works for .hid files.

Table 7	GeneMapper [®]	ID-X Software v1.4 verification	testing

Computers used Table 8 Configuration of test computers

	Computer Configuration								
Testing Category	Make/ Model	Processor (CPU)/ Speed	Memory (RAM)	Operating System (OS)/ Service Pack (SP)					
Data Collection Software v4	Dell [®] OntiPlex [®] XF	Intel [®] Core [™] 2 Duo E8400	4 Gh	Windows [®] 7 Professional OS					
3500 Data Collection Software v2	(4 computers)	3 GHz	4 05	(SP1), 32-bit					
GeneMapper [®] <i>ID-X</i> Software v1.4	Dell [®] Latitude [®] E6500	Intel [®] Core [™] 2 Duo P8700 2.53 GHz	3.48 Gb	Windows [®] 7 Professional OS (SP1), 32-bit					
	Dell [®] Latitude [®] E6500	Intel [®] Core [™] 2 Duo P8700 2.53 GHz	3.48 Gb	Windows [®] XP Professional OS (SP3), 32-bit					
GeneMapper [®] <i>ID-X</i> Software v1.3	Dell [®] OptiPlex [®] XE	Intel [®] Core [™] 2 Duo E8400 3 GHz	4 Gb	Windows [®] XP Professional OS (SP2), 32-bit					

Samples used for concordance testing

A total of 3149 sample files (.fsa and .hid) were used in the sizing and genotyping concordance test. These samples were analyzed using both GeneMapper[®] *ID-X* Software versions 1.3 and 1.4. The Genotypes and Sizing tables were exported and compared using Beyond Compare[®] Software version 3.2.4 to determine whether any differences in data output resulted. The peak heights, peak areas, data points, sizes, allele names, and all the PQV scores were compared between the two software versions.

Table 9 Number of sample files (.fsa and .hid) by type used in concordance testing. The CE instrument, Data Collection software version, and AmpFt/STR[®] kit used to generate data are noted.

Instrument/ Data Collection Software	AmpF <i>t</i> STR [®] Kit	Single Source	Sensitivity	Mixture	Low Quality DNA	LOR	OMR	Spike	Good Ladder	Low Quality Ladder	Positive	Negative	Total
310 Genetic	COfiler®	16	6	5	12	_	_	_	8	_	1	1	49
Analyzer Data Collection	Profiler Plus [®]	16	6	6	12		_	_	8	_	1	1	50
Software v3.0/3.1	Identifiler®	16	6	6	12	_	_	_	15	—	1	1	57
	SGM Plus®	16	8	6	12	_	_	_	5	—	1	1	49
	SEfiler™	16	5	6	12	_	_	_	5	—	1	1	46
	Yfiler®	80	_	—	_	_	_	_	6	_	1	1	88
	MiniFiler™	30	_	—	—	_	_	_	7	—	1	1	39
3100 Genetic	COfiler®	16	6	6	12	_	_	_	3	—	1	1	45
Analyzer Data Collection	Profiler Plus®	16	6	6	12	_	_	_	3	_	1	1	45
Software v1.1/2.0	Identifiler®	16	6	6	12	_	_	_	3	—	1	1	45
	SGM Plus®	16	6	6	12	_	_	_	3	—	1	1	45
	SEfiler™	16	6	6	12	_	_	-	3	—	1	1	45
3100- <i>Avant</i> ™ Genetic Analyzer Data Collection	COfiler®	16	6	6	12	_	_	_	3	—	1	1	45
	Profiler Plus®	16	6	6	12	_	_	_	3	_	1	1	45
Software v2	Identifiler®	16	6	6	12	_	—	_	3	_	1	1	45

Instrument/ Data Collection Software	AmpF <i>t</i> STR® Kit	Single Source	Sensitivity	Mixture	Low Quality DNA	LOR	OMR	Spike	Good Ladder	Low Quality Ladder	Positive	Negative	Total
3130 <i>xl</i> Genetic Analyzer	Profiler Plus [®]	_	_	_	_	_	_	_	48	_	_	_	48
Data Collection	Identifiler®	93	24	12	30	12	10	9	48	58	1	1	298
Software v3.0	SGM Plus®	-	_	—	—	_	_	_	32	—	—	_	32
	SEfiler™	_	_	_	_	_	_	_	16	—	—	_	16
	Yfiler®	10	_	2	—	_	_	16	32	—	1	1	62
	MiniFiler™	10	_	2	_	_	_	_	32	_	1	1	46
	Sinofiler™	113	36	14	—	_	_	_	48	—	—	6	217
	NGM SElect [™] Express	100	_	_	_	-	_	_	12	-	—	-	112
3130 <i>xl</i> Genetic	Yfiler®	_	_	_	_	-	_	_	48	_	45	3	96
Analyzer Data Collection Software v3.1.1	NGM SElect [™]	_	_	_	_	_	_	_	48	_	45	3	96
3730 DNA Analyzer Data Collection Software v3.0	ldentifiler [®]	90	48	_	_	_	_	_	48	_	1	1	188
3730 DNA Analyzer Data Collection Software v3.1.1	ldentifiler®	_	_	_	_	_	_	_	48	_	45	3	96
3130 <i>xl</i> Genetic	SGM Plus®	60	_			_	_	_	12	_	12	12	96
Analyzer Data Collection Software v4	ldentifiler [®] Plus	60	_	_	_	-	_	-	12	-	12	12	96
	Yfiler®	60	_	—	—	-	_	-	12	_	12	12	96
	NGM [™] SElect	60	_	_	_	-	_	-	12	_	12	12	96

Instrument/ Data Collection Software	AmpF <i>t</i> STR® Kit	Single Source	Sensitivity	Mixture	Low Quality DNA	LOR	OMR	Spike	Good Ladder	Low Quality Ladder	Positive	Negative	Total
3730 DNA Analyzer Data Collection Software v4	ldentifiler [®]	60	_	_	_	_	_	_	12	_	12	12	96
3500xL Genetic Analyzer	Identifiler [®] Plus	84	_	_	_	_	_	-	12	—	_	_	96
Data Collection Software v1	Identifiler [®] Direct	84	_	_	_	_	_	-	12	_	_	_	96
	NGM™	84	_	—	—	_	_	_	12	_	-	—	96
	NGM SElect [™] Express	52	_	_	_		_	-	8	_	_	4	64
3500xL Genetic	SGM Plus®	60	_	_	_	_	_	_	12	_	12	12	96
Analyzer Data Collection Software v2	Identifiler [®] Plus	60	_	_	_	_	_	-	12	—	12	12	96
	Identifiler [®] Direct	60	_	_	_	_		_	12	_	12	12	96
	NGM SElect [™]	60	-	-	—	_	_	-	12	-	12	12	96
Total		1578	187	107	186	12	10	25	690	58	262	146	3149

Samples used for GlobalFiler[™] Kit Express genotyping testing

A total of 1990 sample files (.fsa and .hid) were used in the sizing and genotyping concordance test. These samples were analyzed using both GeneMapper[®] *ID-X* Software versions 1.3 and 1.4. The Genotypes and Sizing tables were exported and compared using Beyond Compare[®] Software version 3.2.4 to determine whether any differences in data output resulted. The peak heights, peak areas, data points, sizes, allele names, and all the PQV scores (except for ACC and AN) were compared between the two software versions. The results for the sensitivity samples, allelic ladders, positive and negative controls were also visually inspected for accuracy.

Table 10 Number of sample files (.fsa and .hid) by type used in GlobalFiler[™] Express Kit testing. The CE instrument and Data Collection software version used to generate data are noted.

Instrument/ Data Collection Software	Single Source	Sensitivity	Mixture	Allelic Ladder	Positive	Negative	Total
3130 <i>xl</i> Genetic Analyzer Data Collection Software v4	250	20	40	96	6	6	418
3730 DNA Analyzer Data Collection Software v4	250		_	192	6	6	454
3500xL Genetic Analyzer	250	20	_	—	6	6	418
Data Collection Software v1							
3500 Genetic Analyzer	250	20	40	96	6	6	418
Data Collection Software v2							
3500xL Genetic Analyzer	250	20	40	96	6	6	282
Data Collection Software v2							
Total	1250	80	120	480	30	30	1990

Samples used for Spike enable/ disable testing

- 64 data files with spikes generated with existing kits
- 45 data files with spikes generated with the GlobalFiler[™] Express Kit

Samples used for
ACC and AN testingThe 80 sensitivity samples listed in Table 10 were visually inspected for ACC and AN
PQV result accuracy.

Legacy samples used for Mixture analysis testing A historical mixture sample data set was used to verify the concordance of the mixture analysis results between the GeneMapper[®] *ID-X* Software versions 1.3 and 1.4. The data set included 2 contributor mixtures made from 8 pairs of genomic DNA samples prepared in 11 mixture ratios: 1:0, 1:1, 1:2, 1:3, 1:5, 1:9, 9:1, 5:1, 3:1, 2:1, and 0:1. The 1:0 and 0:1 mixtures were used as 1 contributor (single-source) samples as well as the known samples. The data set also included a sample with a 3 contributor mixture in a mixture ratio of 1:1:2, and a sample triallelic for marker D7S820. The mixture samples were amplified with the AmpF*t*STR[®] Identifiler[®] (1 ng and 0.125 ng), Profiler Plus[®], COfiler[®], and SGM Plus[®] PCR amplification kits. The samples were collected from a 3130*xl* Genetic Analyzer.

The following mixture analysis features and number of sample files were tested:

- Mixture Interpretation Threshold (MIT) pruning and sample segregation testing 467 sample files
- Pattern extraction comparison 389 sample files
- Random Match Probability (RMP), Combined Probability of Inclusion/Exclusion (CPI/CPE), and Likelihood Ratio (LR) calculations 30 sample files
- Known matching 60 sample files
- Multiple kit merging 8 pairs of sample files

Mixture Analysis log files were generated from both software versions with the same sample file sets. These files were compared using the Beyond Compare[®] Software v3.2.4. The comparison tool lined up the text files from the two software versions, and compared the file contents for concordance.

Sample name	Gender	Mixture ratio	DNA input ng:ng	Contributor 1 (µL)	Contributor 2(µL)
H15 H1	ММ	0:1	0.0:0.1	0	10
H31 H30	FF	1:1	0.5:0.5	5	5
H3 H23	M F	1:2	0.33:0.67	3.3	6.7
H26 H6	M F	1:3	0.25:0.75	2.5	7.5
H20 H24	FF	1:5	0.17:0.83	1.7	8.3
		1:7	0.125:0.875	1.25	8.75
		1:9	0.1:0.9	1	9
		1:0	1.0:0.0	10	0
Total	-	_	_	24.5	55.25

GlobalFiler[™] Express samples used for Mixture

Analysis

Data Collection
Software settings
used to run
GlobalFiler™
Express samples

Genetic Analyzer	Run modules and conditions
3500	 HID36_POP4 Injection conditions: 1.2 kV/15 sec Dye Set J6
3500xL	 HID36_POP4xl Injection conditions: 1.2 kV/24 sec Dye Set J6
3130 <i>xl</i>	 HIDFragmentAnalysis36_P0P4 Injection conditions: 3 kV/10 sec Dye Set J6
3730	 GeneMapper_36_POP7 Injection conditions: 2 kV/10 sec Dye Set J6

GeneMapper[®] *ID-X* Software v1.4 analysis settings for GlobalFiler[™] Express data

- GlobalFiler_Express_v1.1X panel, AmpFLSTR_Bins_v3X bin, and AmpFLSTR_Bins_v3X stutter files
- GS600_LIZ_(60-460) size standard

IMPORTANT! Before using the Normalization option, perform appropriate internal validation studies.

3500 and 3130	3730
Analysis Method Editor	Analysis Method Editor
General Allele Peak Detector Peak Quality SQ & GQ Settings Peak Detection Algorithm: Advanced Ranges Peak Detection Analysis Sizing Peak Amplitude Thresholds: Full Range Partial Sizes Start Size: 60 Stop Pt: 10000 Stop Size: 500 Pi 175 Smoothing and Baselining Min. Peak Half Wid 2 Pts	General Allele Peak Detector Peak Quality SQ & GQ Settings Peak Detection Algorithm: Advanced Peak Detection Peak Detection Analysis Sizing Peak Amplitude Thresholds: Full Range Partial Sizes Start Size: 60 Stop Pt: 10000 Stop Size: 500 P: 200 Smoothing and Baselining Y: 200 O: 200
Smoothing None Ight Light Heavy Polynomial Degree: 3 Baseline Windo 33 Size Calling Method Peak Start: 0.0 2nd Order Least Squa Peak End: 0.0 Ocubic Spline Interpola Local Southern Met Global Southern Met Eactory Defaults	Smoothing None Light Polynomial Degree: Baseline Windo 33 Baseline Windo 33 Size Calling Method Peak Start: 2nd Order Least Squa 0.0 2nd Order Least Squa Normalization Cubic Spline Interpola Use Normalization, if appl Local Southern Met Global Southern Me Eactory Defaults
Save As Save Cancel Help	Save As Save Cancel Help

IMPORTANT! Before analyzing 3730 data, see "3730 DNA Analyzer allelic ladder failures" on page 57.

Results All metrics were met as described in Table 11. In all cases, the contents of the genotypes table from v1.3 and v1.4 software match each other.

Table 11	Summary of	of data	collection	software	verification	testing	results
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Testing Categories	Subcategories	Expected Outcome	Result
3130/3730 Data Collection software v4 Ru ins co co and sa 3500 Data Collection Software v2 Software v2 3500 Data Collection Software v1 Ge Ge Size Size Size Software Size	Run setup, instrument control, and data collection of 5-dye and 6-dye samples.	Proper operation and data collection of samples processed with existing AmpF <i>t</i> STR [®] Kits and the GlobalFiler [™] Express Kit.	Pass. For more information, see "Capillaries Viewer issue in Data Collection Software v4" on page 57.
	Genotyping	100% concordance between new and earlier versions of Data Collection Software.	Pass. For more information, see "3730 DNA Analyzer allelic ladder failures" on page 57 and "3730 DNA Analyzer sizing failures" on page 60.
		100% concordance between 3130, 3730, and 3500 instruments.	Pass
	Sizing precision	 Standard deviation of mean size within a run is ≤0.15 bp for all alleles in the allelic ladder. Size range within a run is ≤0.5 bp for the largest allele in the allelic ladder. 	Pass
	Sensitivity	Signal intensity of 6-dye samples meets specifications with no allelic dropout at 125 pg total DNA input	Pass

Testing Categories	Subcategories	Expected Outcome	Result
GeneMapper [®] <i>ID-X</i> Software v1.4 testing GlobalFiler [™] Express Kit	Allelic ladder genotyping	 100% concordance for sizing, genotyping, and PQV scoring between GeneMapper[®] <i>ID-X</i> Software v1.3 and v1.4 (without ACC). 100% accurate allele calling, PQV scoring, and PQV flagging for 20 allelic ladders from each instrument. 	Pass. For more information, see "3730 DNA Analyzer allelic ladder failures" on page 57.
	Sample genotyping	 100% concordance of allele calls between single-source (population) and positive control sample and corresponding allele calls generated with Identifiler[®], NGM SElect[™], and Yfiler[®] Kits. 100% concordance of sizing, genotyping, and PQV scoring between GeneMapper[®] <i>ID-X</i> Software v1.3 and v1.4 (without ACC). 100% accurate allele calling, PQV scoring, and PQV flagging for all sensitivity samples, 1 positive control, and 1 negative control from each instrument. 	Pass. For more information, see "3730 DNA Analyzer allelic ladder failures" on page 57.
	Mixture Analysis	All mixture analysis calculations and flags are 100% accurate when compared to visual inspections or results obtained with third-party tools when using the same analysis methods and thresholds.	Pass
Concordance testing with GeneMapper [®] <i>ID-</i> <i>X</i> Software v1.3	Genotyping, peak detection, PQVs	 typing, peak tion, PQVs 100% concordance of allele calls with Sample Spike Detection enabled. 100% concordance of peak height, area and data points with and without normalization. 100% concordance of all PQV scores, including SQ, with Sample Spike Detection enabled. 	
	Mixture Analysis	100% concordance of mixture analysis results, calculations of MIT pruning, sample segregation, pattern extraction, UI flag, Known matching, RMP, CPI, LR, and multi-kit merging.	Pass

 Table 12
 Summary of GeneMapper[®] ID-X Software v1.4 testing GlobalFiler[™] Express Kit verification testing

Testing Categories	Subcategories	Expected Outcome	Result
Verification of new v1.4 software features and updates	ACC and AN PQVs, Y Marker check box in Panel Manager (new)	 100% concordance of allele calls compared to results from Yfiler[®] kit data and visual inspections. The ACC values and flags are 100% accurate. 	Pass
	Spike Detection disable/enable function for samples (new)	 SPK flag is N/A when spike detection is disabled with and without the presence of a spike. SPK flag is Check when spikes are present in a marker and sample Spike Detection is enabled. 	Pass
	SPK PQV for markers that contain a spike but no alleles (update)	 SPK flag is Check for markers that contain a spike but no alleles. SPK flag is N/A when spike detection is disabled with and without the presence of a spike. 	Pass
	Define New Sample Path function	Supports .hid files.	Pass

Testing observations

- Capillaries Viewer issue in Data Collection Software v4
- 3730 DNA Analyzer allelic ladder failures
- 3730 DNA Analyzer sizing failures

Capillaries Viewer issue in Data Collection Software v4

The first time you add capillaries in the Capillaries Viewer (displayed by selecting Capillaries Viewer in the left navigation pane), the software may incorrectly display dye colors in some of the capillaries. This is a display issue only. The sample file (.fsa file) is written correctly and the data will display correctly in GeneMapper[®] *ID-X* Software. To correct the colors, refresh the display by clicking on another window, then clicking on the Capillary Viewer again.



3730 DNA Analyzer allelic ladder failures

The GeneMapper[®] *ID-X* Software uses an Allelic Ladder Quality Assessment to help ensure the allelic ladders used for sizing are of acceptable quality. One of the metrics used is base-pair spacing: within each marker, the base pair spacing between any two ladder alleles is within the expected range (specified in the panel used to analyze).

On the 3730 Genetic Analyzer with POP-7[™] polymer, the D2S441 and D1S1656 markers in some allelic ladder samples did not pass the base-pair spacing quality assessment when using Light Smoothing:

- Figure 2 shows the spacing rule failure for the D2S441 marker.
- Figure 3 shows the spacing rule failure for the D1S1656 marker, with an additional peak height ratio quality assessment failure caused by incorrect allele assignments.







Figure 3 Example of base pair spacing error and incorrect allele assignments in the D1S1656 marker

The instances of spacing failures were significantly reduced by using the None setting instead of the Light setting for Smoothing in the Peak Detector tab of the analysis method as shown in the following table.

 Table 13
 Number and type of failures by Smoothing method used (out of 192 total allelic ladders)

Failure and marker	Smoothing setting/number of allelic ladder failures	
	Light	None
Spacing failure with D2S441	5	1
Missing allele/spacing failure with D1S1656	9	1

IMPORTANT! Using No Smoothing can increase baseline noise. Perform appropriate validation studies before using this setting. For more information on smoothing, refer to the *GeneMapper® ID-X Software v1.0 Reference Guide* (Pub. no. 4375671).

Considerations when using the None setting for Smoothing:

- Using a Global Cut-Off setting in the Analysis Method Allele tab (for example, a setting of 20%) may mitigate the increased baseline noise caused by the use of the None setting for Smoothing.
- If you use a Global Cut-Off setting that is lower than any marker-specific stutter setting for any locus, you should still apply the Marker-Specific Stutter Ratios (Analysis Method Allele tab). For example, if a stutter ratio is 12% but the Global Cut-Off setting is 10%, you should still apply the Marker-Specific Stutter Ratio of 12% for the locus (to ensure stutter peaks between 10–12% are not labeled).

3730 DNA Analyzer sizing failures

Due to the small fragment sizes analyzed by the GlobalFiler[®] Express kit, we did observe that the 60 base-pair peak in the GS600v2 size standard can migrate close to the primer peak region (Figure 4). One sample out of 250 in our validation study failed sizing with the default size-standard definition (60 to 460 bp) because the 60 bp size-standard peak fell within the primer region and was not accurately identified as a size standard peak.

This issue can be addressed by either of the following steps:

- Re-inject samples that fail to recognize the 60 base-pair peak.
- Use the 80 to 460 bp size-standard definition after performing appropriate validation studies (as a general rule, the 60 base-pair peak is not required for accurate fragment sizing using the 3rd Order Least Squares sizing method).

Figure 4 Raw data example illustrating the migration of the 60-base-pair size-standard peak into the primer-peak region.



Conclusions	•	The GeneMapper [®] <i>ID-X</i> Software v1.4 can be used to process sample files generated on all HID CE instruments and with existing AmpFℓSTR [®] kits and the GlobalFiler [™] Express Kit.
	•	The same results for sizing, genotyping, and mixture analysis were obtained using GeneMapper [®] ID -X Software versions 1.4 and 1.3.
	•	All updates to GeneMapper [®] <i>ID-X</i> Software v1.4 were successfully and correctly implemented without deleterious effects on other software functionality.

• The 3130 and 3730 Data Collection Software v4 and 3500 Data Collection v2 can be used to collect and analyze data generated with existing AmpFlSTR[®] kits and the GlobalFiler[™] Express Kit. All updates to data collection software were successfully and correctly implemented without deleterious effects on other software functionality.

Based on the nature of the modifications addressed in this update, and the testing that we performed, it is recommended that users evaluate this software as it pertains to their laboratory workflow to demonstrate concordance to previously validated GeneMapper[®] *ID-X* Software versions. Laboratories should determine the appropriate level of testing required based on their internal software validation guidelines and those of the appropriate governing agencies.



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