

# 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.

## 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 GlobalFiler™ or GlobalFiler™ 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® size standards	<ul style="list-style-type: none"> <li>• GS600_LIZ+Normalization_{60-460}</li> <li>• GS600_LIZ_{60-460}</li> </ul>
Panels, bins, table settings	Updated for the GlobalFiler™ Express Kit
Plot settings	Updated for the GlobalFiler™ Express Kit  <b>IMPORTANT!</b> 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](#).
- **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.

### Issues addressed in GeneMapper® ID-X Software v1.4

## 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 <sup>†</sup>
Table settings	Mixture Analysis analysis Method <sup>†</sup>
Plot settings	Known reference profiles for Mixture Analysis <sup>†</sup>
Matrix	Audit map configuration <sup>†</sup>

<sup>†</sup> 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 documentation

- For more information on features, updates, and known issues for GeneMapper® ID-X Software v1.4, see the following:
  - *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 context-sensitive help in the software application, click  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](http://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](mailto: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](http://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.
- Download software updates and patches.

## 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™	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

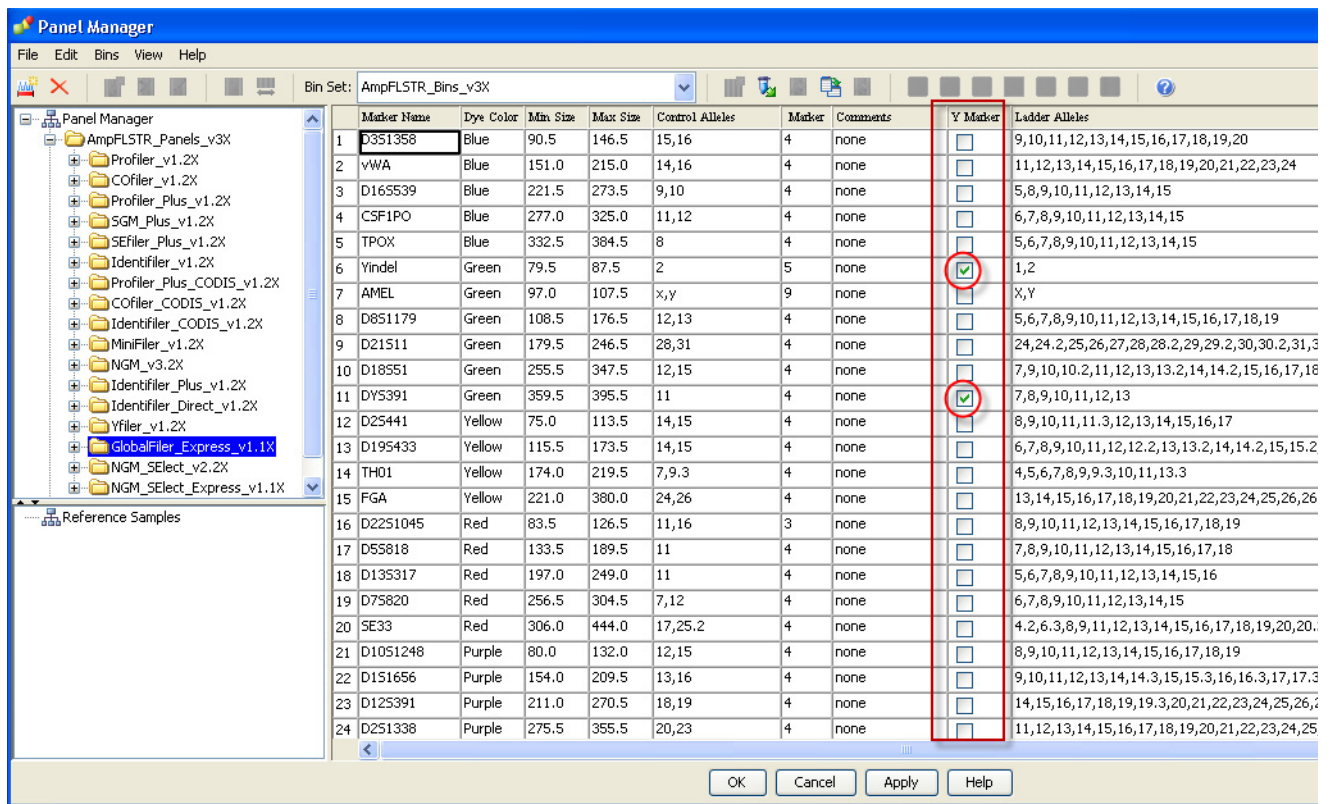
## Panel Manager

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 AmpFSTR® 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








### Using the new Y marker functions with the AmpFISTR® Yfiler® 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: <ul style="list-style-type: none"> <li>Amelogenin genotype is not X, X or X,Y (for example it is X,OL, OL,OL, or Y only - no X allele detected).</li> <li>Amelogenin genotype is X or X,X but one or more Y markers contain called alleles.</li> <li>Amelogenin genotype is X,Y and one or more Y markers do not contain called alleles.</li> </ul> <p><b>Note:</b> Peaks identified and labeled by the software as spikes are not considered in the ACC PQV.</p>
NA	<ul style="list-style-type: none"> <li>Negative control.</li> <li>Allelic Ladder.</li> <li>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 AmpFISTR® Yfiler® PCR Amplification Kit, which does not contain Amelogenin).</li> </ul>
 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.



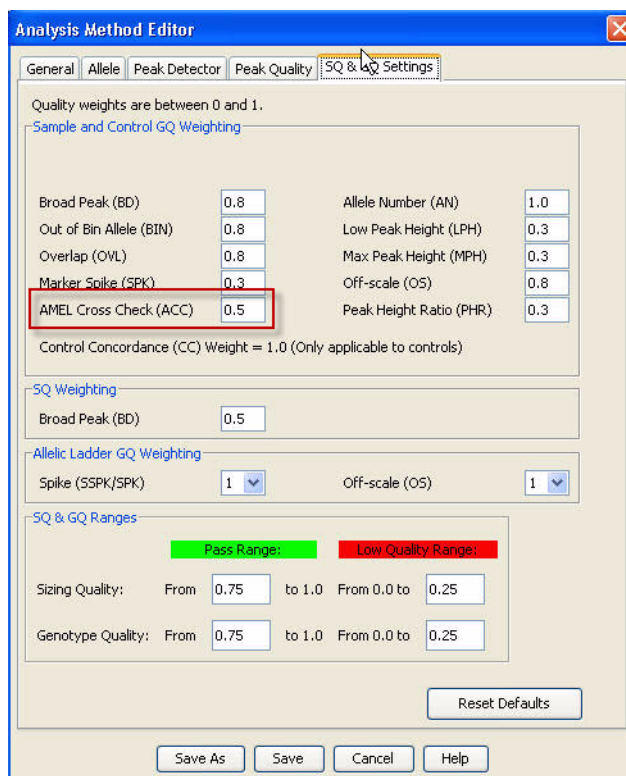
Table 1 ACC results for the GlobalFiler™ Express Kit

Number of alleles detected Amelogenin† X, Y			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 

† 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.



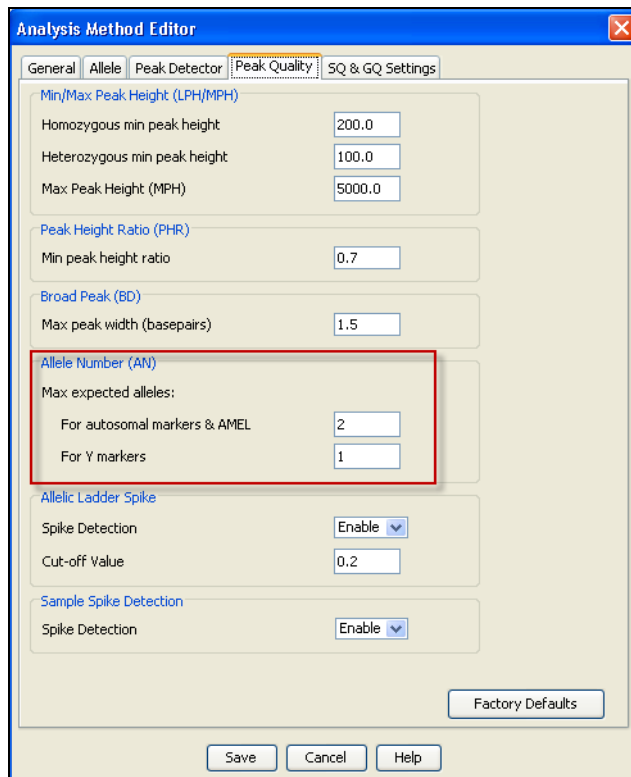
## Modified Allele Number PQV (AN)


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 	<ul style="list-style-type: none"> <li>More than the Max Expected Alleles are detected for any markers specified as Y markers in the Panel Manager.</li> <li>More than the Max Expected Alleles are detected for Autosomal/Amelogenin markers.</li> <li>No alleles are detected for autosomal or amelogenin markers.</li> <li>No X allele is detected in Amelogenin.</li> </ul>
 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.



**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  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.



## 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® .NET Framework 2.0 or later	Microsoft® .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.

### TCP/IP

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.

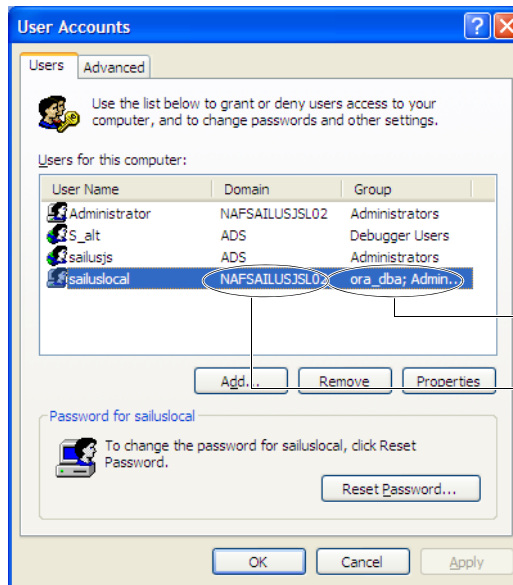
A local computer account may be different from the account you normally use to log in to the computer. The local account:

- 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.)

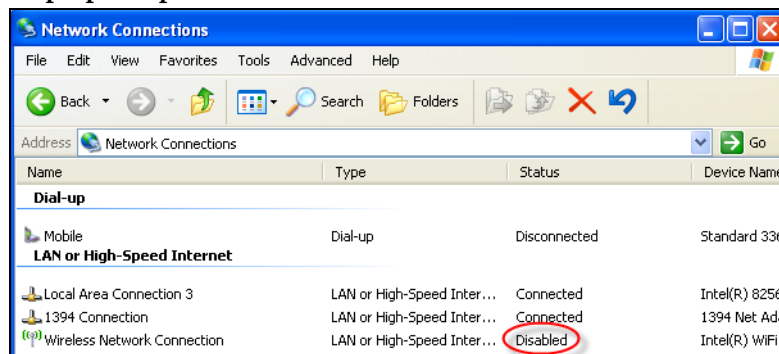


Belongs to the Administrators

Domain is the same as the computer name

### 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.



## 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

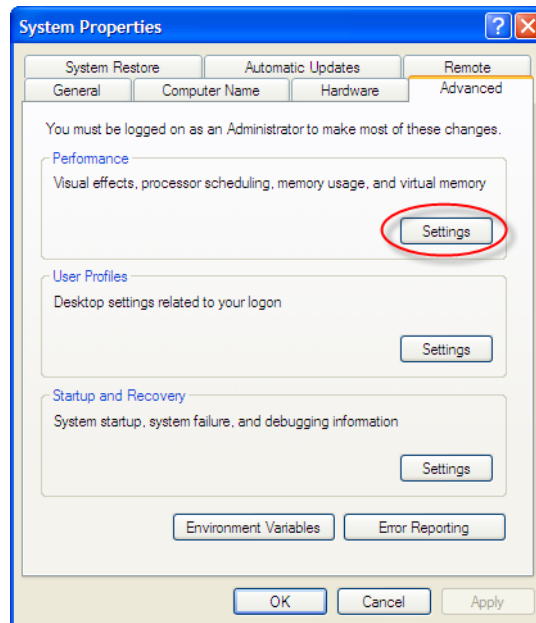
Uninstall GeneMapper® ID-X Software, any other programs that use Oracle databases, and any existing versions of Oracle databases, whether Life Technologies products or products from other companies. Go to **Start ▶ Control Panel ▶ Add or Remove Programs**.

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).

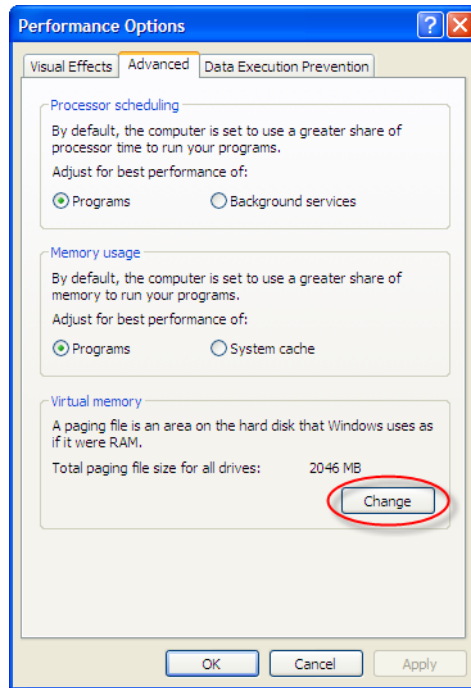
If it is still listed, manually uninstall the software (see [“If the GeneMapper® ID-X Software is still listed after uninstalling \(tested on Windows® XP only\)”](#) on page 38).

## Check virtual memory settings

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



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



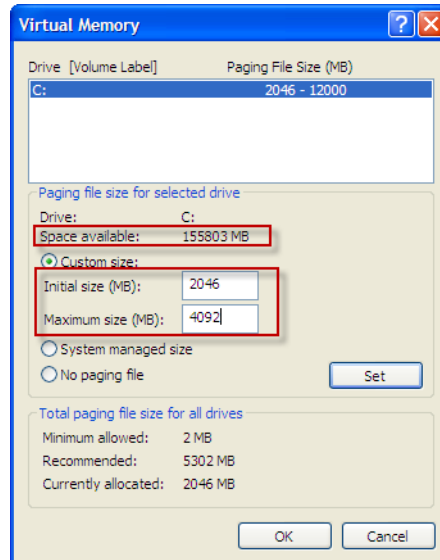
3. In the Virtual Memory dialog box, select the **C:** drive. Click the **Custom size** radio button. Specify **2046** MB for initial and **4092** for maximum size.

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**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.

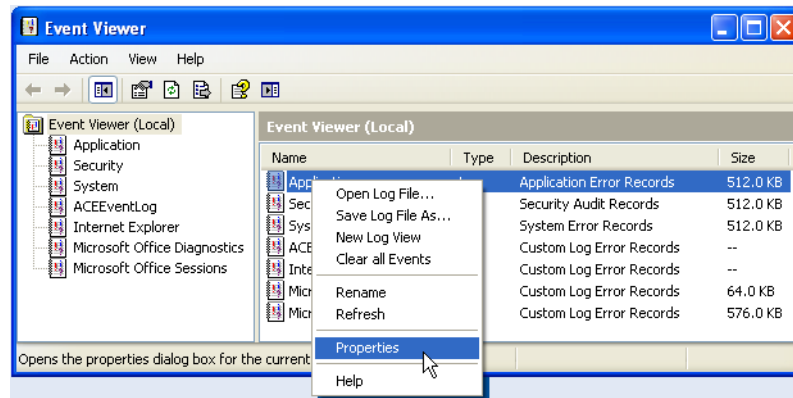


4. Click **Set**, then click **OK**.

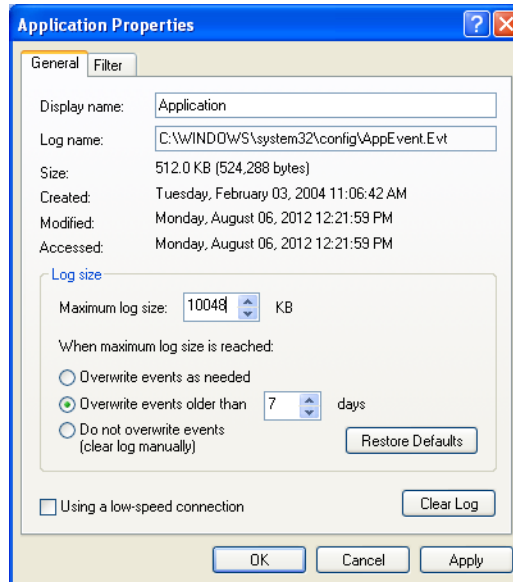
These settings are not activated until you restart the computer.

### Clear Windows® XP application and system logs

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



3. In the Application Properties dialog box, set the Maximum Log Size to **10048**, then click **Clear Log**.

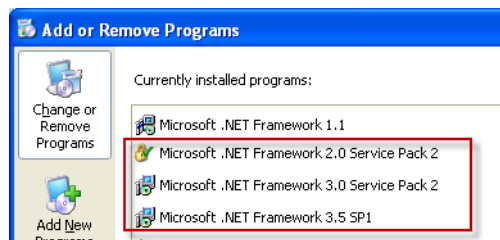


4. Click **OK**.
5. Right-click **System**, then select **Properties**.
6. In the System Properties dialog box, set the Maximum Log Size to **10048**, then click **Clear Log**.
7. Click **OK**.

### Check Microsoft .NET Framework version

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

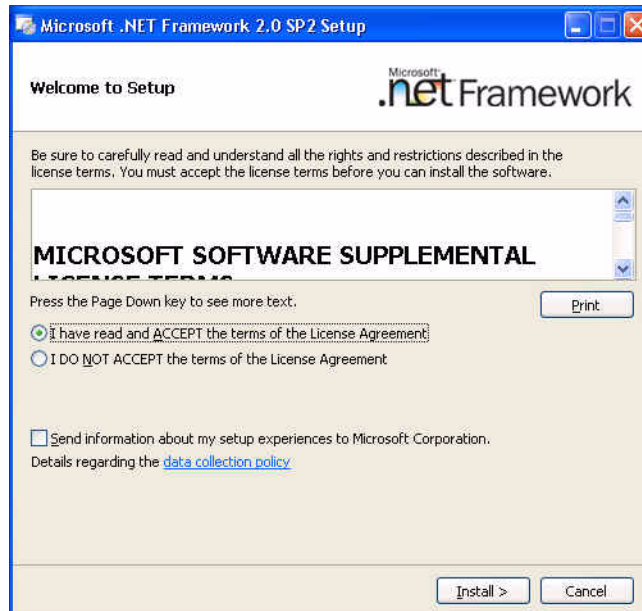
1. Select **Start** ▶ **Settings** ▶ **Control Panel** ▶ **Add or Remove Programs**.
2. Scroll down and determine if a version of 2.0 or later is installed. (There may be multiple versions installed. Do not remove any versions of the software.)



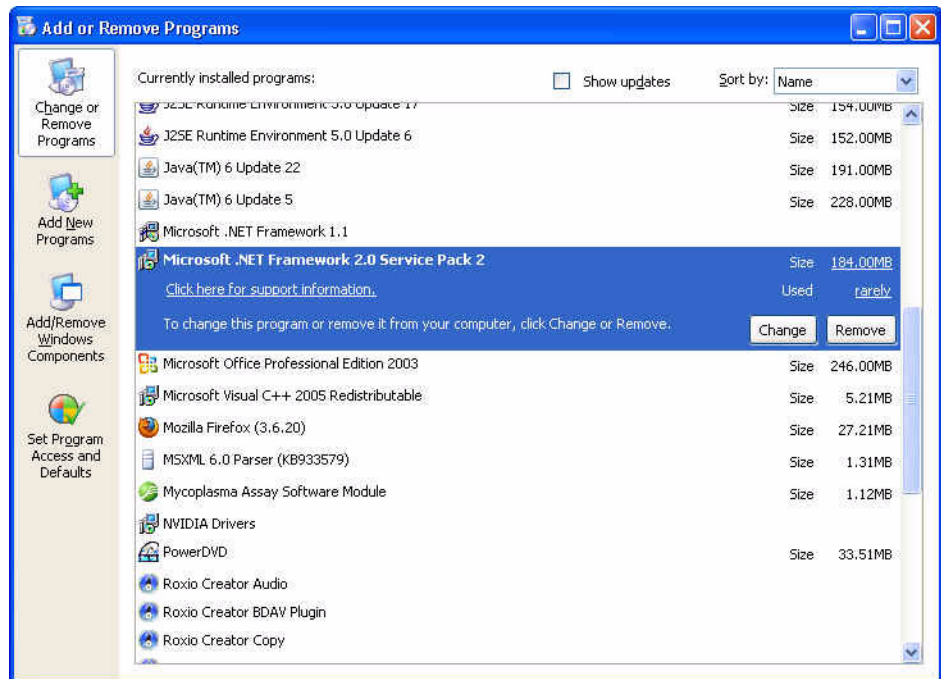
Version 2.0 or higher is required

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**.



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



**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

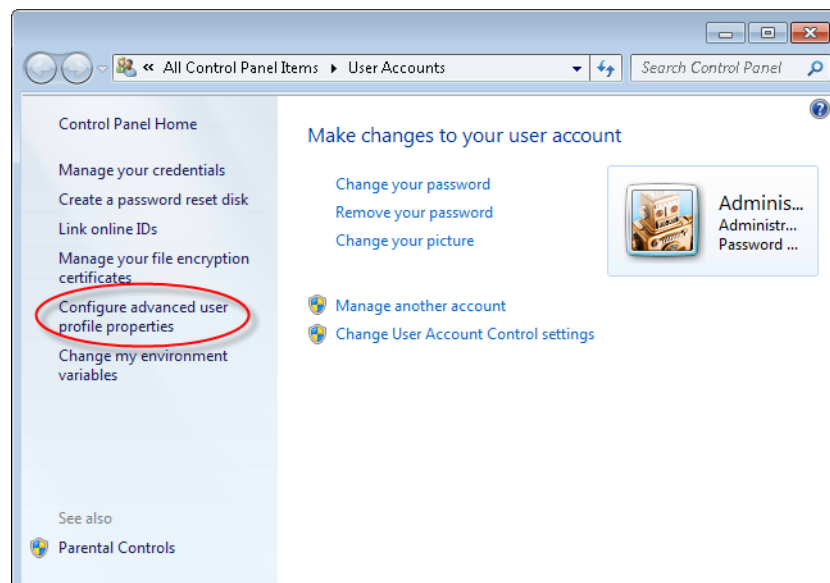
You must log on to the local computer using a local account with administrator privileges (read, write, and execute [rwx] permissions). The local computer is typically identified in the log in dialog box by the text “(this computer)” after the computer name

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

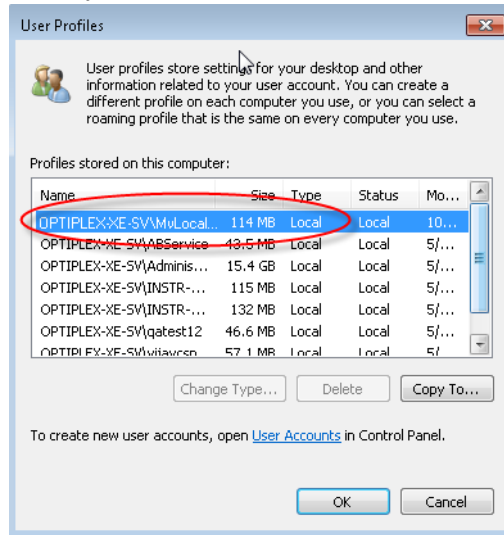
- Can not include network domain policies that restrict access to the install drive of the local computer account.
- Can not restrict access to operating system firewall or other security configurations.

### Check Local status

1. Select  **Control Panel** **User Accounts**. Click **Configure advanced user profile properties**.

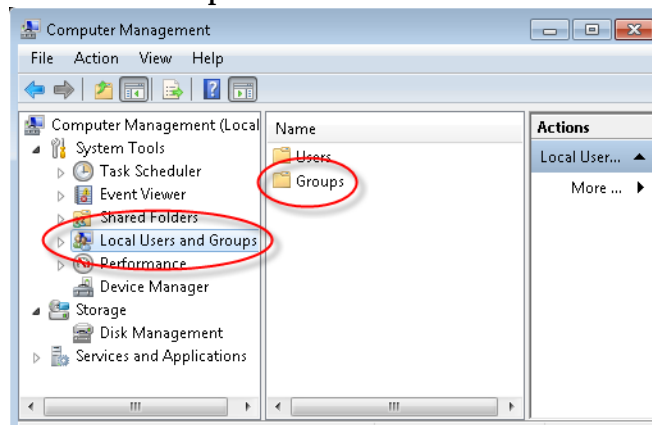


2. Select your local user account and ensure that the Type is Local.

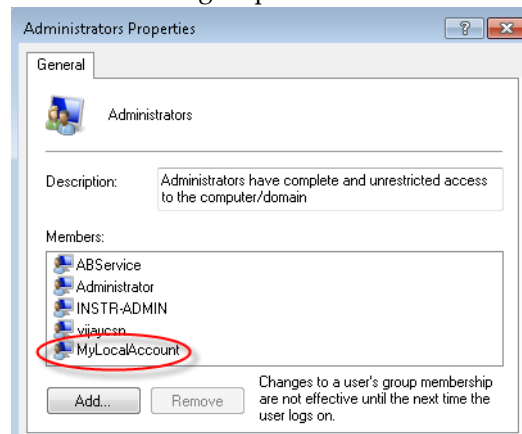


### Check Administrator privileges

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

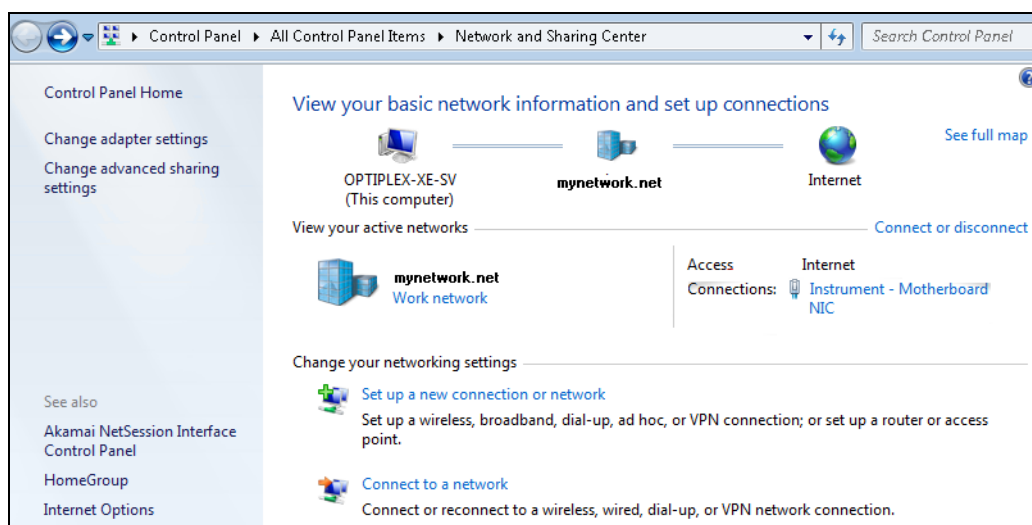


3. Double-click **Administrators**. Ensure that your local account is listed in the Administrators group.



## 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

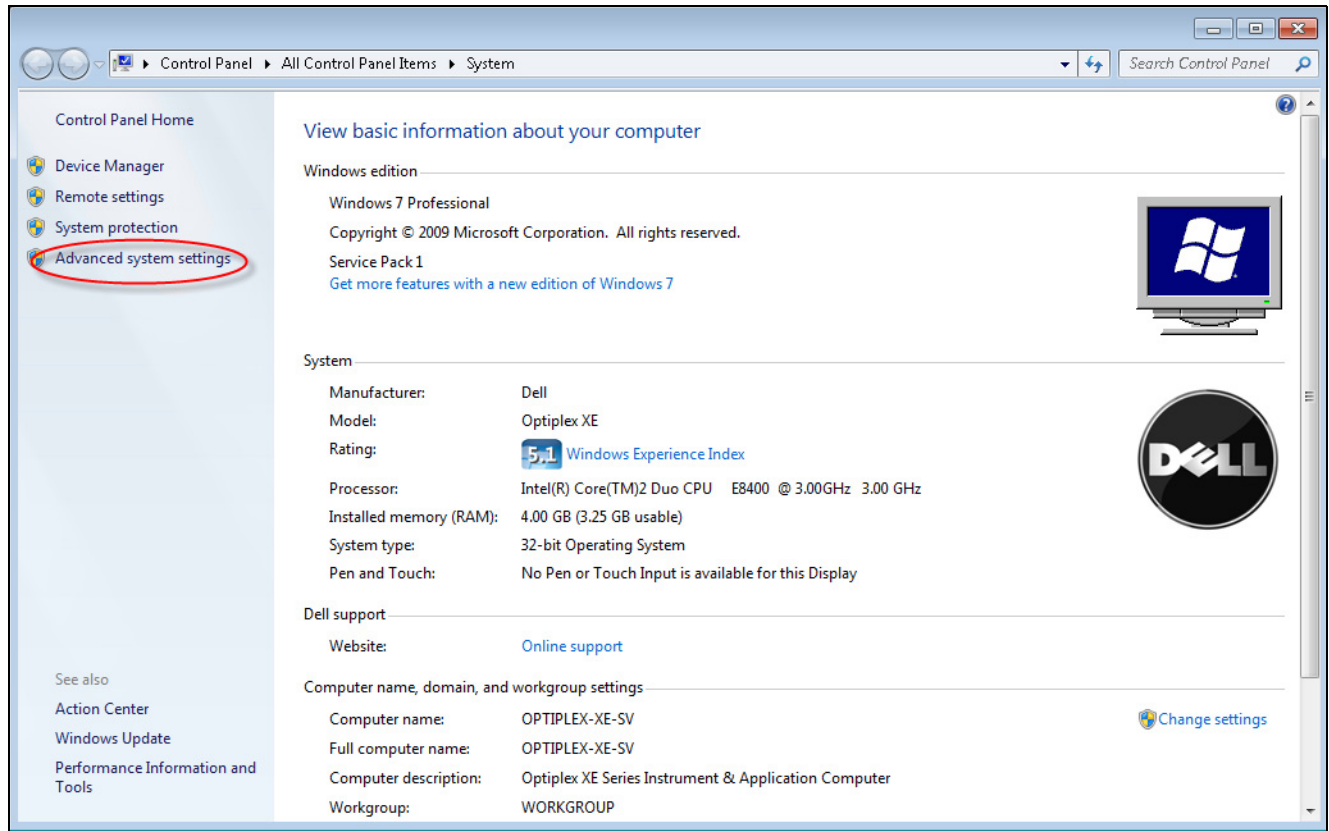
Uninstall GeneMapper® ID-X Software, any other programs that use Oracle databases, and any existing versions of Oracle databases, whether Life Technologies products or products from other companies. Go to **Start ▶ Control Panel ▶ Add or Remove Programs**.

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).

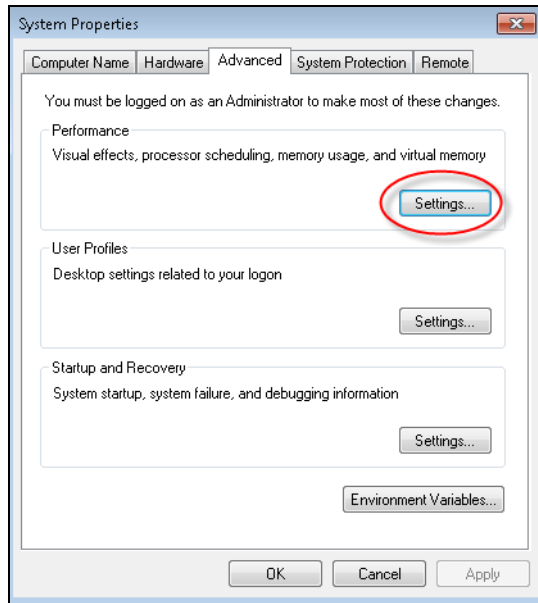
If it is still listed, manually uninstall the software (see “If the GeneMapper® ID-X Software is still listed after uninstalling (tested on Windows® XP only)” on page 38).

## Check virtual memory settings

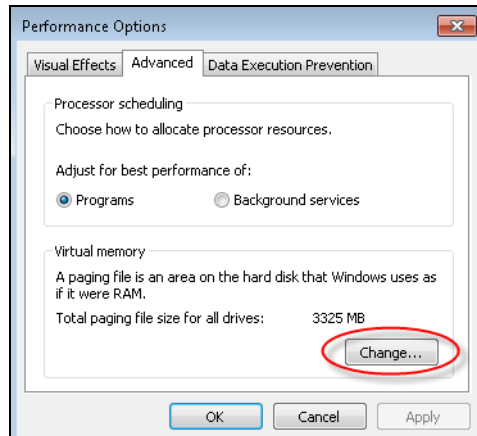
1. On the desktop, right-click **My Computer**, then click **Advanced System Settings**.



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



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



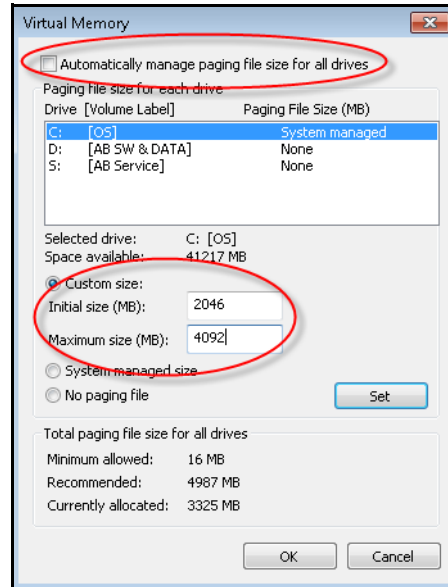
4. In the Virtual Memory dialog box, deselect the Automatically Manage paging file size for all drives check box. Select the **C:** drive. Click the **Custom size** radio button. Specify **2046 MB** for initial and **4092** for maximum size.

---

**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.

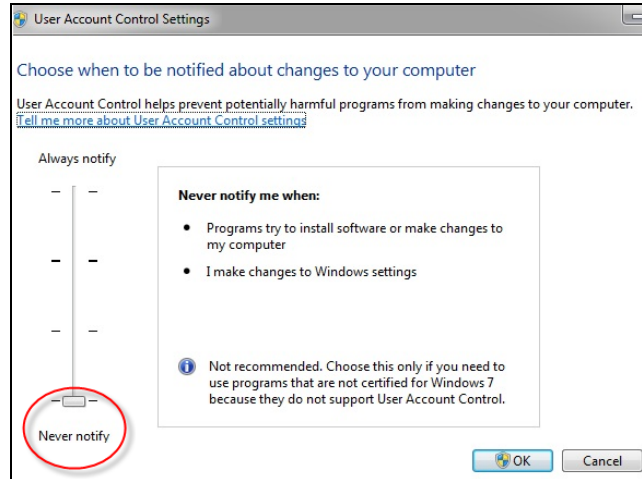


5. Click **Set**, then click **OK**.

These settings are not activated until you restart the computer.


## Check notification settings

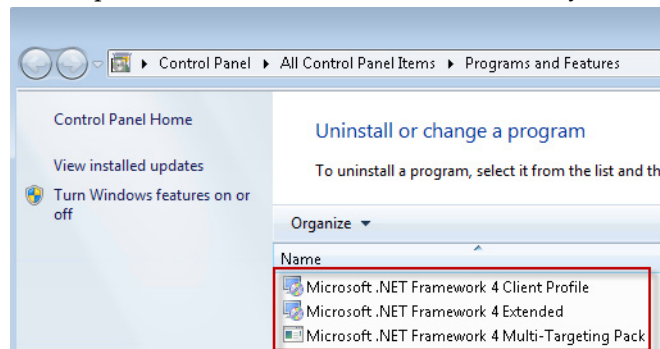
1. Select  ► **Control Panel** ► **User Accounts**. Click **Change User Account Settings**.
2. In the User Account Control Settings, drag the slider to the bottom position **Never Notify**.



## Check Microsoft .NET Framework version

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

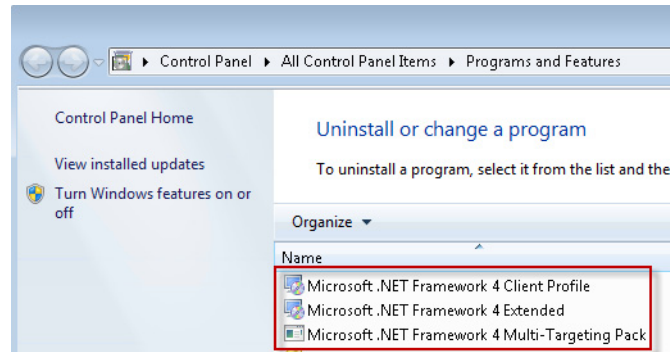
1. Select  ► **Control Panel** ► **User Programs and Features**.
2. Scroll down and determine if a version of 2.0 or later is installed. (There may be multiple versions installed. Do not remove any versions of the software.)



Version 2.0 or higher is required

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**.

5. After installation completes, verify the Microsoft .NET Framework 2.0 SP2 was successfully installed (select  ► **Control Panel** ► **User Programs and Features**).



**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

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**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](#)).

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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® ID-X Software installation

Use 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	Scenario		Choose DVD	Steps
GeneMapper® ID-X Software Full installation	Full installation	<b>Stand Alone Computer</b> without any version of GeneMapper® ID-X Software or Data Collection Software installed	GeneMapper® ID-X Software v1.4 Full Part no. 4479707	<ol style="list-style-type: none"> <li>1. Log in to the local computer (not a network domain) using an account with Administrator privileges.</li> <li>2. Insert the GeneMapper® ID-X Software v1.4 Full DVD and follow the instructions. Installation may take up to 1 hour to complete.</li> <li>3. Enter the Registration Code to launch the software.</li> </ol>
	Full installation to a computer installed with GeneMapper® ID Software v3.2	<b>Stand Alone Computer</b> with GeneMapper® ID Software v3.2.x installed	GeneMapper® ID-X Software v1.4 Full Part no. 4479707	<ol style="list-style-type: none"> <li>1. Log in to the local computer (not a network domain) using an account with Administrator privileges.</li> <li>2. Insert the GeneMapper® ID-X Software v1.4 Full DVD and follow the instructions. The software detects the GeneMapper® ID Software v3.X.</li> <li>3. When prompted, export the GeneMapper® ID 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.</li> <li>4. Un-install the GeneMapper® ID Software v3.2 (go to the Windows® <b>Control Panel</b>, then select <b>Add or Remove Programs</b>).</li> <li>5. Restart the computer, then log in to the local computer using an account with Administrator privileges.</li> <li>6. Install the GeneMapper® ID-X Software v1.4 Full version from the Full DVD. Installation may take up to 1 hour to complete.</li> <li>7. Enter the Registration Code to launch the software.</li> </ol>

Table 3 Client installation scenarios and steps

Installation Type	Scenario		Choose DVD	Steps
GeneMapper® ID-X Software Client installation	Client installation	<b>Stand Alone Computer</b> without any version of GeneMapper® ID-X Software installed	GeneMapper® ID-X Software v1.4 1-Client Part no. 4479711 5-Client Part no. 4479708 10-Client Part no. 4479709	<ol style="list-style-type: none"> <li>1. Before installing, perform the procedures in the section appropriate for the computer: <ul style="list-style-type: none"> <li>• “Procedures to perform before installation: Windows® XP Operating System (OS)” on page 13.</li> <li>• “Procedures to perform before installation: Windows® 7 Operating System (OS)” on page 20.</li> </ul> </li> <li>2. Install a full version of the software before the client version (see Table 2 on page 29).</li> <li>3. Log in to the local computer (not a network domain) using an account with Administrator privileges.</li> <li>4. Insert the GeneMapper® ID-X Software v1.4 Client DVD and follow the instructions. Installation takes about 15 minutes to complete.</li> <li>5. Enter the Registration Code to launch the software.</li> </ol>

Installation Type	Scenario		Choose DVD	Steps
GeneMapper® ID-X Software Client installation	Client installation to a computer with GeneMapper® ID Software v3.2	<b>Stand Alone Computer</b> with GeneMapper® ID Software v3.2.x installed	GeneMapper® ID-X Software v1.4 1-Client Part no. 4479708  5-Client Part no. 4479708  10-Client Part no. 4479709	<ol style="list-style-type: none"> <li>1. Before installing, perform the procedures in the section appropriate for the computer: <ul style="list-style-type: none"> <li>• “Procedures to perform before installation: Windows® XP Operating System (OS)” on page 13.</li> <li>• “Procedures to perform before installation: Windows® 7 Operating System (OS)” on page 20.</li> </ul> </li> <li>2. Log in to the local computer (not a network domain) using an account with Administrator privileges.</li> <li>3. Insert the GeneMapper® ID-X Software v1.4 Full DVD and export the GeneMapper® ID 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.</li> <li>4. Un-install the GeneMapper® ID Software v3.2 (go to the Windows® <b>Control Panel</b>, then select <b>Add or Remove Programs</b>).</li> <li>5. Restart the computer, then log in to the local computer using an account with Administrator privileges.</li> <li>6. Insert the GeneMapper® ID-X Software v1.4 Client DVD and follow the instructions. Installation takes about 15 minutes to complete.</li> <li>7. Enter the Registration Code to launch the software.</li> </ol>

## 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 upgrade scenarios and steps

Installation Type	Scenario	Choose DVD	Steps
Upgrade to GeneMapper® ID-X Software Full installation	Upgrade GeneMapper® ID-X Software v1.0.1 or later Full install on a <b>stand-alone computer</b>	GeneMapper® ID-X Software Version 1.4 Full Upgrade Part no. 4479715	<ol style="list-style-type: none"> <li>1. Before installing, perform the procedures in the section appropriate for the computer: <ul style="list-style-type: none"> <li>• <a href="#">“Procedures to perform before installation: Windows® XP Operating System (OS)”</a> on page 13.</li> <li>• <a href="#">“Procedures to perform before installation: Windows® 7 Operating System (OS)”</a> on page 20.</li> </ul> </li> <li>2. Log in to the local computer using an account with Administrator privileges.</li> <li>3. Insert the GeneMapper® ID-X Software Full Upgrade DVD and follow the instructions.</li> <li>4. 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.)</li> </ol>

Table 5 Client upgrade scenarios and steps

Installation Type	Scenario	Choose DVD	Steps
Upgrade to GeneMapper® ID-X Software Client	Upgrade GeneMapper® ID-X Software v1.0.1 or later Client installed on a <b>stand-alone computer</b>	GeneMapper® ID-X Software Version 1.4 Client Upgrade Part no. 4479710	<ol style="list-style-type: none"> <li>Before installing, perform the procedures in the section appropriate for the computer: <ul style="list-style-type: none"> <li>“Procedures to perform before installation: Windows® XP Operating System (OS)” on page 13.</li> <li>“Procedures to perform before installation: Windows® 7 Operating System (OS)” on page 20.</li> </ul> </li> <li>Upgrade a full version of the software before the client version (see Table 4 on page 33).</li> <li>Log in to the local computer using an account with Administrator privileges.</li> <li>Insert the GeneMapper® ID-X Software Client Upgrade DVD and follow the instructions. The software detects the previous version of GeneMapper® ID-X Software.</li> <li>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.)</li> </ol>

## Procedures to perform after installation

### Reset file and folder permissions after installation (Client installation)

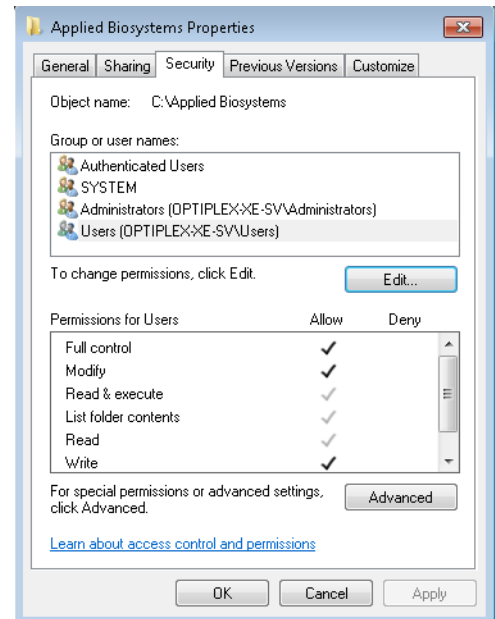
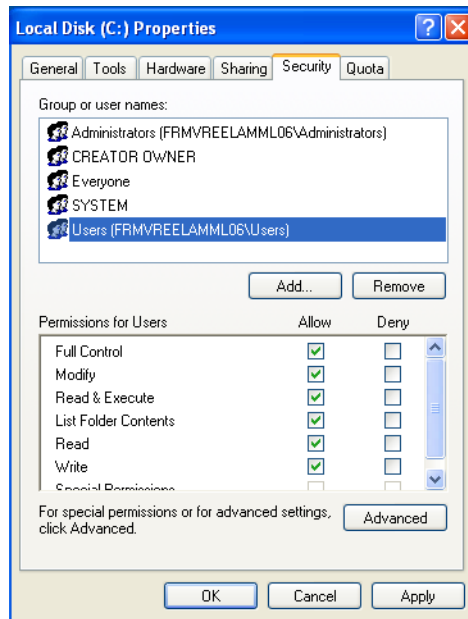
The client installer specifies folder privileges at the time of the GeneMapper® ID-X Software installation.

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:

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

4. **Windows 7 OS only:** Click **Edit**.
5. In the bottom pane, select **Full Control**.



**Reset antivirus, firewall, and network computer settings**

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

**Import GlobalFiler™ stutter files**

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 HID Updater on 3500 Series instruments**

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.

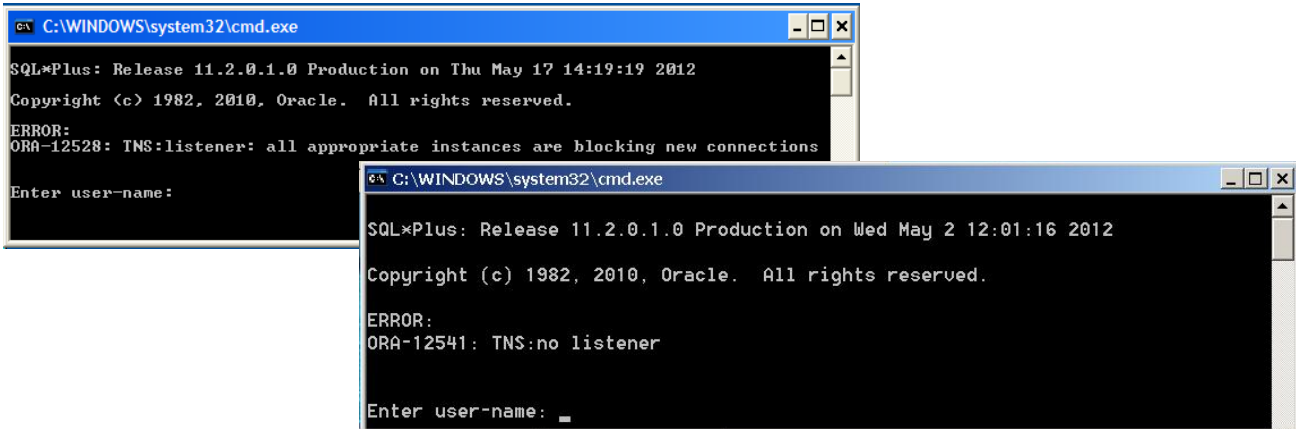
**Note:** If you have a new instrument installed by a Life Technologies representative, the updater may have been run during installation.

1. Obtain the HID Updater 3500 DC v2.0 from [www.lifetechnologies.com/support](http://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.

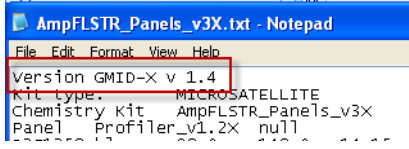
# Troubleshooting

## Symptoms and causes

Symptom	Possible cause	Action
ORA-12528 and ORA-12541 Oracle® errors displayed during installation	Problem with Oracle® software installation.	Contact Life Technologies.





"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	<ol style="list-style-type: none"> <li>1. Cancel the installation.</li> <li>2. Install the required version. See <a href="#">"Check Microsoft .NET Framework version" on page 18.</a></li> <li>3. Start the installation again.</li> </ol>
GeneMapper® ID-X Software will not start after installation	Uninstallation of the previous version of GeneMapper® ID-X Software failed.  <b>Note:</b> In most cases, uninstallation should succeed. However, third-party software, firewall interference, and other situations may interfere with successful uninstallation.	Uninstall the software. See <a href="#">"Uninstall the GeneMapper® ID-X Software" on page 38.</a>  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.	Modify network security settings. See <a href="#">"Enable communication with port 1521 Windows® XP OS" on page 39</a> or <a href="#">"Enable communication with port 1521 Windows® 7 OS" on page 39.</a>
	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 lost. Please restart the application. This message may appear multiple times.” message	Network communication is interrupted.	Restart the software. Restart Oracle services (see <a href="#">“Restart Oracle services” on page 43</a> ).
	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 connection with the database	Anti-virus software is interfering with communication.	Use less restrictive anti-virus settings. 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 <a href="#">“Reset file and folder permissions after installation (Client installation)” on page 34</a> .
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. <b>Note:</b> 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® ID-X Software.
Version error displayed when you import a panel file (this message differs from the message displayed in earlier versions of the software)	The version text in the panel .txt file is not present. 	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.	<ol style="list-style-type: none"> <li>In the Project window, select <b>Admin ▶ Audit Manager ▶ Report</b>.</li> <li>Log in to the Audit Manager.</li> <li>In the Audit History Viewer, <b>File ▶ Edit Query</b>, leave the default settings, then click <b>OK</b>.</li> <li>Select <b>File ▶ Execute Query</b>.</li> </ol>
Small markers and low molecular weight microvariant alleles are not displayed in plots when using the default 6-dye plot setting	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 Software

- Restart the computer and log on using a local computer administrator account (see [“Check user access” on page 13](#) or [page 20](#)).
- Ensure that no programs or applications are running.
- Disable any antivirus software (including antimalware software).
- Select  ▶ **Control Panel ▶ Uninstall a Program**. Select **GeneMapper® ID-X Software**, then click **Uninstall**.
- Restart the computer and log on using a local computer administrator account.
- Confirm that the software has been uninstalled: select  ▶ **Control Panel ▶ Uninstall a Program**. If GeneMapper® ID-X Software is still listed, go to [“If the GeneMapper® ID-X Software is still listed after uninstalling \(tested on Windows® XP only\)”](#) below.

### If the GeneMapper® ID-X Software is still listed after uninstalling (tested on Windows® XP only)

- Ensure antivirus/antimalware software is disabled.
 

**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.
- Confirm the Virtual Memory settings are correct ([“Check virtual memory settings” on page 15](#)).
- Run the Remove Oracle utility:
  - Insert the GeneMapper® ID-X Software Full or Full Upgrade Installation DVD in the computer DVD drive, right-click on the drive icon, then select **Explore**.
  - Navigate to **Utilities ▶ RemoveOracle.exe**.
  - Copy RemoveOracle.exe to the desktop.
  - Double-click **RemoveOracle.exe** (a black box appears for a few seconds and disappears).
- Navigate to and delete the entire **x:\AppliedBiosystems** folder.
- Restart the computer and log on using a local computer administrator account.

## 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.

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**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.

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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 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.

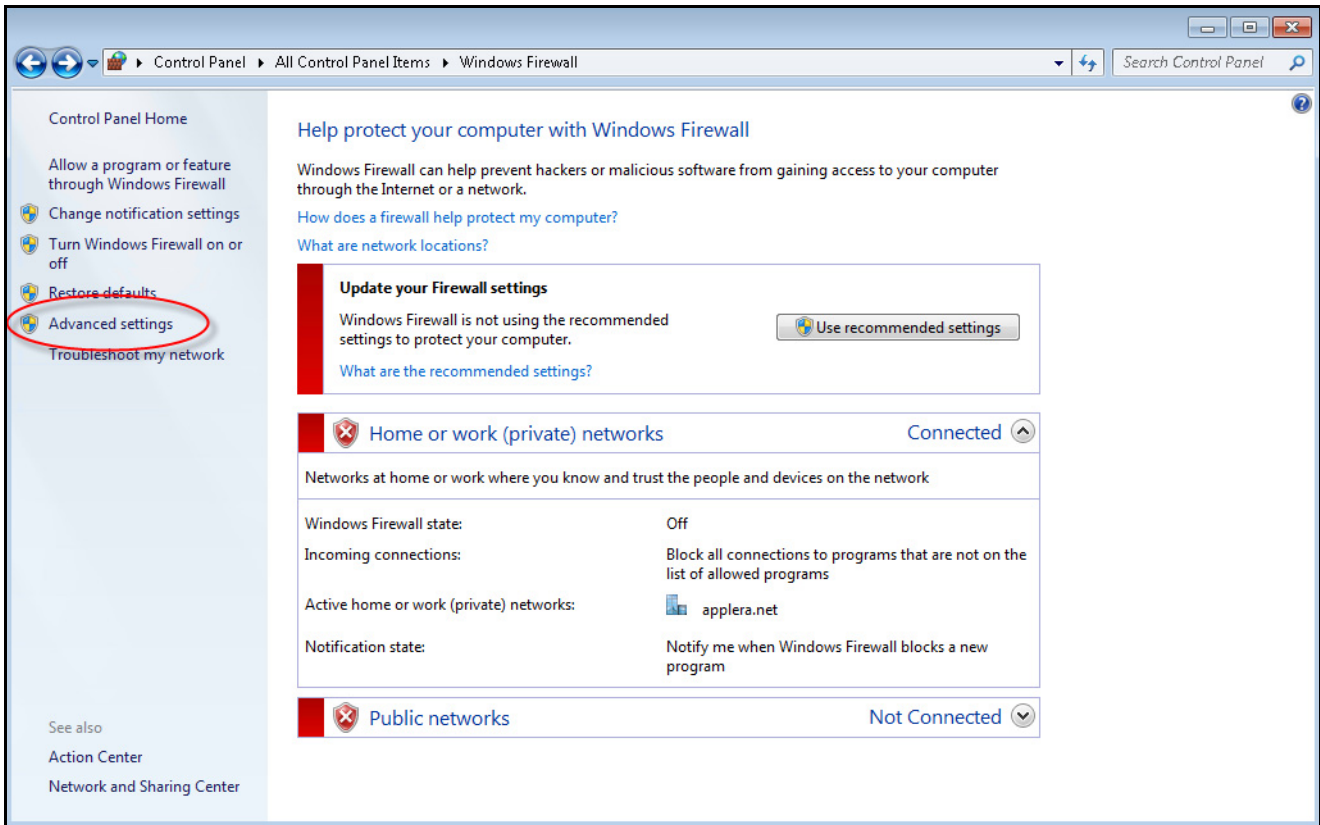
However, if the software does not start or a “No databases found” message is displayed after installation, modify settings to enable communication with port 1521.

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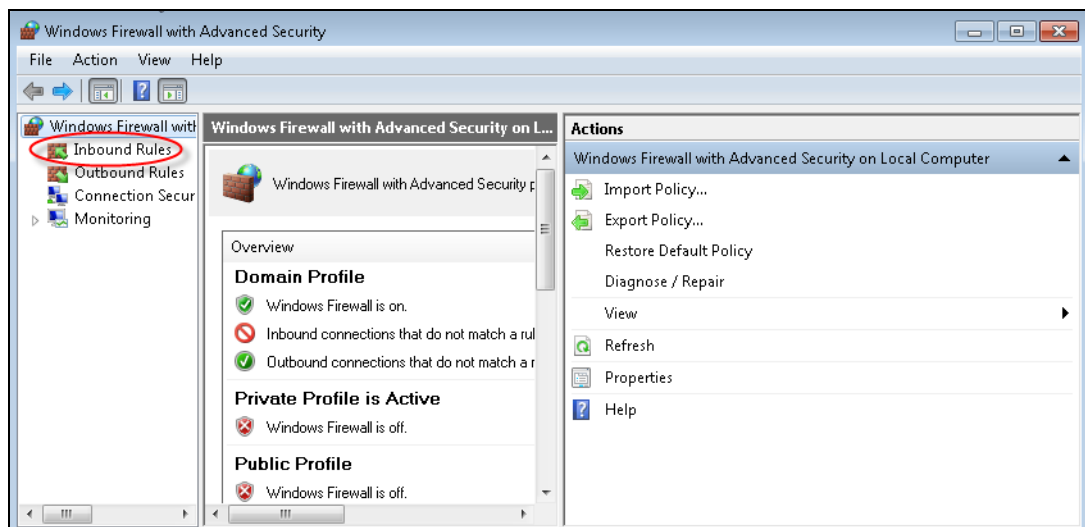
**IMPORTANT!** In addition to Windows security settings, some third-party anti-virus or firewall applications may affect port 1521. If you are running, third-party anti-virus or firewall applications, modify settings for those applications to enable communication with port 1521.

---

1. Select  ▶ **Control Panel ▶ Security ▶ Windows Firewall**. Click **Advanced Settings**.

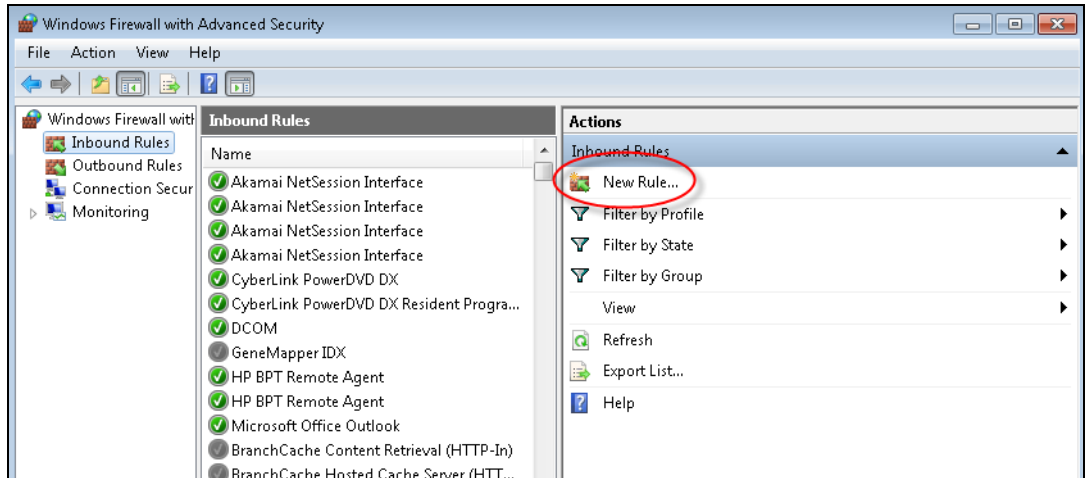


2. In the Windows Firewall with Advanced Security window, click **Inbound Rules**.

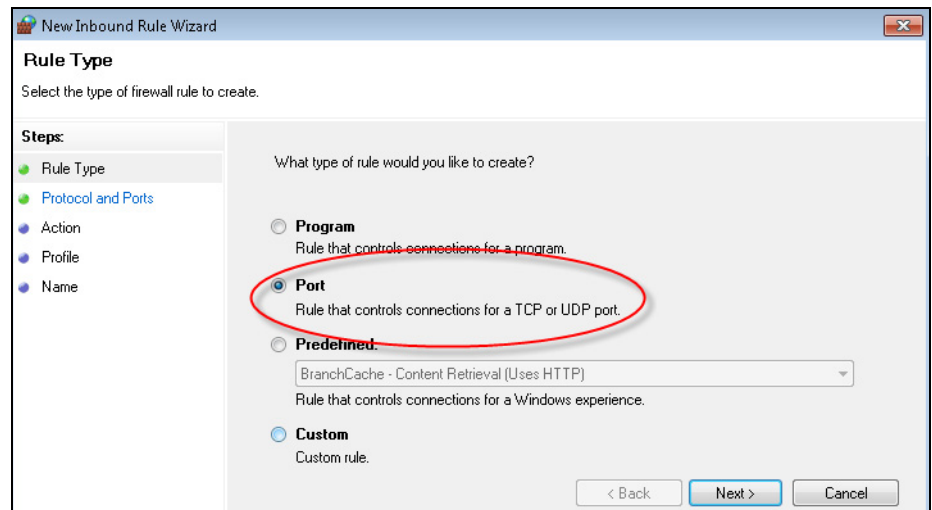




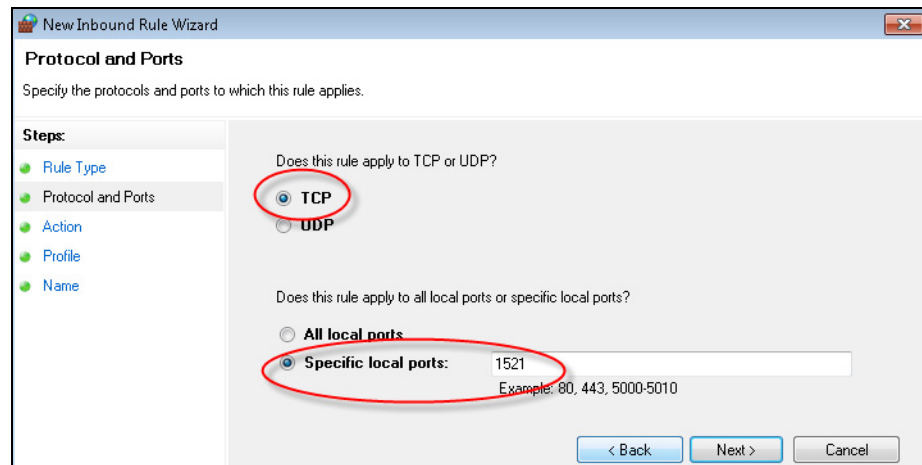
3. Click New Rule.



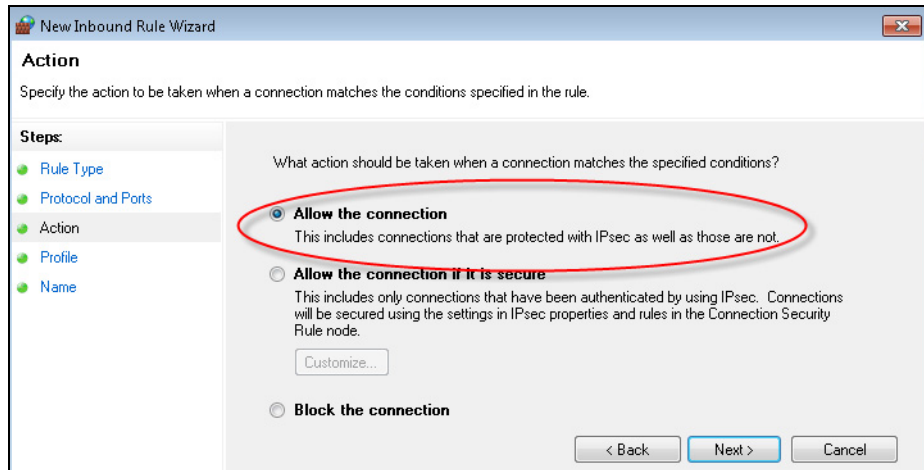
4. Select Port, then click Next.



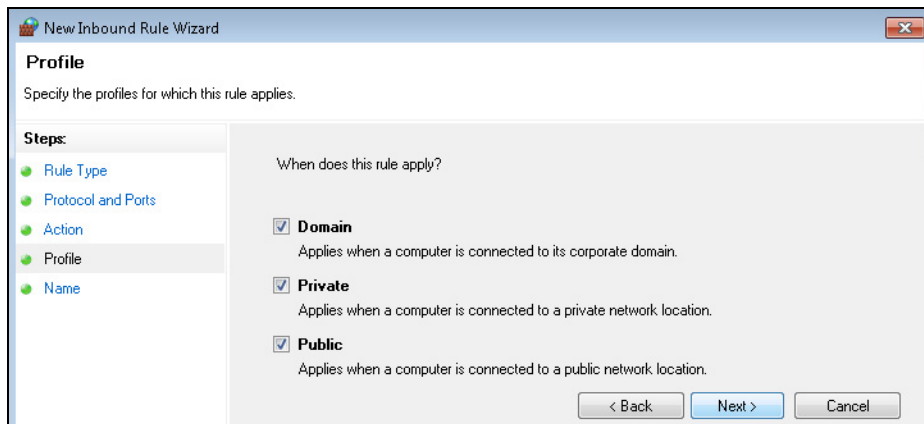
5. Select TCP, then type 1521 in the Specific Local Ports, then click Next.



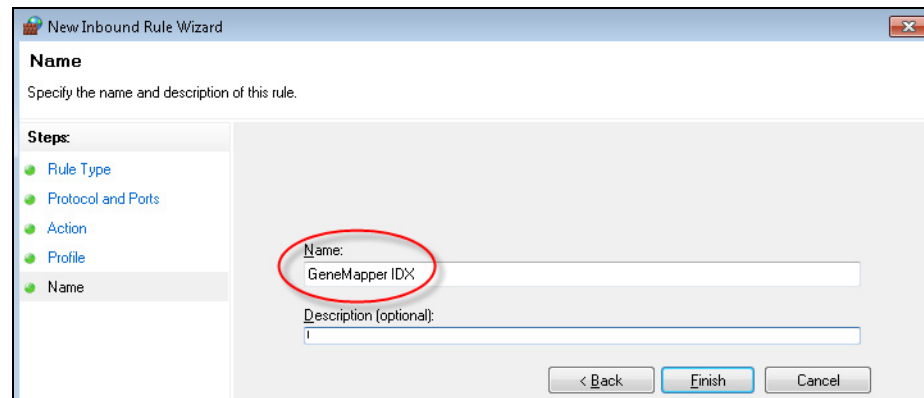
- In the Action page, select **Allow the connection**, then click **Next**.



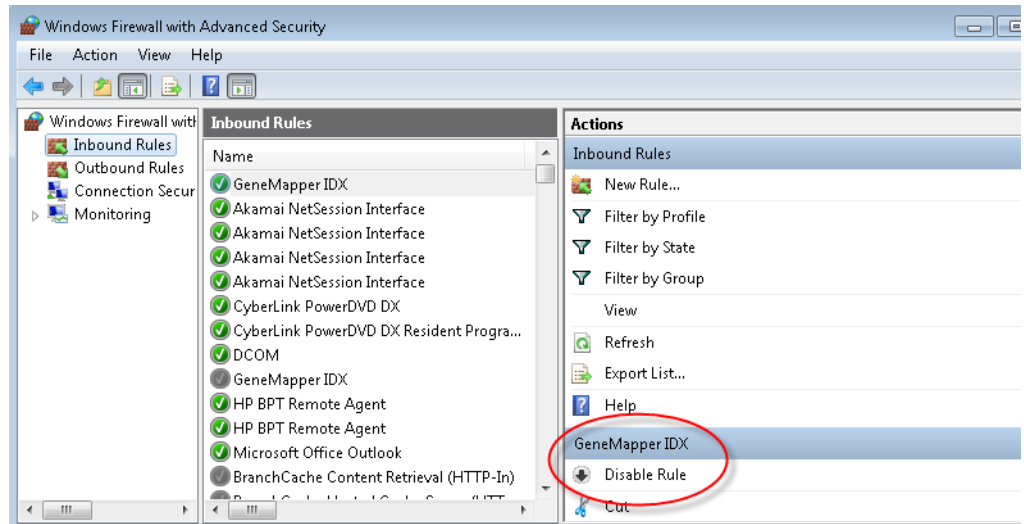
- In the Profile page, leave the default settings selected, then click **Next**.



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



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).



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

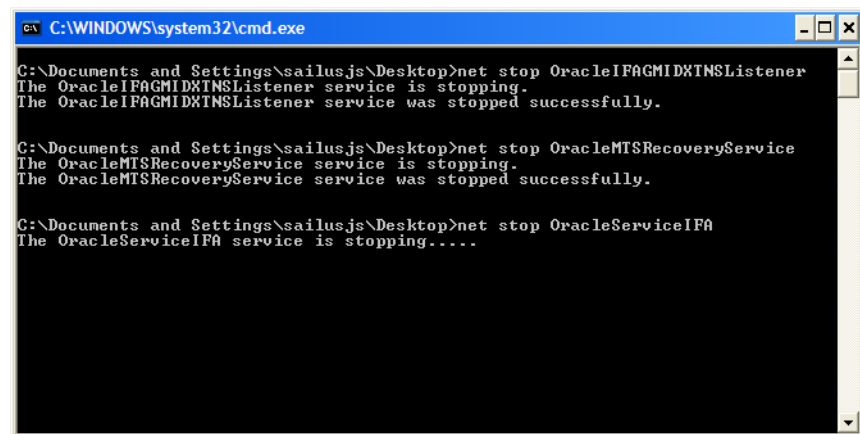
## Restart Oracle services

If a “The database connection has been lost” message is displayed, restart Oracle services 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.)

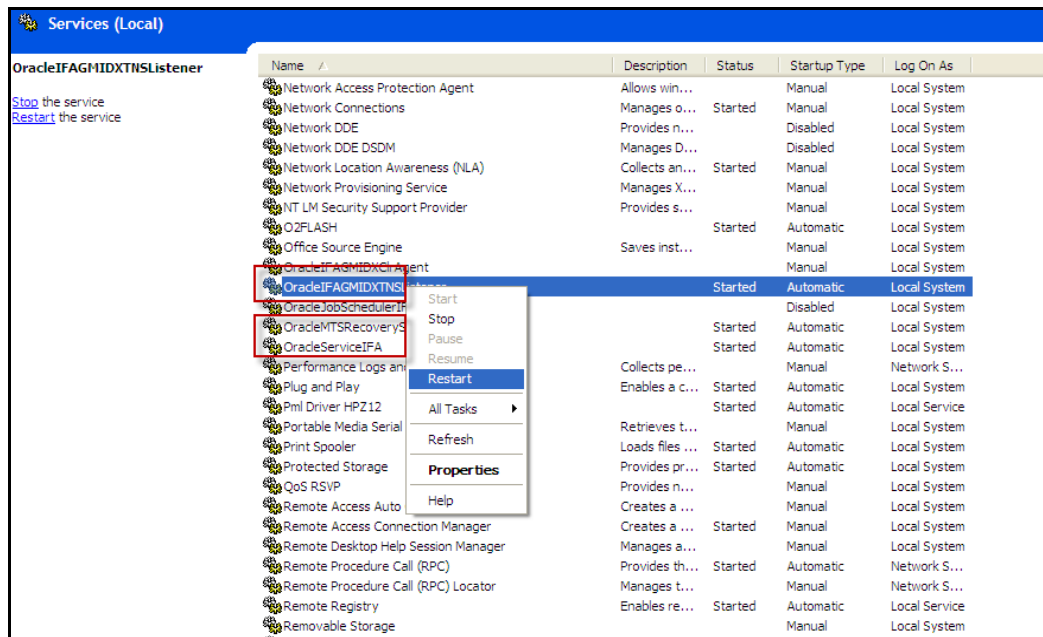
The following window is displayed for ~2 minutes as the services restart.



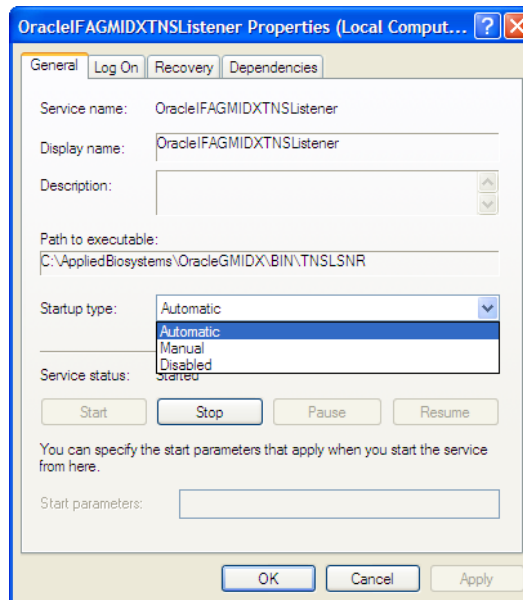
3. When the window closes, start the GeneMapper® ID-X Software.

### 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



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.



4. Start the GeneMapper® ID-X Software.

## Software verification testing


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### 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 3500 Data Collection Software v1	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 AmpFISTR® PCR Amplification Kit and the GlobalFiler™ Express Kit.
	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.

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

Testing Categories	Subcategories	Test Description
GeneMapper® ID-X Software v1.4 testing with the GlobalFiler™ Express Kit	Allelic ladder genotyping	<ul style="list-style-type: none"> <li>Compare the allelic ladder run sizing, genotyping, and PQV scoring between v1.3 and v1.4 (without ACC).</li> <li>Visually inspect 20 allelic ladders from each instrument for proper allele calling, PQV scoring, and PQV flagging.</li> </ul>
	Sample genotyping	<ul style="list-style-type: none"> <li>Compare the single-source (population) and positive control sample allele calls: <ul style="list-style-type: none"> <li>To corresponding allele calls generated with Identifiler®, NGM SElect™, and Yfiler® Kits.</li> <li>Between instruments.</li> </ul> </li> <li>Compare the single-source (population), positive control sample, and sensitivity sample: sizing, genotyping, and PQV scoring between v1.3 and v1.4 (without ACC).</li> </ul>
GeneMapper® ID-X Software v1.4 testing GlobalFiler™ Express Kit	Mixture Analysis	<p>Evaluate for accurate results:</p> <ul style="list-style-type: none"> <li>MIT pruning and sample segregation.</li> <li>Pattern extraction, PHR, residual, Mx and Avg Mx calculation, and flags and values.</li> <li>Individual data files for RMP, CPI, LR, and multiple-kit merging calculations.</li> </ul>
Concordance testing of legacy kit data with GeneMapper® ID-X Software v1.3	Sizing and genotyping	<ul style="list-style-type: none"> <li>Export Genotype and Sizing tables and compare peak heights, areas, data points, sizes, allele names, and PQV scores.</li> <li>Compare the 310 matrix results.</li> </ul>
	Mixture analysis	Compare mixture analysis calculations and flags using the same analysis methods and thresholds.
Verification of new v1.4 software features and updates	ACC and AN PQVs, Y Marker check box in Panel Manager (new)	<ul style="list-style-type: none"> <li>Process GlobalFiler™ Express Kit data with the GlobalFiler panel and bins.</li> <li>Visually verify the accuracy of the ACC and AN flag results.</li> </ul>
	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 rules)	<ul style="list-style-type: none"> <li>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).</li> <li>Confirm SPK flag is N/A for any sample type where spike detection is disabled.</li> </ul>
	Define New Sample Path function	Define New Sample Path function works for .hid files.

## Computers used

**Table 8** Configuration of test computers

Testing Category	Computer Configuration			
	Make/ Model	Processor (CPU)/ Speed	Memory (RAM)	Operating System (OS)/ Service Pack (SP)
Data Collection Software v4	Dell® OptiPlex® XE (4 computers)	Intel® Core™2 Duo E8400 3 GHz	4 Gb	Windows® 7 Professional OS (SP1), 32-bit
3500 Data Collection Software v2				
GeneMapper® ID-X 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® ID-X 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 AmpF®STR® kit used to generate data are noted.

Instrument/ Data Collection Software	AmpF®STR® Kit	Single Source	Sensitivity	Mixture	Low Quality DNA	LOR	OMR	Spike	Good Ladder	Low Quality Ladder	Positive	Negative	Total
310 Genetic Analyzer Data Collection Software v3.0/3.1	COfiler®	16	6	5	12	—	—	—	8	—	1	1	49
	Profiler Plus®	16	6	6	12	—	—	—	8	—	1	1	50
	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 Analyzer Data Collection Software v1.1/2.0	COfiler®	16	6	6	12	—	—	—	3	—	1	1	45
	Profiler Plus®	16	6	6	12	—	—	—	3	—	1	1	45
	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-Avant™ Genetic Analyzer Data Collection Software v2	COfiler®	16	6	6	12	—	—	—	3	—	1	1	45
	Profiler Plus®	16	6	6	12	—	—	—	3	—	1	1	45
	Identifiler®	16	6	6	12	—	—	—	3	—	1	1	45



Instrument/ Data Collection Software	AmpF/STR® Kit	Single Source	Sensitivity	Mixture	Low Quality DNA	LOR	OMR	Spike	Good Ladder	Low Quality Ladder	Positive	Negative	Total
3130xl Genetic Analyzer	Profiler Plus®	—	—	—	—	—	—	—	48	—	—	—	48
Data Collection Software v3.0	Identifiler®	93	24	12	30	12	10	9	48	58	1	1	298
	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
	NGMSElect™ Express	100	—	—	—	—	—	—	12	—	—	—	112
3130xl Genetic Analyzer Data Collection Software v3.1.1	Yfiler®	—	—	—	—	—	—	—	48	—	45	3	96
	NGM SElect™	—	—	—	—	—	—	—	48	—	45	3	96
3730 DNA Analyzer Data Collection Software v3.0	Identifiler®	90	48	—	—	—	—	—	48	—	1	1	188
3730 DNA Analyzer Data Collection Software v3.1.1	Identifiler®	—	—	—	—	—	—	—	48	—	45	3	96
3130xl Genetic Analyzer Data Collection Software v4	SGM Plus®	60	—	—	—	—	—	—	12	—	12	12	96
	Identifiler® Plus	60	—	—	—	—	—	—	12	—	12	12	96
	Yfiler®	60	—	—	—	—	—	—	12	—	12	12	96
	NGM™ SElect	60	—	—	—	—	—	—	12	—	12	12	96

Instrument/ Data Collection Software	AmpFISTR® 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	Identifiler®	60	—	—	—	—	—	—	12	—	12	12	96
3500xL Genetic Analyzer  Data Collection Software v1	Identifiler® Plus	84	—	—	—	—	—	—	12	—	—	—	96
	Identifiler® Direct	84	—	—	—	—	—	—	12	—	—	—	96
	NGM™	84	—	—	—	—	—	—	12	—	—	—	96
	NGMSElect™ Express	52	—	—	—	—	—	—	8	—	—	4	64
3500xL Genetic Analyzer  Data Collection Software v2	SGM Plus®	60	—	—	—	—	—	—	12	—	12	12	96
	Identifiler® Plus	60	—	—	—	—	—	—	12	—	12	12	96
	Identifiler® Direct	60	—	—	—	—	—	—	12	—	12	12	96
	NGM SElect™	60	—	—	—	—	—	—	12	—	12	12	96
<b>Total</b>		1578	187	107	186	12	10	25	690	58	262	146	<b>3149</b>

**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.

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

**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 testing**

The 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 AmpFSTR® Identifiler® (1 ng and 0.125 ng), Profiler Plus®, COfiler®, and SGM Plus® PCR amplification kits. The samples were collected from a 3130xl 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.

### GlobalFiler™ Express samples used for Mixture Analysis

Sample name	Gender	Mixture ratio	DNA input ng:ng	Contributor 1 (µL)	Contributor 2(µL)
H15 H1	M M	0:1	0.0:0.1	0	10
H31 H30	F F	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	F F	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

### Data Collection Software settings used to run GlobalFiler™ Express samples

Genetic Analyzer	Run modules and conditions
3500	<ul style="list-style-type: none"> <li>• HID36_POP4 Injection conditions: 1.2 kV/15 sec</li> <li>• Dye Set J6</li> </ul>
3500xL	<ul style="list-style-type: none"> <li>• HID36_POP4xl Injection conditions: 1.2 kV/24 sec</li> <li>• Dye Set J6</li> </ul>
3130xl	<ul style="list-style-type: none"> <li>• HIDFragmentAnalysis36_POP4 Injection conditions: 3 kV/10 sec</li> <li>• Dye Set J6</li> </ul>
3730	<ul style="list-style-type: none"> <li>• GeneMapper_36_POP7 Injection conditions: 2 kV/10 sec</li> <li>• Dye Set J6</li> </ul>

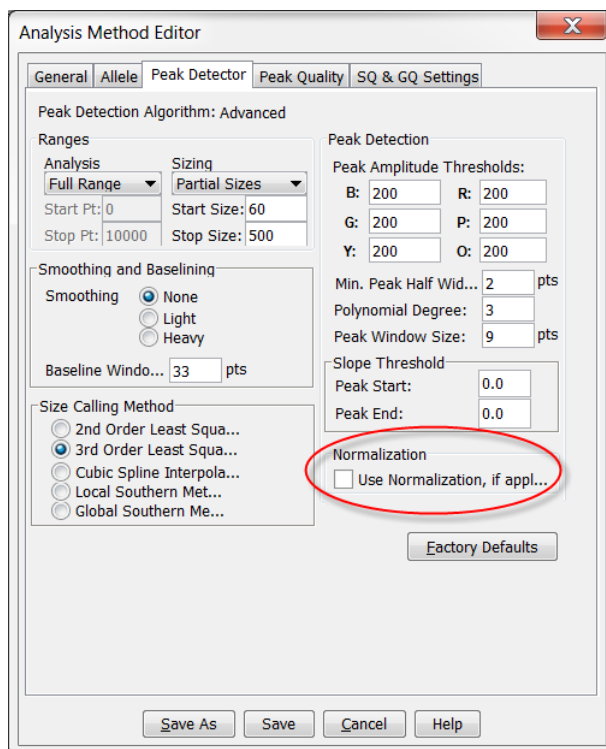
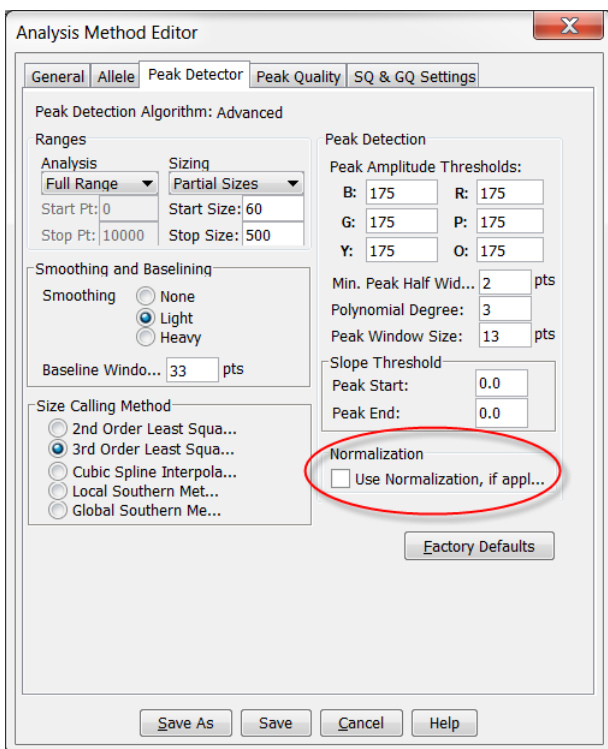
**GeneMapper® ID-X  
Software v1.4  
analysis settings  
for GlobalFiler™  
Express data**

- 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



**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 data collection software verification testing results

Testing Categories	Subcategories	Expected Outcome	Result
3130/3730 Data Collection software v4 3500 Data Collection Software v2 3500 Data Collection Software v1	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/STR® Kits and the GlobalFiler™ Express Kit.	Pass. For more information, see <a href="#">“Capillaries Viewer issue in Data Collection Software v4”</a> on page 57.
	Genotyping	100% concordance between new and earlier versions of Data Collection Software.	Pass. For more information, see <a href="#">“3730 DNA Analyzer allelic ladder failures”</a> on page 57 and <a href="#">“3730 DNA Analyzer sizing failures”</a> on page 60.
		100% concordance between 3130, 3730, and 3500 instruments.	Pass
	Sizing precision	<ul style="list-style-type: none"> <li>Standard deviation of mean size within a run is <math>\leq 0.15</math> bp for all alleles in the allelic ladder.</li> <li>Size range within a run is <math>\leq 0.5</math> bp for the largest allele in the allelic ladder.</li> </ul>	Pass
	Sensitivity	Signal intensity of 6-dye samples meets specifications with no allelic dropout at 125 pg total DNA input	Pass

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

Testing Categories	Subcategories	Expected Outcome	Result
GeneMapper® ID-X Software v1.4 testing GlobalFiler™ Express Kit	Allelic ladder genotyping	<ul style="list-style-type: none"> <li>• 100% concordance for sizing, genotyping, and PQV scoring between GeneMapper® ID-X Software v1.3 and v1.4 (without ACC).</li> <li>• 100% accurate allele calling, PQV scoring, and PQV flagging for 20 allelic ladders from each instrument.</li> </ul>	Pass. For more information, see <a href="#">“3730 DNA Analyzer allelic ladder failures”</a> on page 57.
	Sample genotyping	<ul style="list-style-type: none"> <li>• 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.</li> <li>• 100% concordance of sizing, genotyping, and PQV scoring between GeneMapper® ID-X Software v1.3 and v1.4 (without ACC).</li> <li>• 100% accurate allele calling, PQV scoring, and PQV flagging for all sensitivity samples, 1 positive control, and 1 negative control from each instrument.</li> </ul>	Pass. For more information, see <a href="#">“3730 DNA Analyzer allelic ladder failures”</a> 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® ID-X Software v1.3	Genotyping, peak detection, PQVs	<ul style="list-style-type: none"> <li>• 100% concordance of allele calls with Sample Spike Detection enabled.</li> <li>• 100% concordance of peak height, area and data points with and without normalization.</li> <li>• 100% concordance of all PQV scores, including SQ, with Sample Spike Detection enabled.</li> </ul>	Pass
	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

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)	<ul style="list-style-type: none"> <li>• 100% concordance of allele calls compared to results from Yfiler® kit data and visual inspections.</li> <li>• The ACC values and flags are 100% accurate.</li> </ul>	Pass
	Spike Detection disable/enable function for samples (new)	<ul style="list-style-type: none"> <li>• SPK flag is N/A when spike detection is disabled with and without the presence of a spike.</li> <li>• SPK flag is Check 🚩 when spikes are present in a marker and sample Spike Detection is enabled.</li> </ul>	Pass
	SPK PQV for markers that contain a spike but no alleles (update)	<ul style="list-style-type: none"> <li>• SPK flag is Check 🚩 for markers that contain a spike but no alleles.</li> <li>• SPK flag is N/A when spike detection is disabled with and without the presence of a spike.</li> </ul>	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 2 Example of base pair spacing error in the D2S441 marker

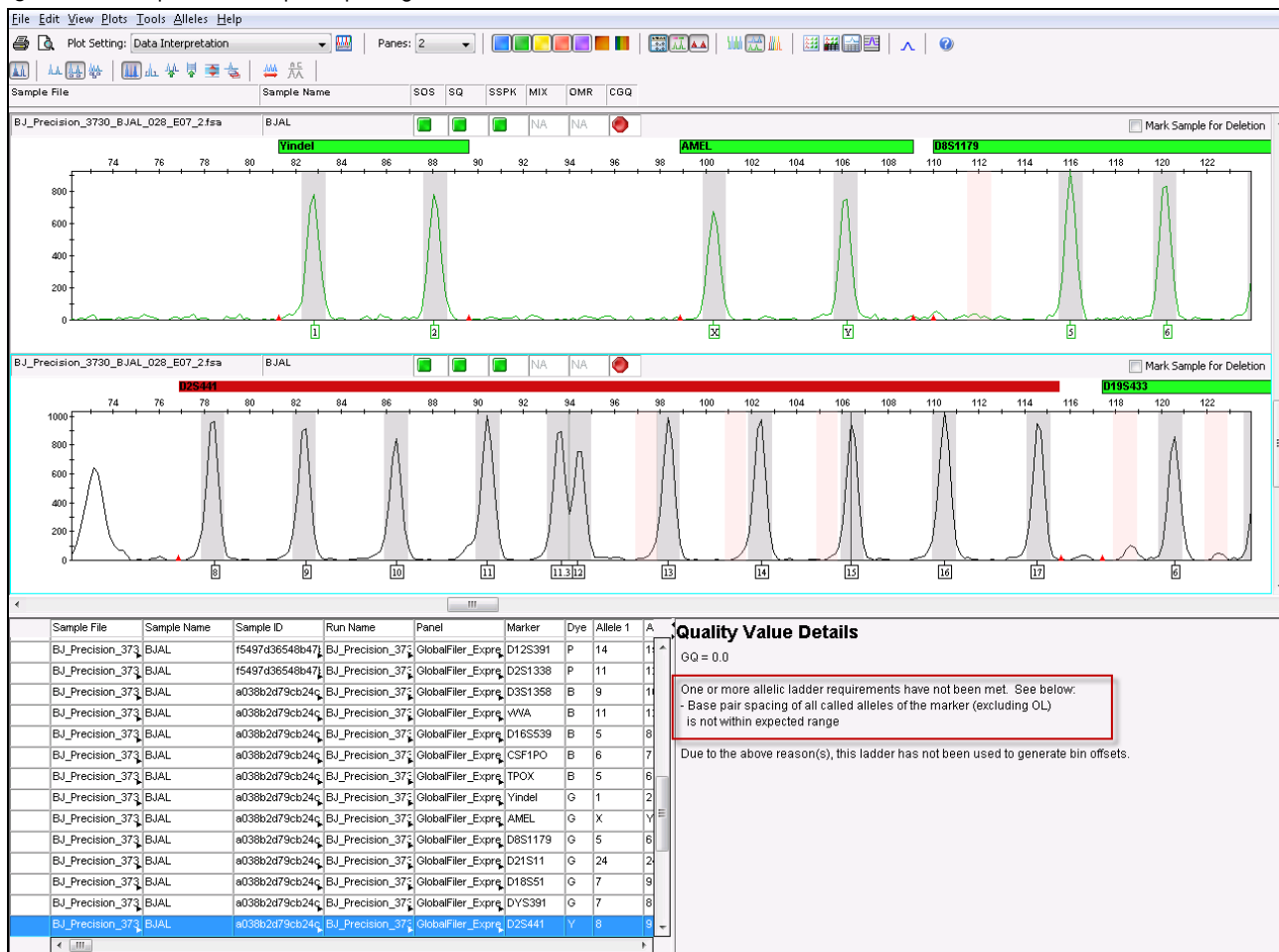
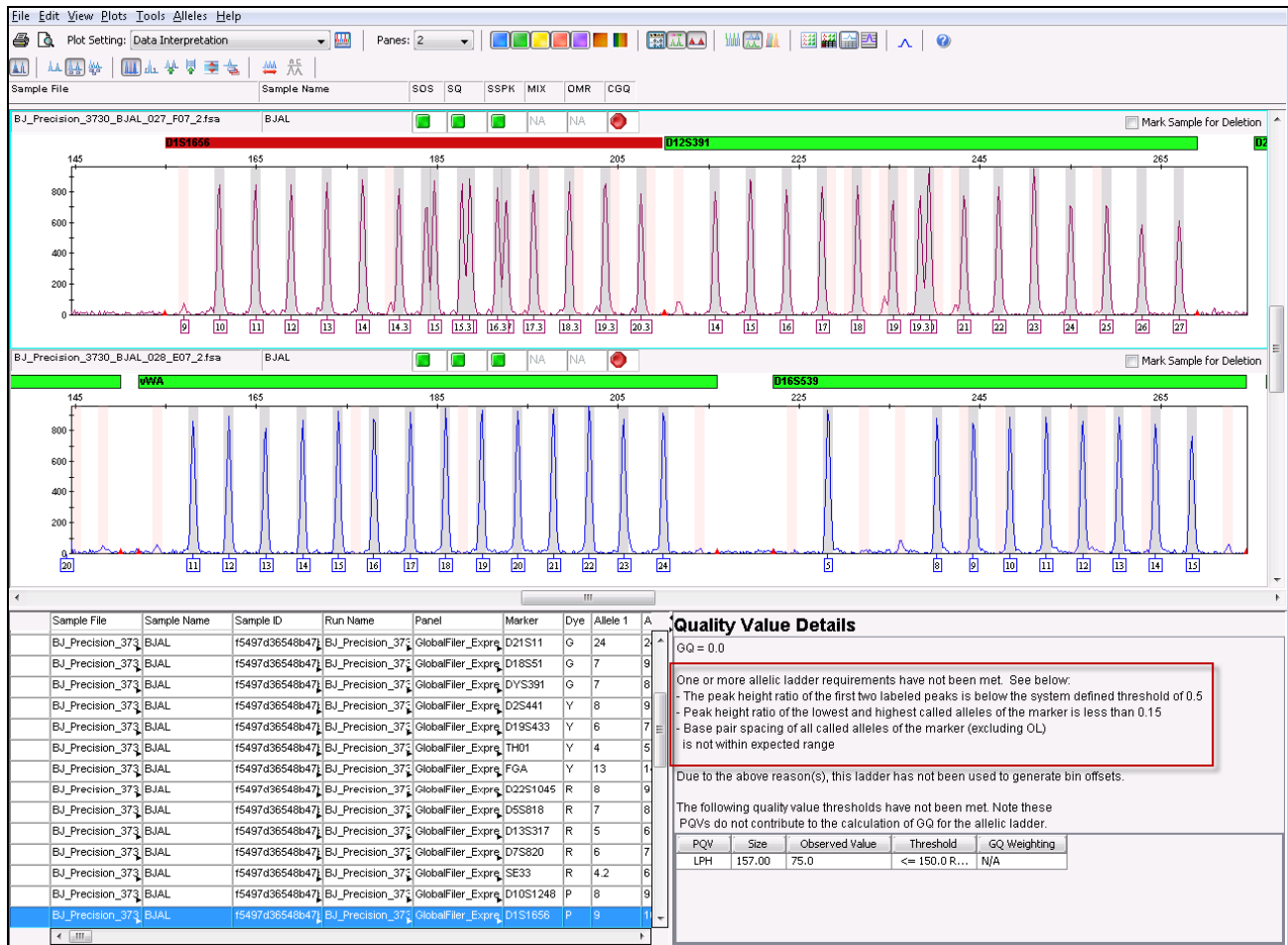


Figure 3 Example of base pair spacing error and incorrect allele assignments in the D1S1656 marker



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).

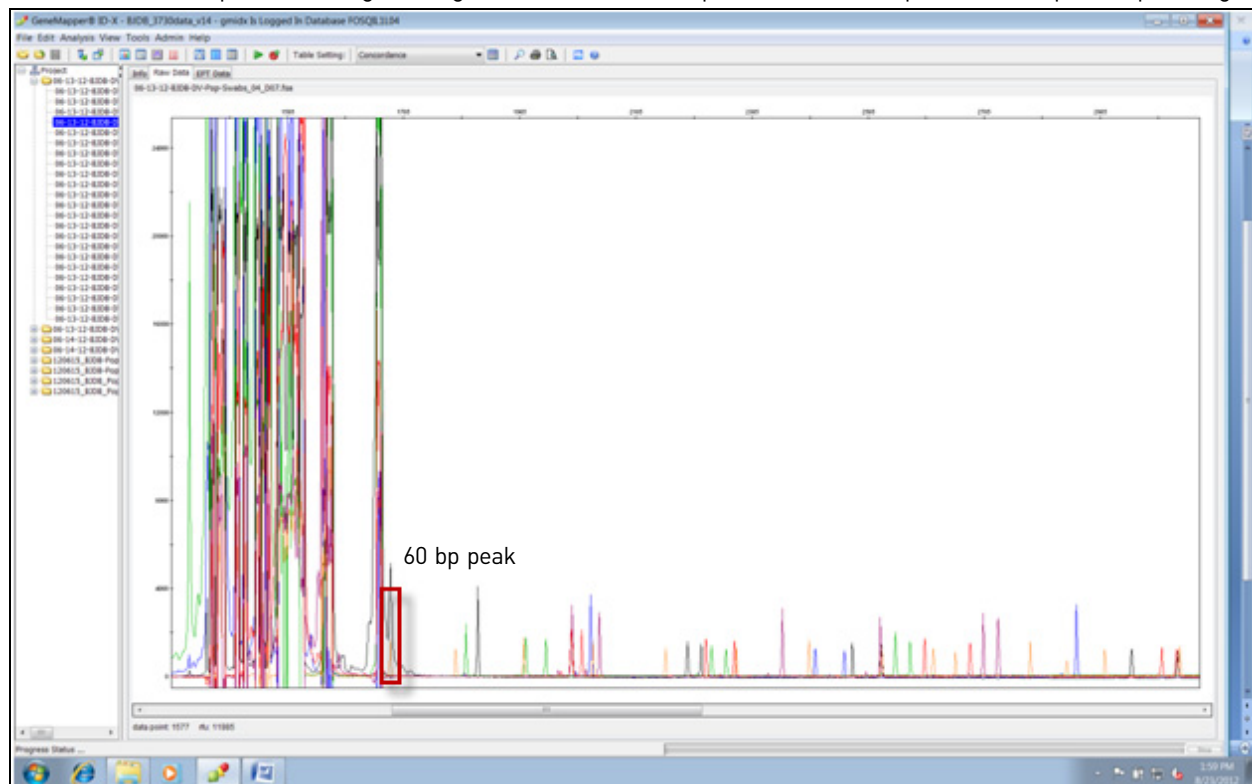
### 3730 DNA Analyzer sizing failures

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® *ID-X* Software v1.4 can be used to process sample files generated on all HID CE instruments and with existing AmpFISTR® 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® *ID-X* 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 AmpFISTR® 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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