

Agilent GeneSpring GT 2 (formerly Varia) Installation Guide

System requirements	3
To upgrade the GeneSpring GT (Varia analysis workbench) Software	4
Step 1. Download the GeneSpring GT (Varia analysis workbench) installation package	10
Step 2. Install GeneSpring GT 2 (Varia analysis workbench)	11
Step 3. Enter license information	16
Step 4. Configure GeneSpring GT (Varia analysis workbench)	19
Step 5. Download genome data	20
Contacting Agilent Technical Support	25

GeneSpring GT (Varia analysis workbench) is a genetic analysis software tool. Use this manual to install:

- the standalone version of GeneSpringGT
- the GeneSpring client, if you have the Agilent GeneSpring License Manager (GSLM)

Download the GeneSpring (Varia) installation package from our Web site:

<http://www.chem.agilent.com/cag/bsp/SiG/Products/2/DemoDownload.asp>



Agilent Technologies

NOTE

Agilent Technologies acquired Silicon Genetics in 2005. The name of Silicon Genetics Varia will be changed to Agilent GeneSpring GT in future releases. This document might refer to both Varia and Agilent during this transition period.

System requirements

This section lists the system requirements for Windows and Mac OS machines.

Windows systems

The following are *minimum* requirements for GeneSpring GT (Varia analysis workbench) software:

- Windows XP, 2000, or Server 2003
- 1024 MB RAM
- Pentium IV processor (or equivalent)
- 2-4 GB disk space (for the complete human or mouse genomes).
- 1024x768 pixel resolution and 16-bit color.

Macintosh systems

The following are *minimum* requirements for GeneSpring GT (Varia analysis workbench) software:

- Mac OS X
- 1024 MB RAM
- 250 MB disk space (for GeneSpring (Varia) with the supplied Crohn's genome).
- 2-4 GB disk space (for the complete human or mouse genomes).
- 1024x768 pixel resolution and 16-bit color strongly recommended.

To upgrade the GeneSpring GT (Varia analysis workbench) Software

If you are migrating from GeneSpring (Varia) Version 1 to Version 2, follow the steps in this section.

NOTE

In GeneSpring GT (Varia analysis workbench) 1, the default destination directory was **Program Files\Silicon Genetics\Varia** on Windows systems (not available on Mac OS).

In GeneSpring GT (Varia) 2, the default destination directory is **..\Agilent\GeneSpring GT (Program Files\Agilent\GeneSpring GT** on Windows systems; **/Users/<user login name>/Agilent/GeneSpring GT** on Mac OS X.

Agilent recommends that you use the default directory, **Agilent**, for Version 2, and keep your **Silicon Genetics** directory as a backup.

NOTE

If you renew your license, you do not have to go through the installation process to enter your new license info. Instead, when Agilent sends you the **licensekey.txt** file, download it to your GeneSpring GT (Varia) directory (by default, **..\Agilent\GeneSpring GT\data**). Click the GeneSpring GT icon to start the program.

The complete path is **Program Files\Agilent\GeneSpring GT\data** on Windows systems, and **/Users/<user login name>/Agilent/GeneSpring GT/data** on Mac OS X systems.

You do not need to remove the previous install of Varia to run GeneSpring GT 2. If you want to uninstall GeneSpring GT (Varia), Agilent recommends that you run the **Uninstaller.exe** file provided in the **..\SiliconGenetics\Uninstaller Data** directory.

If you are upgrading from an older version, this path is likely to be different from the one you originally used. Users who upgrade will not modify any of the files in their original installation directory by doing so.

- 1 Log in as a user with read/write privileges (such as **Administrator** on Windows systems).
- 2 Quit any applications you are running.

- 3 Do not use the same name for the Varia 1 and GeneSpring GT 2 directories. Using the same name for both directories would result in important files being overwritten:
 - **..\Varia\data\variapreferences** file
 - **..\Varia\data\Programs** directory
 - **..\Varia\data\Script** directory
 - **..\Varia\data\Chron** genome directory
 - **..\Varia\data\Cache** directory
- 4 Use **Add-Remove Programs** to remove the previous installation of Varia software.
- 5 In your Web browser, go to <http://www.chem.agilent.com/cag/bsp/SiG/Products/2/DemoDownload.asp> and complete the online form to download GeneSpring GT 2 (Varia).
- 6 Download the GeneSpring GT (Varia analysis workbench) software. See “[Step 1. Download the GeneSpring GT \(Varia analysis workbench\) installation package](#)” on page 10.
- 7 Complete the installation. See “[Step 2. Install GeneSpring GT 2 \(Varia analysis workbench\)](#)” on page 11.
- 8 If you are using a complete human genome, complete the steps in “[To upgrade to the Build 35 genome](#)” below.
- 9 To port your Varia 1 data to GeneSpring GT 2, complete the following steps:
 - a Copy the **Homo Sapiens build 34v2 dbSNP 119** directory from ..\Silicon Genetics\Varia\Data to ..\Agilent\GeneSpring GT\Data.
 - b Copy the **..\Varia\data\variapreferences** file to ..\Agilent\GeneSpring GT\Data; do not rename the file. Doing this overwrites the newer file, but retains the preferences you specified in Version 1.
 - c Copy and paste all your Version 1 directories, *except the Cache directory*, into the new **Agilent** directory.

GeneSpring GT 2 creates a new **Cache** directory when you use the product.

To upgrade to the Build 35 genome

GeneSpring GT 2 includes a more recent build of the human genome, Build 35. Users are encouraged to begin using this genome, as it contains a more exhaustive list of variations and uses a more recent alignment to describe the human sequence.

Agilent strongly recommends that you do not attempt to transfer data generated in build 34 (such as variation lists, samples, experiments, haplotype map, and sequence region lists) directly into the Build 35 genome. If you want to re-analyze your data using Build 35, re-import your data, starting from the raw text files generated from the original genotyping technology.

NOTE

Do not simply export a **.zip** file from an old genome and drag it into the new genome. Instead, import data from the original raw data files. One reason for this is that any variations that were in the original data files, but not in the original genome, were ignored in that genome. If those variations are available in the new genome, they will be included when the user imports the raw data.

Genetic maps appropriate to the genome will be incorporated into new genomes Agilent releases.

Pedigrees are an exception to this rule, provided that you remove the links to the old samples and replace them with links to new samples.

Several changes in Build 35 make it impossible to compare data generated using NCBI Build 34 (in Varia 1) and using Build 35. For example, with the new alignment (in Build 35), the physical positions of many SNPs have been updated. This means that existing haplotype maps will contain blocks that include non-adjacent loci. In other cases, two different SNPs in Build 34 (with different RS numbers) have been assigned to the same physical location in Build 35. Therefore, the safest method to analyze data in Build 35 is to re-import it from raw data files.

Agilent converts each new NCBI build into a format that GeneSpring GT can use.

- 1 Install Build 35 as a new genome. See “[Step 5. Download genome data](#)” on page 20.
- 2 If you have modified your previous version of the genome (for example, by adding custom variations), transfer the modifications into the new genome. You will not need to repeat all of your changes in the new genome.
 - a Open the genome folder in the `..\Varia\data` directory.
 - b Copy the modifications to Build 34. The name of the file to copy ends with `_diff.txt`.
 - c Copy the file ending with `_diff.txt` into the genome folder of the new genome. See Figure 2.
 - d Modify the `..\GeneSpring GT\data\<genome name>*.genomedef` file in the new genome.
 - Open the new genome’s `.genomedef` file in a text editor.
 - Under the line that begins `Variations :`, add the following line:

```
VariationsCustom : <name-of-the-*_diff.txt-file>
```

For example:

```
VariationsCustom : Homo Sapiens Build 33 12.1.2003_diff.txt
```

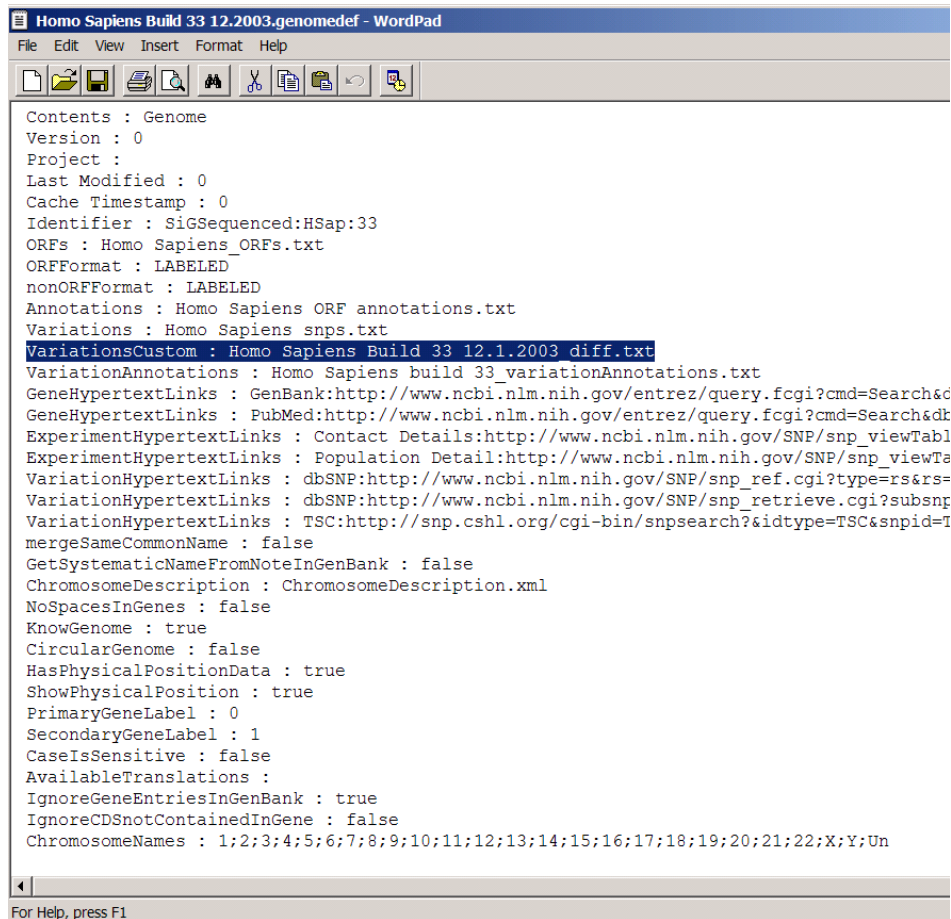


Figure 1 Editing the **genomedef** file

3 Re-import the original raw data from the old genome into the new genome.

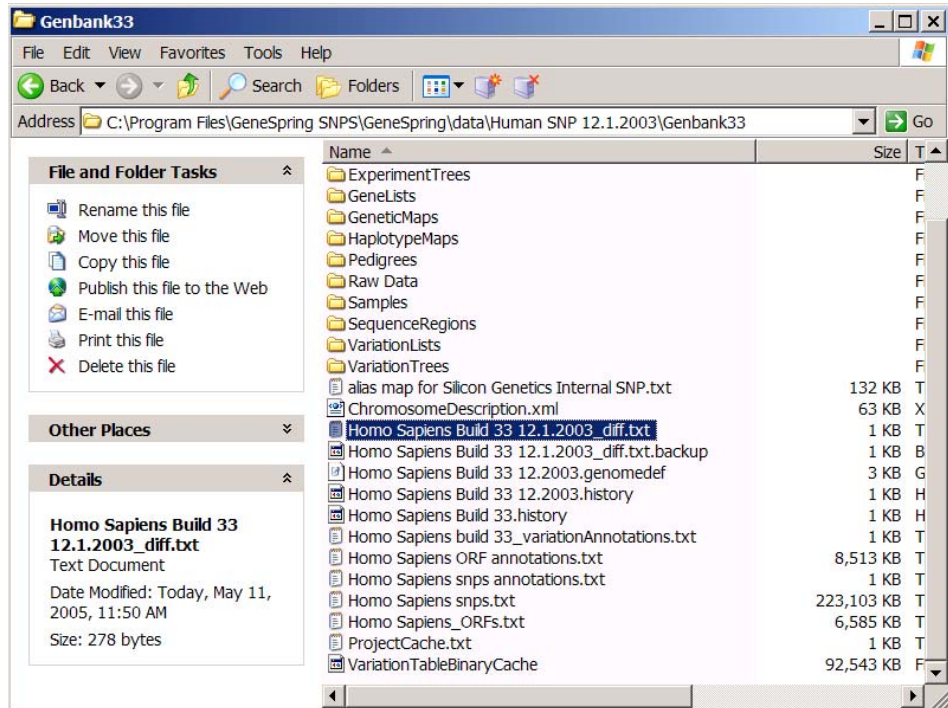


Figure 2 Preparing to re-import data from the old genome into the new genome

- 4 You will need to recreate the results of analyses (such as Haplotyped Data, variation lists, and sequence regions), using the “new” data. See the Varia Analysis Workbench User’s Guide.

NOTE

If any of the variations have changed location (and many do in new assembly builds), the results of the analyses on the same data (with no new variations) will still be different.

Step 1. Download the GeneSpring GT (Varia analysis workbench) installation package

- 1 Open your Web browser and copy the following URL into the URL field:
<http://www.chem.agilent.com/cag/bsp/SiG/Products/2/DemoDownload.asp>
- 2 Complete the online form and click **Submit**.
To clear the form and start over, click **Reset**.
- 3 Download the **GeneSpring GT2_0 Installer**, and proceed to “[Step 2. Install GeneSpring GT 2 \(Varia analysis workbench\)](#)” below.

Step 2. Install GeneSpring GT 2 (Varia analysis workbench)

By default, the GeneSpring GT (Varia analysis workbench) installation program installs three items in the main directory (..\Agilent) on Windows systems, and two items on Mac OS X systems:

- A **GeneSpring GT** folder: contains such files as the installation program, sample data, and help files.
- A **GeneSpring_GT_InstallLog.xml** file, which summarizes the install process
- Windows only: A Java folder (**gsgtjre**): contains Java-related files and libraries. (A java folder is not included with the GeneSpringGT for Macintosh installer because Mac OS X already has its own java—Apple’s Java 1.4.2_09.)

The default destination directory is **Program Files\Agilent\GeneSpringGT** on Windows systems; **/Users/<user login name>/Agilent/GeneSpringGT** on Mac OS X.

- 1** Make sure you are logged on as a user with read/write privileges (such as **Administrator** on Windows systems).
- 2** Make sure your system meets the minimum requirements listed in “[System requirements](#)” on page 3.
- 3** Close all applications, and run **GeneSpring GT.exe**.
- 4** The installation program displays an introductory page. Click **Next**.

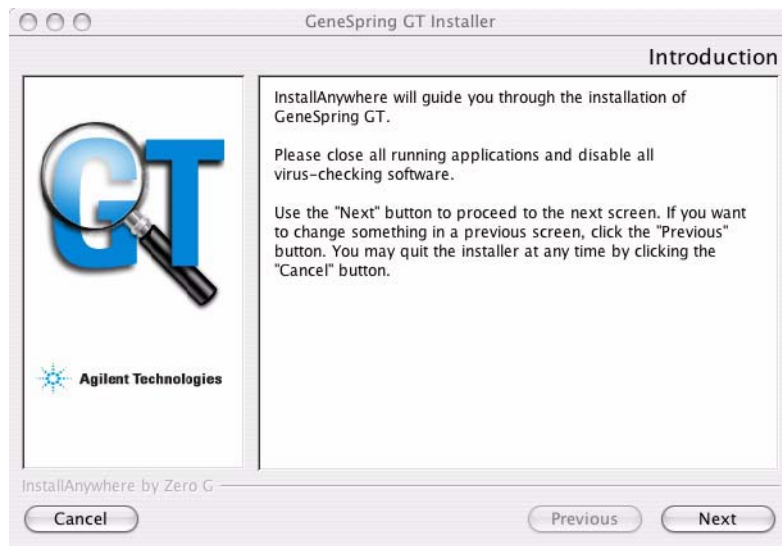


Figure 3 The introductory GeneSpring GT (Varia analysis workbench) installation page.

- 5** Read the terms of the license agreement. Click **I accept...** or **I do not accept...**. You must accept the terms of the license agreement in order to continue with installation.
- 6** Click **Next**.
- 7** Read the Version Notes/Important Info page, and click **Next** until the installer displays the Choose Install Folder page.

NOTE

Macintosh users: Be sure to read items 4 and 5 in the Version Notes.

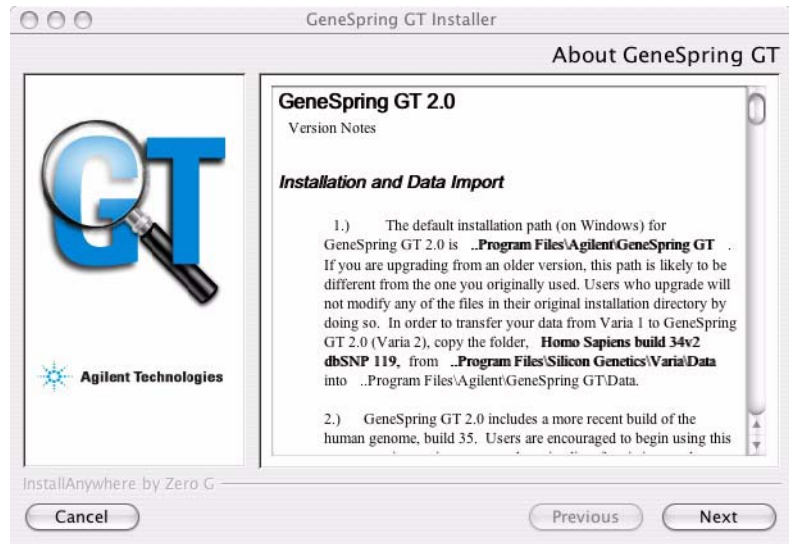


Figure 4 The Version Notes page.

- 8** Specify where the system should install the GeneSpring (Varia) software.
 - Agilent recommends that you accept the default location (on Windows: **C:\Program Files\Agilent**. On Mac OS: **/Users/<user login name>/Agilent/GeneSpringGT**).
 - To specify a different location, click **Choose**.
 - To reinstate the default location, click **Restore Default Folder**.
- 9** Click **Next**.

10 Review the **Pre-Installation Summary** page.

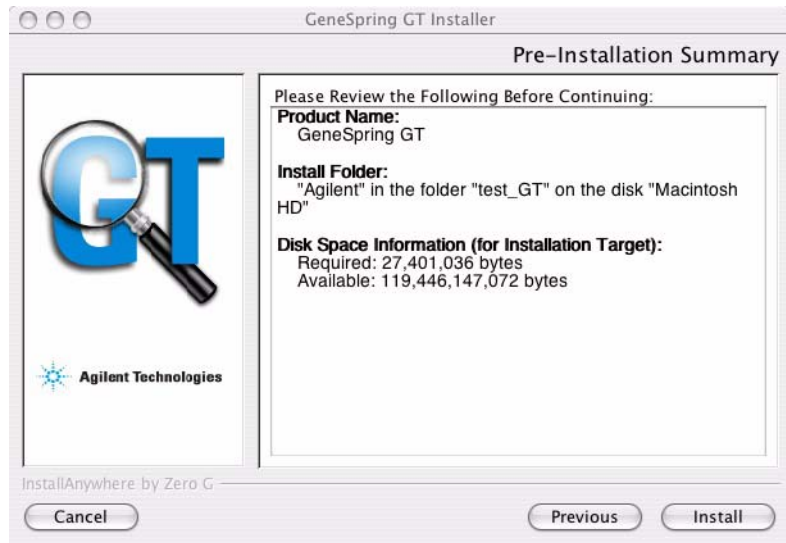


Figure 5 The **Pre-Installation Summary** page.

- If the information is correct, click **Install**.
- If the information is not correct, click **Previous** as many times as necessary and make the appropriate changes.

11 After installing GeneSpring, the installer displays the **Version Notes** page again ([Figure 4](#) on page 13). Click **Next**.

12 The next installer page asks if you would like to view the QuickStart Guide. Click **Yes** or **No** and then click **Next**

13 The installer displays a reminder for you to download a genome. This is optional, but most users do so.

NOTE

You can click on the Web link in the installer to download a genome. However, if you do so, you must complete the GeneSpringGT installation when you are finished downloading the genome.

See [“Step 5. Download genome data”](#) on page 20 for information about downloading a genome.

14 Click **Done** on the **Install Complete** page of the installer.

The system launches GeneSpring (Varia) automatically.

15 Enter license information. See [“Step 3. Enter license information”](#) on page 16.

16 GeneSpring GT (Varia) displays a **Helpful Hint** dialog box. Click **OK** to continue without reading the hints, and **Details** to read them.

17 Select the genome to open. If you have not downloaded a complete genome, select **Crohns Mini-Genome** and click **OK**.

18 Configure GeneSpring (Varia) for compatibility with your system. Follow the steps in [“Step 4. Configure GeneSpring GT \(Varia analysis workbench\)”](#) on page 19.

19 If you will be using a complete genome, do one of the following if you have not already done so:

a Download the genome data. See [“Step 5. Download genome data”](#) on page 20.]

b If you are migrating from GeneSpring GT (Varia) Version 1 to Version 2, and you are using the human genome, complete the steps in [“To upgrade to the Build 35 genome”](#) on page 6.

Step 3. Enter license information

You need to enter Agilent-supplied license information to use GeneSpring GT (Varia analysis workbench).

If you downloaded GeneSpring (Varia) on a trial basis, you can use the product for one day, but you need to purchase a license to continue to use it.

NOTE

If you renew your license in order to upgrade from GeneSpring GT Version 1 to Version 2, you do not have to go through the installation process to enter your new license info. Instead, when Agilent sends you the **licensekey.txt** file, download it to your GeneSpring GT (Varia) directory (by default, ..\Agilent\data).

- 1 Click the GeneSpring GT icon to start the program, if it is not already started.



Figure 6 The GeneSpring GT desktop icon

- 2 When you start GeneSpring (Varia) for the first time, or before you have a permanent license, the system displays the **Permanent license entry** dialog box (Figure 7).



Figure 7 Permanent license entry dialog box

- 3 If you click **No**, the system displays the **Online Demo License Registration** form (Figure 8). Complete the form, click **Submit Registration**, and continue with step 6.

When you complete this form, Agilent sets up a temporary license for you, and automatically makes it permanent when you purchase the license. You do not need to enter a separate “permanent license” later.

Online Demo License Registration

Please fill out the following form to request your free demo license. Bold entries are required. Please use only standard Roman characters for all fields.

Title	<input type="text"/>	ZIP/Postal Code	<input type="text"/>
First Name	<input type="text"/>	Country	<input type="text"/>
Last Name	<input type="text"/>	Phone	<input type="text"/>
Company Name	<input type="text"/>	Fax	<input type="text"/>
Department	<input type="text"/>	Email Address	<input type="text"/>
Address	<input type="text"/>	How did you hear about us	Choose below ▾
Address2	<input type="text"/>	Type of Institution	Choose below ▾
City	<input type="text"/>	In what region are you located?	Choose below ▾
State/Province	<input type="text"/>	MicroArray Technology	Choose below ▾

Submit Registration

Figure 8 Online demo license registration form

- 4 If you click **Yes**, the system displays the **Enter License** dialog box (Figure 9).

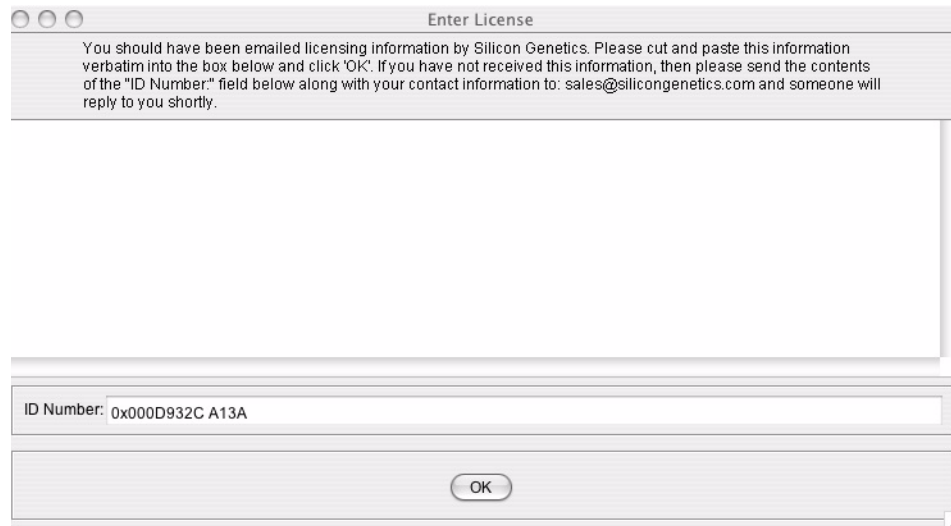


Figure 9 The Enter License dialog box.

- 5 Open the **licensekey.txt** file. Paste the entire contents of **licensekey.txt** into the top text box in the **Enter License** dialog box.

The **ID Number** field displays your computer's Ethernet address.

- 6 The GeneSpring (Varia) program starts, and prompts you to select a genome to open. Select the desired genome and click **OK**.

If you have any problems getting a license to run GeneSpring GT (Varia), contact Agilent technical support (sig_support@agilent.com) and provide them the information (including **ID Number** field) in [step 5](#) above.

Step 4. Configure GeneSpring GT (Varia analysis workbench)

Change the memory preferences

GeneSpring GT (Varia) installation assumes you have the required resources to run the program, as specified on the Agilent GeneSpring Web site. Agilent recommends that you use the default value, but if you need to increase the memory, follow these steps.

- 1 Double-click the GeneSpring GT icon to start the GeneSpring GT (Varia analysis workbench) program.
- 2 Choose **Edit > Preferences**.
- 3 Click the **System** tab.
- 4 Set the value in **Desired Memory Use** to the desired value. Agilent recommends that you use the default value (700 MB), or set it to about 2/3 of your available RAM.
- 5 Click **Apply** or **OK**.

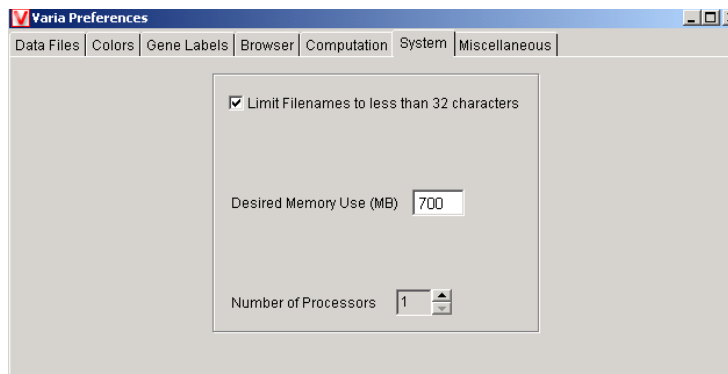


Figure 10 The System tab, where you can specify memory resources for GeneSpring (Varia).

To further optimize performance, you can edit the Java heap size (Windows: **Program Files\Agilent\GeneSpring GT\varia.lax**). *Contact Agilent technical support (sig_support@agilent.com) if you want to do this step.*

Step 5. Download genome data

This install package includes variation data from a small section of Human Chromosome 5 that was used to study Crohn's disease. The installation also includes a small section of sequence that spans the region in question. Agilent provides sample genome data in the installation package, rather than a complete genome, to let you download GeneSpring (Varia) quickly.

Most users will want to download NCBI Build 35 of the complete human genome (the complete human sequence, and the complete list of variations). This file is available from the Agilent Web FTP site using the same password you used to download this install package. You can also download the NCBI Build 32 of the complete mouse genome at the Agilent Web FTP site.

If you want to download a different genome, contact your Agilent representative.

NOTE

If you are migrating from GeneSpring GT Version 1 to 2, do not follow the instructions in this section; instead, follow the instructions in ["To upgrade to the Build 35 genome"](#) on page 6.

NOTE

The genome data files for GeneSpring GT (Varia analysis workbench) are very large (about 1 GB). Be aware that the data might take a long time to download.

- 1 Open a Web browser, and enter the following URL in the address field:
<http://www.chem.agilent.com/Scripts/Generic.ASP?lPage=35399>

2 Double-click the genome (human or mouse) that you want to download.

Download instructions:

1. Download the appropriate installer for your operating system. (Save it somewhere you can find it).
2. Run the Installer file. (Click **View** under **Instructions** below for your specific operating system).
3. Follow the installation wizard.
5. Download the [GeneSpring GT Quick Start Guide](#) to help you start your analysis.


Platform	Installer	Genomes
 Windows	Download (30.5 MBytes)*	Human NCBI Build 35 (994 Mbytes) Mouse NCBI Build 32 (716 Mbytes)


Figure 11 Part of the Agilent FTP site for downloading genomes

3 Specify where you want to download the **.zip** file.

4 Download the genome.

Download instructions:

1. Download the appropriate installer for your operating system. (Save it somewhere you can find it).
2. Run the Installer file. (Click **View** under **Instructions** below for your specific operating system).
3. Follow the installation wizard.
5. Download the [GeneSpring GT Quick Start Guide](#) to help you start your analysis.

Platform	Installer	Genomes
 Windows	Download (30.5 MBytes)*	Human NCBI Build 35 (994 Mbytes) Mouse NCBI Build 32 (716 Mbytes)

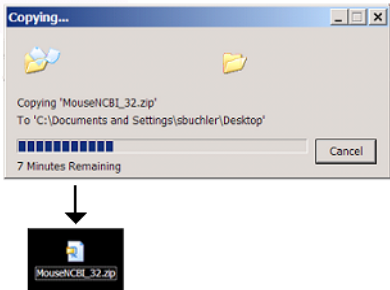


Figure 12 Downloading a genome

- 5 Open GeneSpring GT (Varia). In the GeneSpring GT (Varia) window, do *one* of the following:
 - a Select **File > Import Varia Zip**
 - b Drag the genome **.zip** file into the GeneSpring GT (Varia) window.

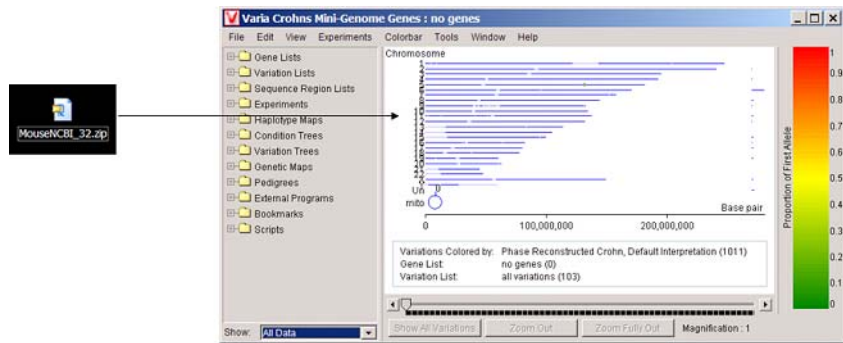


Figure 13 Importing a genome into GeneSpring GT (Varia)

- 6 The system displays a confirmation dialog box. Click **Yes** if you are sure you want to import the specified **.zip** file into the current genome, or **No** to cancel the import.

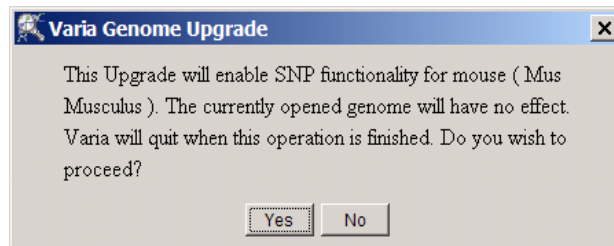


Figure 14 Genome upgrade confirmation dialog box

- 7 After importing the genome, the system prompts you to close GeneSpring GT (Varia). Click **OK**.
- 8 Start GeneSpring (Varia) again. If GeneSpring (Varia) does not prompt you to select a genome upon startup, select **File > Open Genome or Array**, and select the name of the genome you just imported.

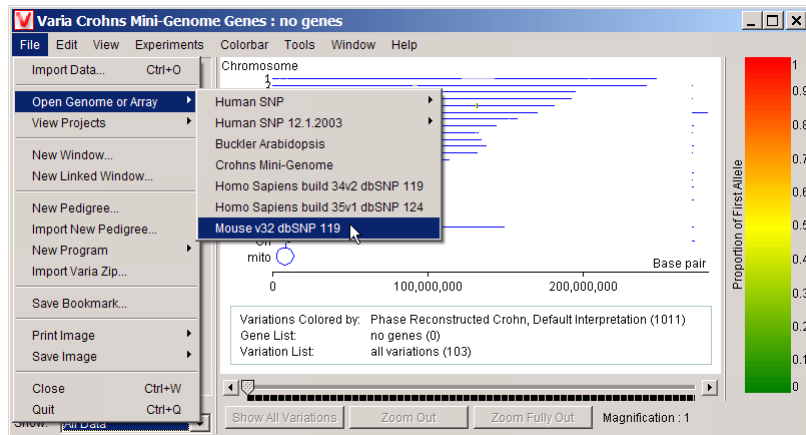


Figure 15 Selecting a genome to open

9 GeneSpring GT (Varia) loads the genome.

To uninstall GeneSpring GT or Varia analysis workbench)

- To uninstall Varia 1, run **Uninstaller.exe**, located in the `..\SiliconGenetics\Uninstaller Data` directory.
- To uninstall GeneSpring GT 2:
 - On Windows systems, run the **Uninstall GeneSpring GT.exe** file provided in the `..\Agilent\GeneSpring GT\Uninstaller Data` directory.
 - On Mac OS X systems, double-click **Uninstall GeneSpring GT** in the `/Users/<user login name>/Agilent/GeneSpringGT/UninstallerData` folder.

Contacting Agilent Technical Support

If you need technical support, contact Agilent at sig_support@agilent.com.

To expedite the support process, follow these steps:

Windows users

- 1 From the GeneSpring (Varia) main window, select **Help > About**.
- 2 Take a screenshot of the splash screen, making sure to note:
 - the license serial number
 - the operating system
 - the current JVM that GeneSpring (Varia) is using
- 3 Exit GeneSpring (Varia).
- 4 Use Notepad to open **Program Files\Agilent\Varia\varia.lax**.
- 5 Scroll to the line `lax.stderr.redirect=`
- 6 Set this value to `console`.
- 7 Scroll to the line `lax.stdout.redirect=`
- 8 Set this value to `console`.
- 9 Save and exit the **varia.lax** file.
- 10 Restart GeneSpring (Varia). See if you can reproduce your problem with the console running.
- 11 Take a screenshot of the console if stack traces or exceptions are thrown.

Macintosh users

- 1 From the GeneSpring (Varia) main window, select **Help > About**.
- 2 Take a screenshot of the splash screen, making sure to note:
 - the license serial number
 - the operating system
- 3 Exit GeneSpring (Varia).
- 4 In the `/Users/<user login name>/Agilent/GeneSpring GT/data` folder, right-click the GeneSpringGT executable icon.
- 5 Select **Show Package Contents**, and open the **Contents** folder.
- 6 Open the **Info.plist** file with TextEdit (right-click **Info.plist** and select **TextEdit**). TextEdit is in the Mac OS `/Applications` folder.
- 7 Scroll to the line `stderr.redirect=`
- 8 Set this value to `console`.
- 9 Scroll to the line `stdout.redirect=`
- 10 Set this value to `console`.
- 11 Save and exit the **Info.plist** file.
- 12 Restart GeneSpringGT (Varia). See if you can reproduce your problem with the console running.
- 13 Take a screenshot of the console if stack traces or exceptions are thrown.