MUTATION Surveyor®

DNA Variant Analysis Software

Importing External Database Annotation

dbSNP, COSMIC, dbNSFP

SOFTGENETICS®

Software PowerTools for Genetic Analysis

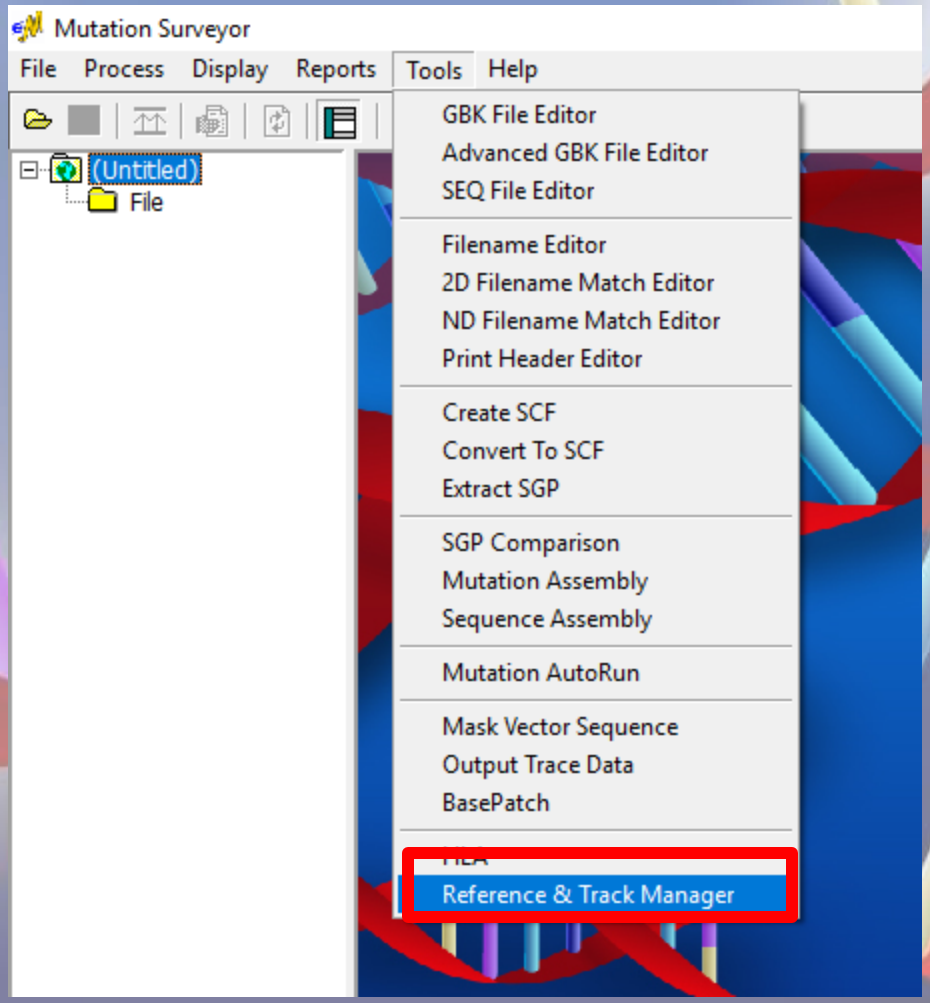
www.softgenetics.com / info@softgenetics.com

Mutation Surveyor Track Manager

- Mutation Surveyor software (5.0 and above) is able to import data from the dbNSFP, dbSNP, and COSMIC databases. Custom variation files may also be imported.
- Importing database information first requires the import of a whole human genome reference. Databases are installed specific to this reference.
- NextGENe software users may import and query data from same directory as NextGENe track manager.

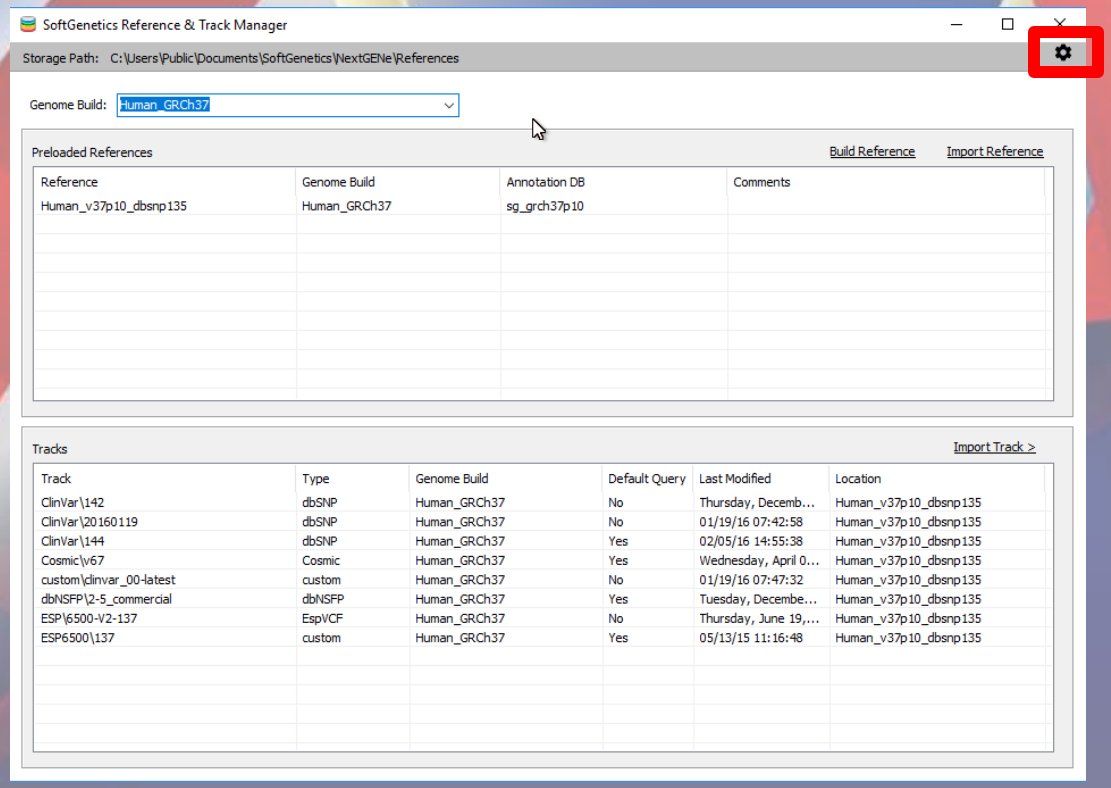
Importing Reference Files

- To import a whole human genome reference, right click Mutation Surveyor icon and select “Run as Administrator”.
- Navigate to the tools menu and select the “Reference & Track Manager” option.



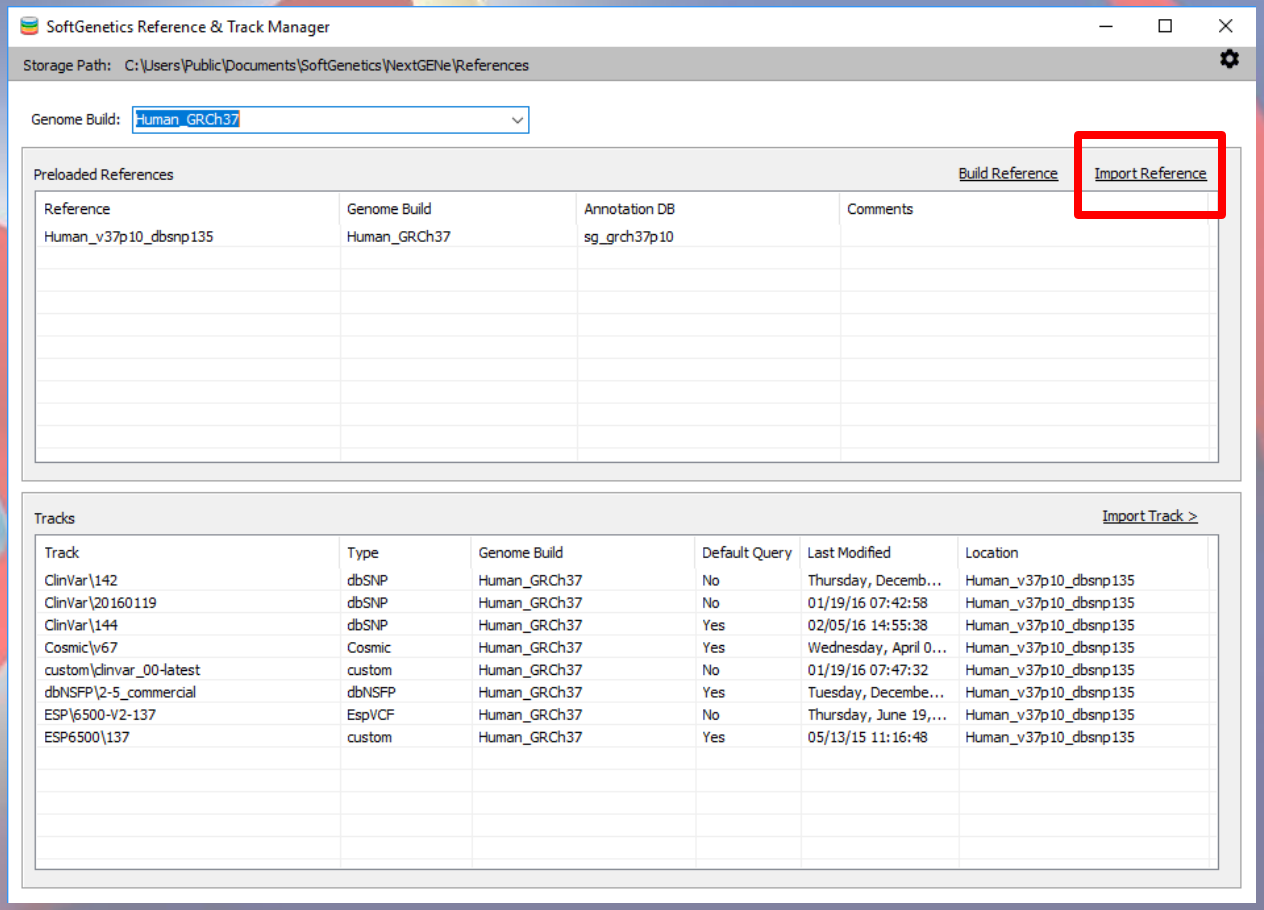
Selecting Reference Files

- If references have previously been imported by NextGENe software, you may select the directory



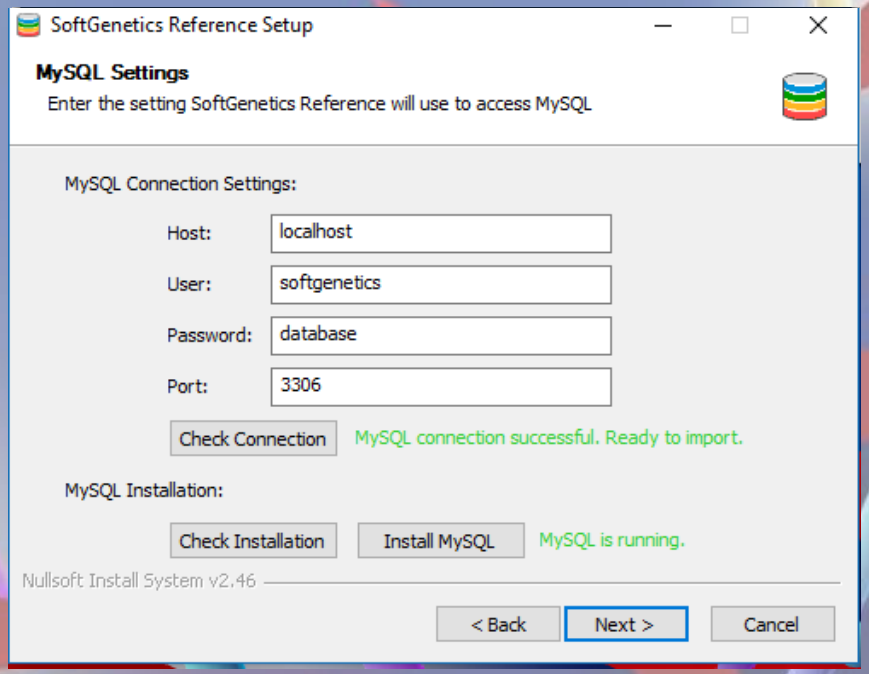
Importing Reference Files

- Click on the Import Reference link



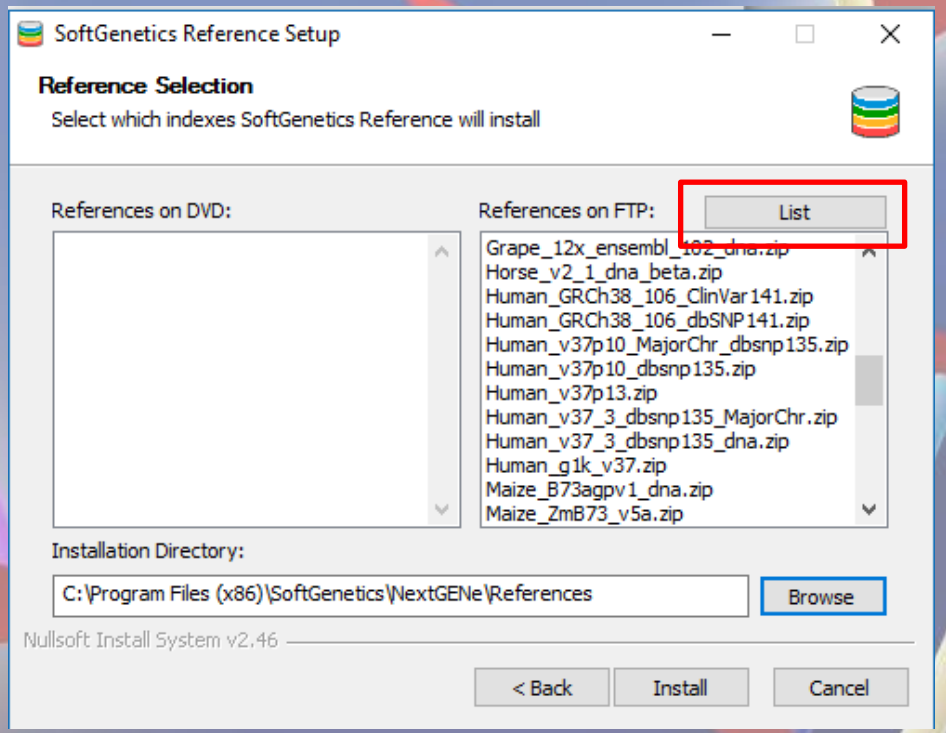
Import Reference Wizard

- Check MySQL connection. If connection failed because MySQL is not installed, click Install MySQL and proceed to next step.
- Messages will be green if the reference is ready for import.
- Click “Next” to continue to reference selection step



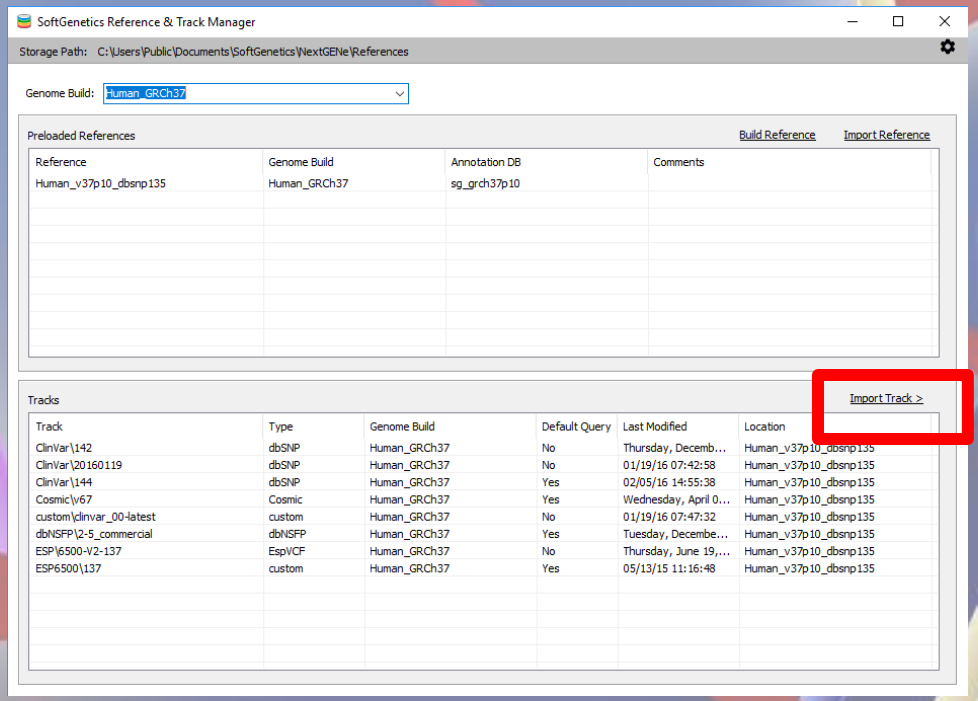
Import Reference Wizard

- To select and download a reference from our FTP server, select the “List” button.
- We recommend downloading Human_v37p13_105.zip.
- If you would like a DVD of a specific reference mailed to you, contact tech_support@softgenetics.com.
- After reference is selected, enter the installation directory at the bottom of the window
- Click install to install reference to directory. This process may take a few hours to complete.



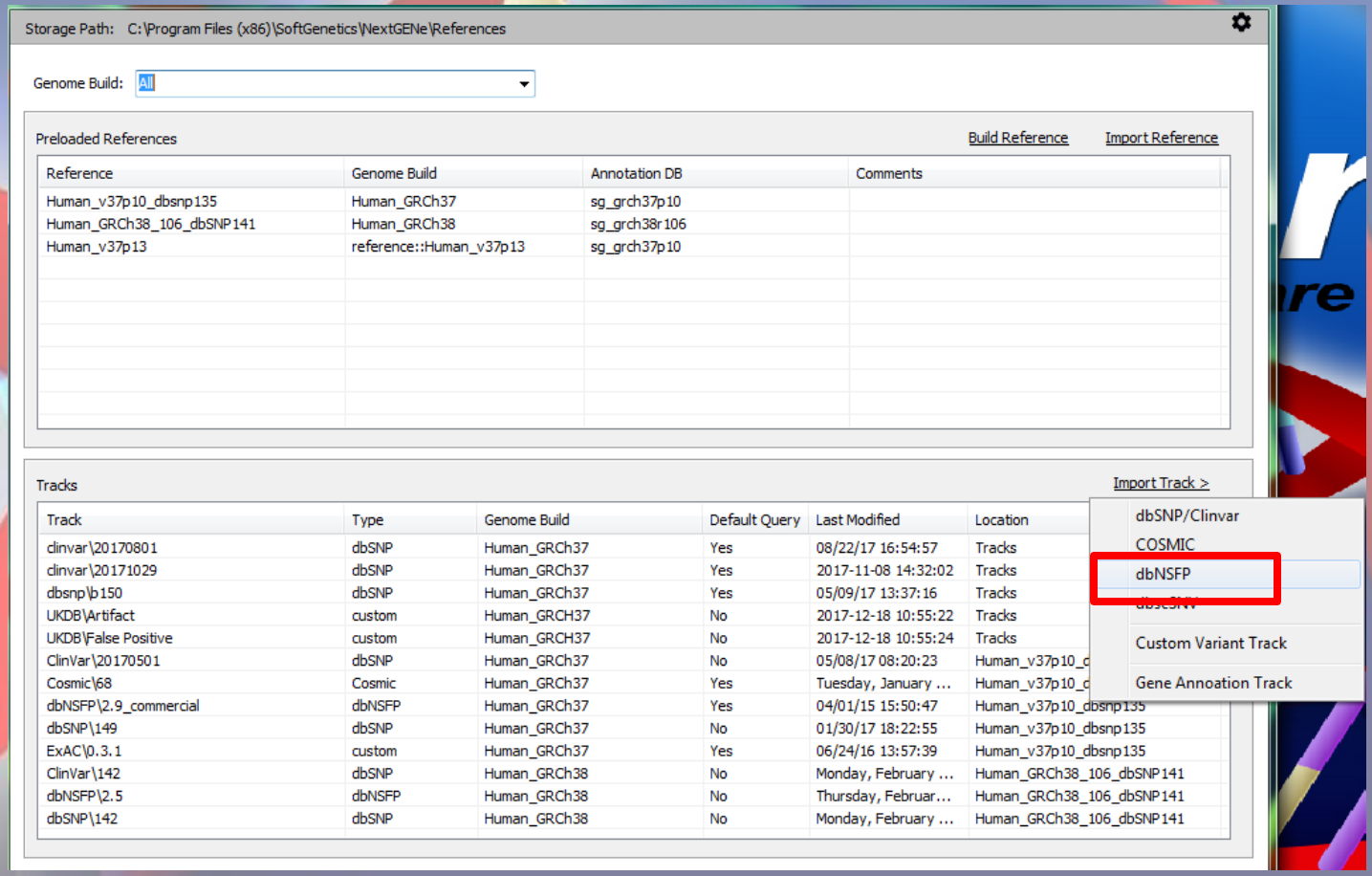
Importing External Databases

- After selecting the reference directory, return to the Track Manager window to import external databases.
- To begin the process, select the Import Tracks link.



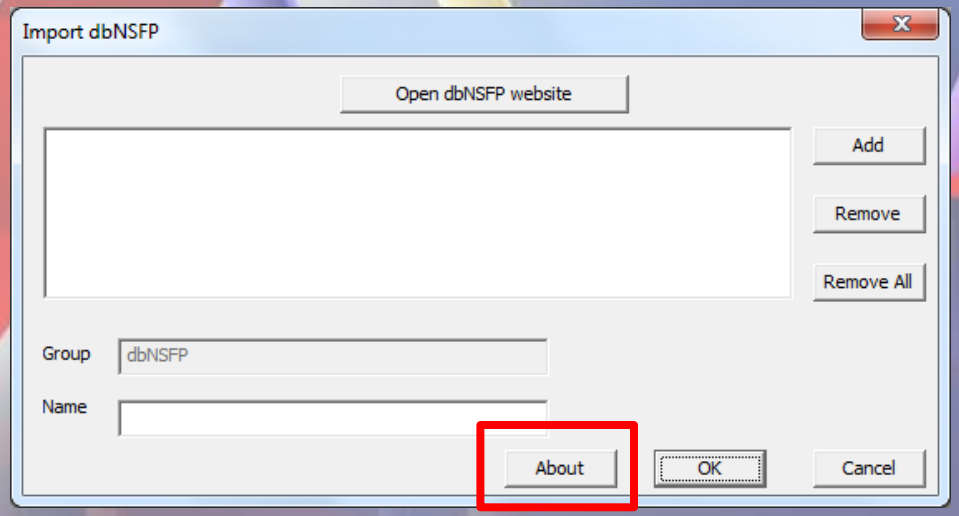
Importing dbNSFP

- Click “Import dbNSFP”



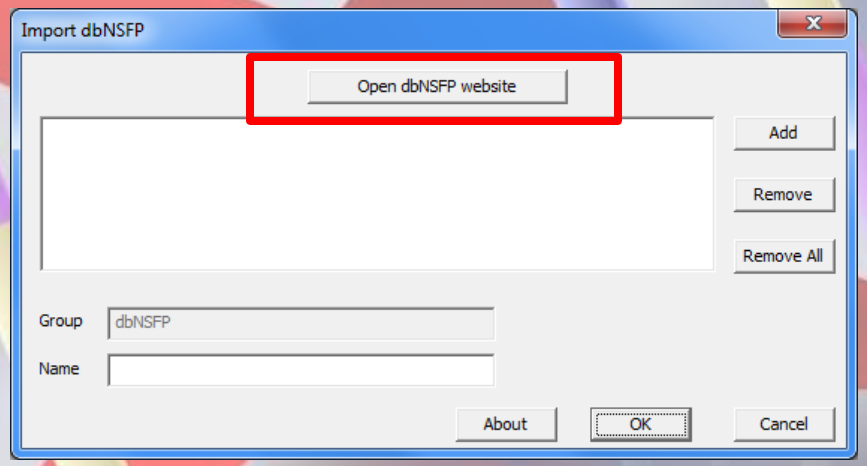
Importing dbNSFP

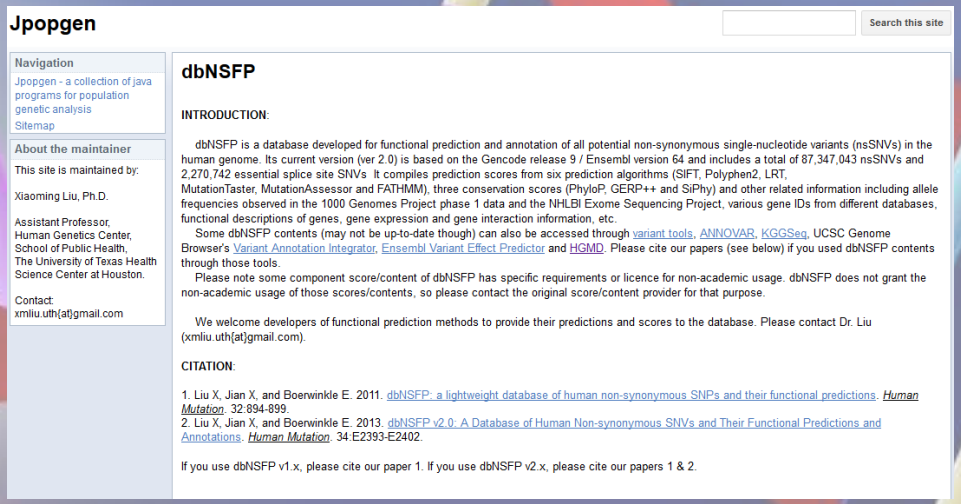
- A link to the paper for dbNSFP can be found by clicking the “About” button in the Import dbNSFP dialog



Importing dbNSFP

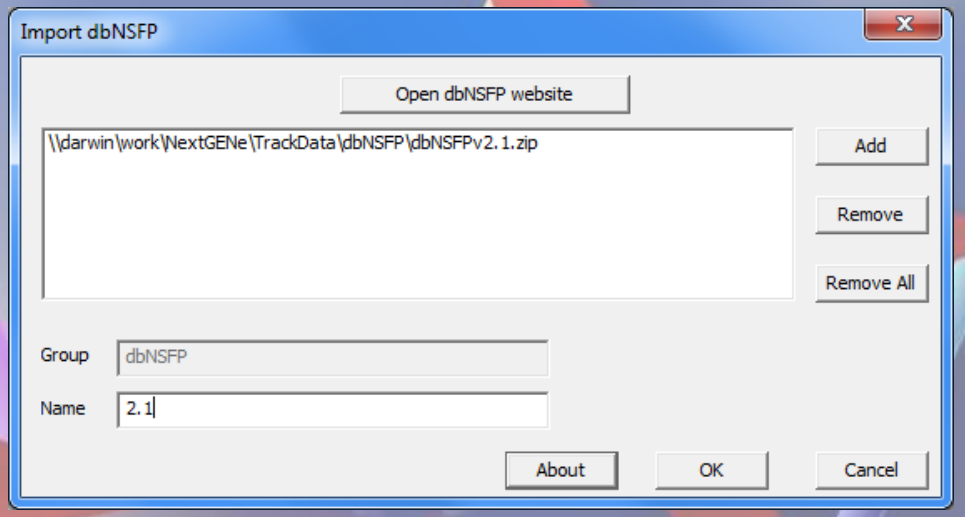
- Click the “Open dbNSFP website” button to download the database from the dbNSFP web page.
- The latest support version is v2.9.





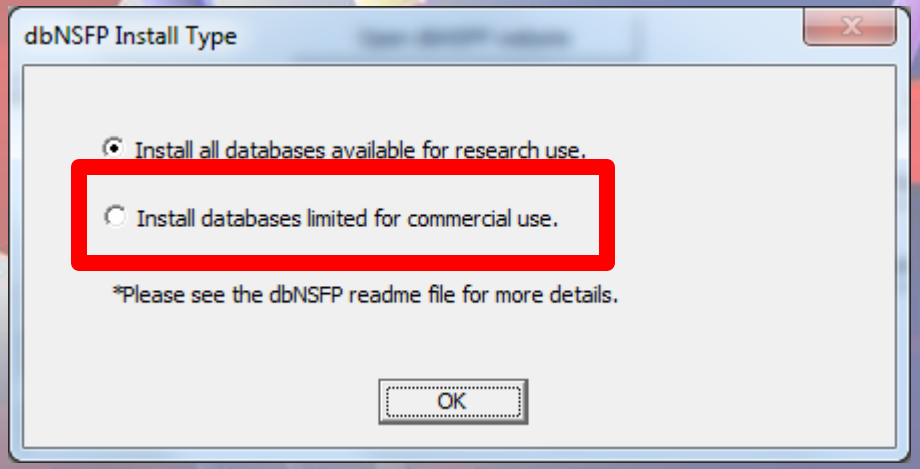
Importing dbNSFP

- Click “Add” to load the file.
- Enter Name of dbNSFP version.
- Click the “OK” button.
- Note: The original files can be deleted once the tracks have finished importing.



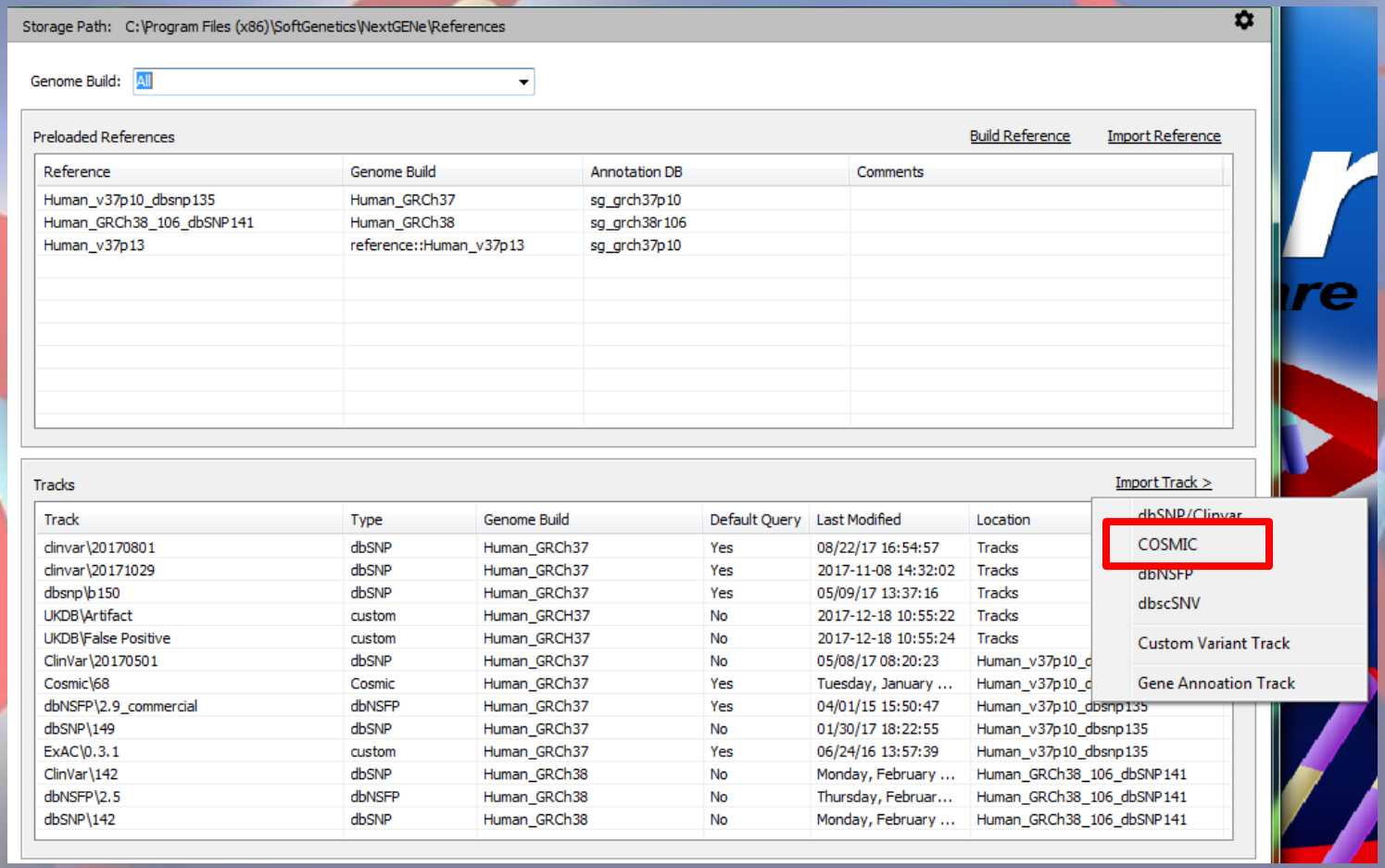
Importing dbNSFP

- Some databases are intended for research use only. Commercial users should install the commercial database.



Importing COSMIC

- Click “Import COSMIC”

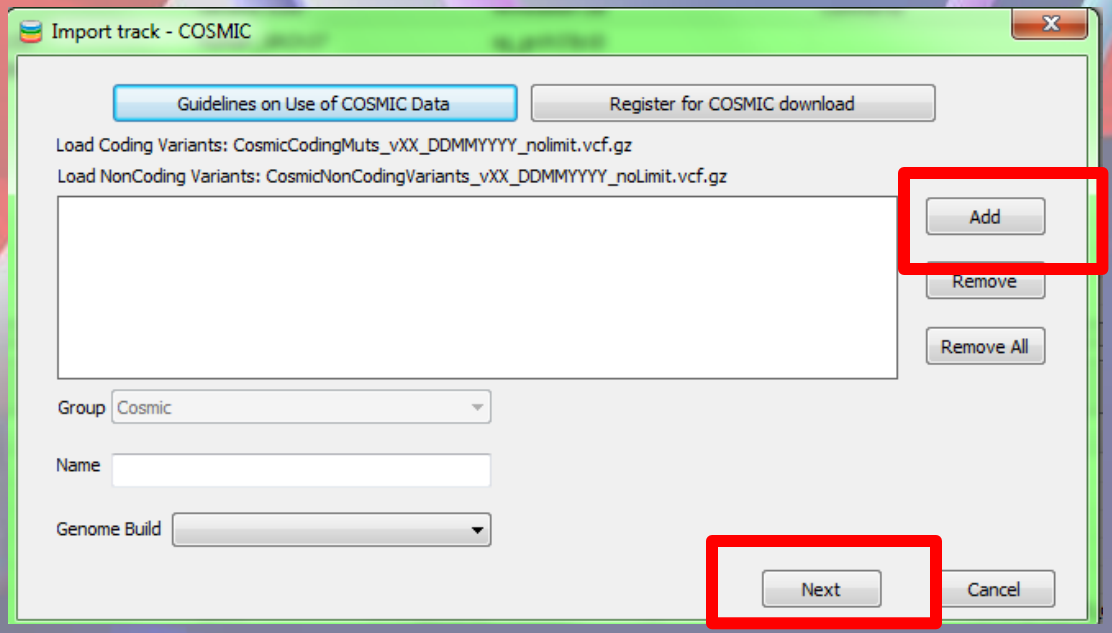


Importing COSMIC

- Registered/Licensed users must login to COSMIC site prior to download and in accordance with the terms and conditions of the licensing policy.
- Expand the VCF files list on the Data Download page.
- You can download COSMIC information for coding variants and/or non coding variants

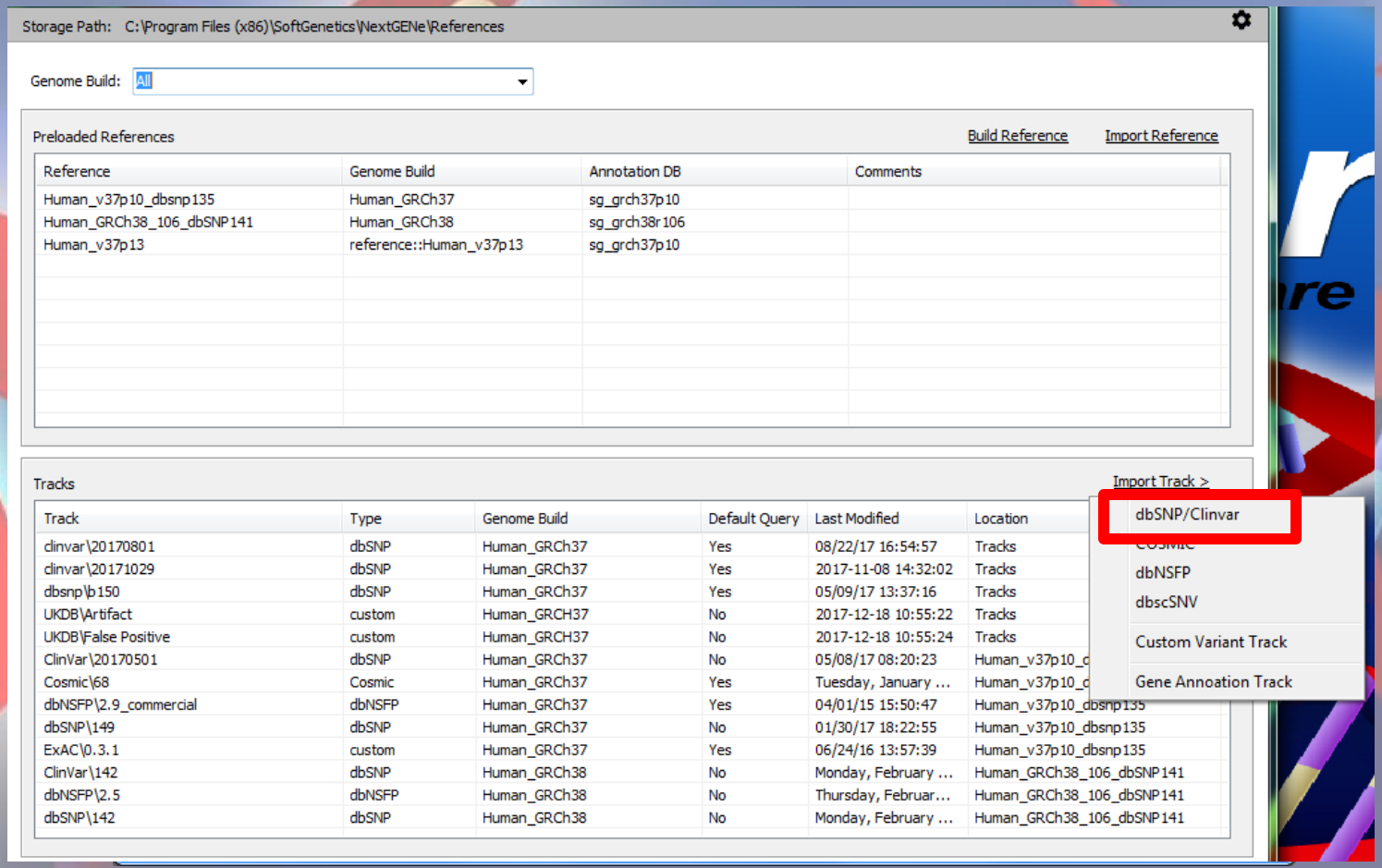
Importing COSMIC

- Click “Add” to load file(s).
- Specify the COSMIC version number or other name.
- Select appropriate genome build from dropdown
- Click “Next”.



Import ClinVar/dbSNP

- Click “Import dbSNP/ClinVar”



Import ClinVar/dbSNP

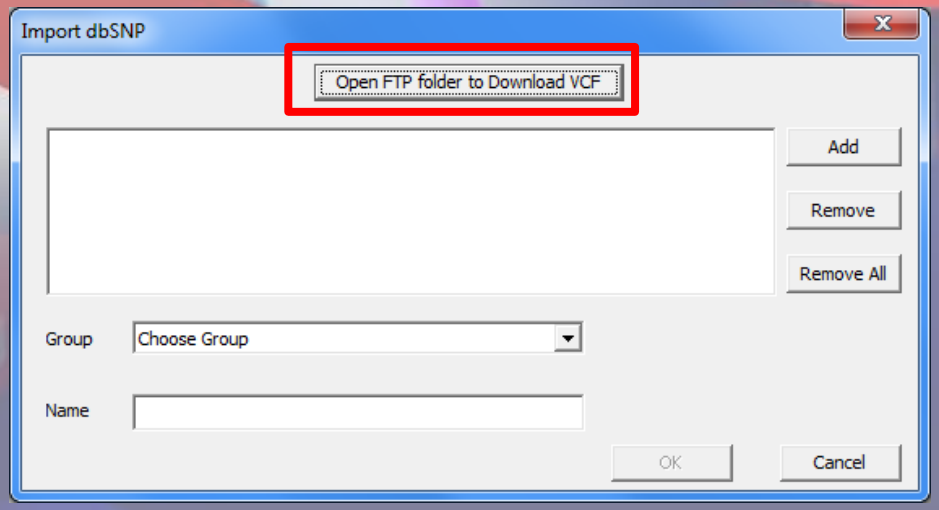
- Download files using these links or by clicking the "Open FTP Folder to Download VCF" button

GRCh37:

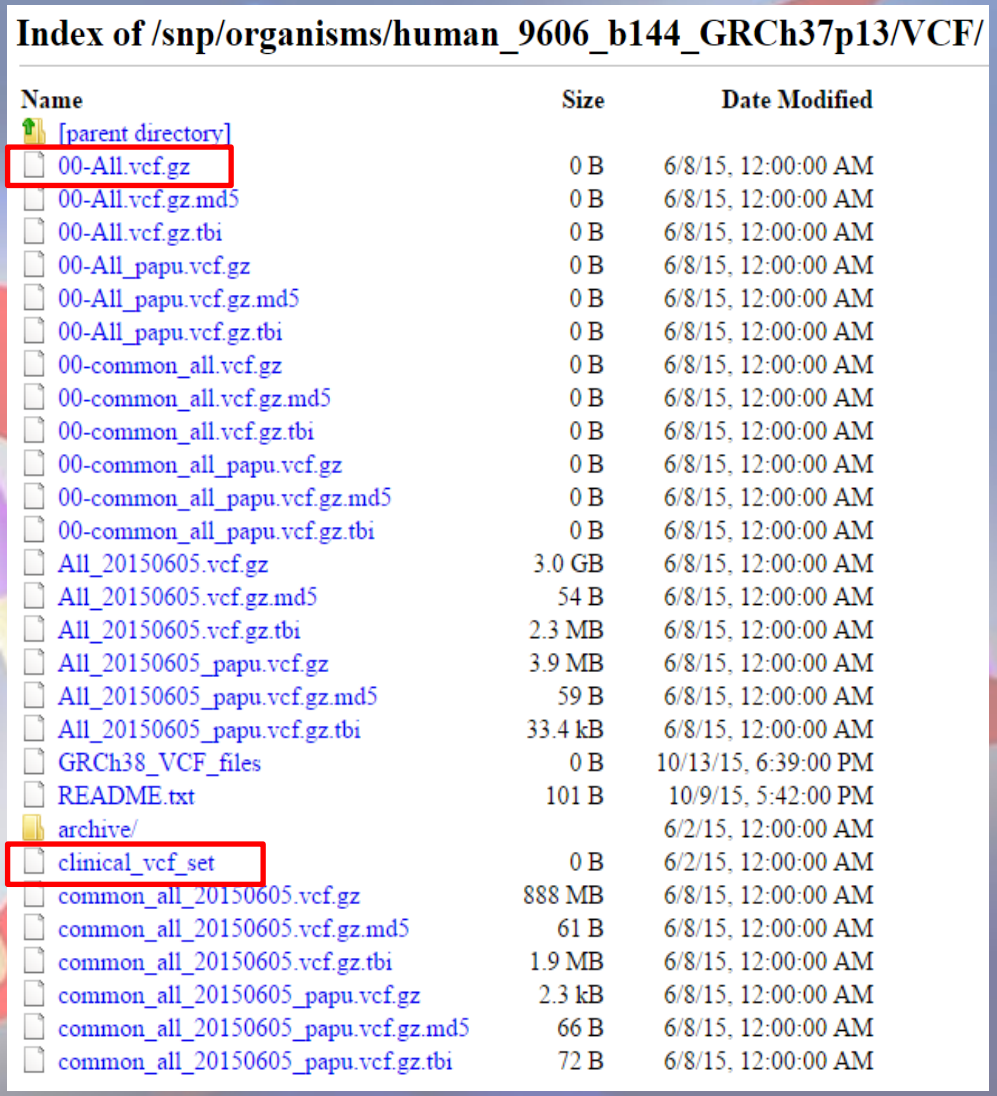
dbSNP: ftp://ftp.ncbi.nlm.nih.gov/snp/organisms/human_9606_b151_GRCh37p13/VCF/00-All.vcf.gz
ClinVar: ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/vcf_GRCh37/clinvar.vcf.gz

GRCh38:

dbSNP: ftp://ftp.ncbi.nlm.nih.gov/snp/organisms/human_9606/VCF/00-All.vcf.gz
ClinVar: ftp.ncbi.nih.gov/pub/clinvar/vcf_GRCh38/clinvar.vcf.gz



Import ClinVar/dbSNP



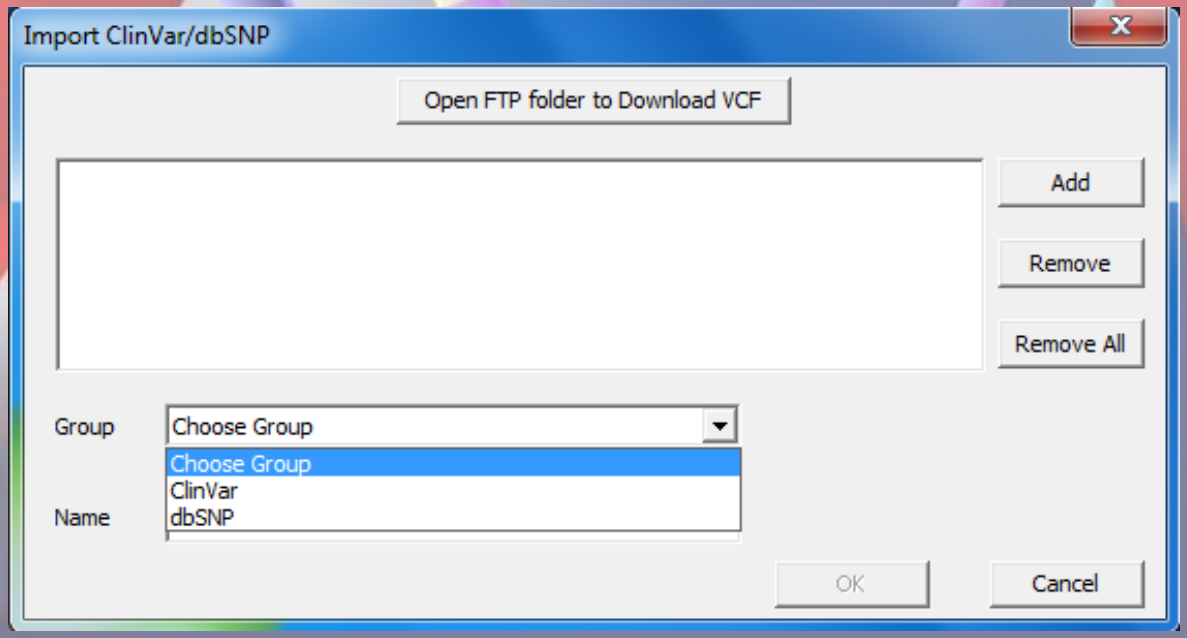
Index of /snp/organisms/human_9606_b144_GRCh37p13/VCF/

Name	Size	Date Modified
[parent directory]		
00-All.vcf.gz	0 B	6/8/15, 12:00:00 AM
00-All.vcf.gz.md5	0 B	6/8/15, 12:00:00 AM
00-All.vcf.gz.tbi	0 B	6/8/15, 12:00:00 AM
00-All_papu.vcf.gz	0 B	6/8/15, 12:00:00 AM
00-All_papu.vcf.gz.md5	0 B	6/8/15, 12:00:00 AM
00-All_papu.vcf.gz.tbi	0 B	6/8/15, 12:00:00 AM
00-common_all.vcf.gz	0 B	6/8/15, 12:00:00 AM
00-common_all.vcf.gz.md5	0 B	6/8/15, 12:00:00 AM
00-common_all.vcf.gz.tbi	0 B	6/8/15, 12:00:00 AM
00-common_all_papu.vcf.gz	0 B	6/8/15, 12:00:00 AM
00-common_all_papu.vcf.gz.md5	0 B	6/8/15, 12:00:00 AM
00-common_all_papu.vcf.gz.tbi	0 B	6/8/15, 12:00:00 AM
All_20150605.vcf.gz	3.0 GB	6/8/15, 12:00:00 AM
All_20150605.vcf.gz.md5	54 B	6/8/15, 12:00:00 AM
All_20150605.vcf.gz.tbi	2.3 MB	6/8/15, 12:00:00 AM
All_20150605_papu.vcf.gz	3.9 MB	6/8/15, 12:00:00 AM
All_20150605_papu.vcf.gz.md5	59 B	6/8/15, 12:00:00 AM
All_20150605_papu.vcf.gz.tbi	33.4 kB	6/8/15, 12:00:00 AM
GRCh38_VCF_files	0 B	10/13/15, 6:39:00 PM
README.txt	101 B	10/9/15, 5:42:00 PM
archive/		6/2/15, 12:00:00 AM
clinical_vcf_set	0 B	6/2/15, 12:00:00 AM
common_all_20150605.vcf.gz	888 MB	6/8/15, 12:00:00 AM
common_all_20150605.vcf.gz.md5	61 B	6/8/15, 12:00:00 AM
common_all_20150605.vcf.gz.tbi	1.9 MB	6/8/15, 12:00:00 AM
common_all_20150605_papu.vcf.gz	2.3 kB	6/8/15, 12:00:00 AM
common_all_20150605_papu.vcf.gz.md5	66 B	6/8/15, 12:00:00 AM
common_all_20150605_papu.vcf.gz.tbi	72 B	6/8/15, 12:00:00 AM

- Scroll down the list of organisms and select the preferred organism and database build.
- Click on the VCF folder option
- Select “00-All.vcf.gz” to begin download of the whole dbSNP database.
- To download ClinVar database, click “clinical_vcf_set” and select the file “clinvar.vcf.gz”
- For information regarding the different VCF files generated in each build, please see NCBI’s Human Variation Sets in VCF Format

Import ClinVar/dbSNP

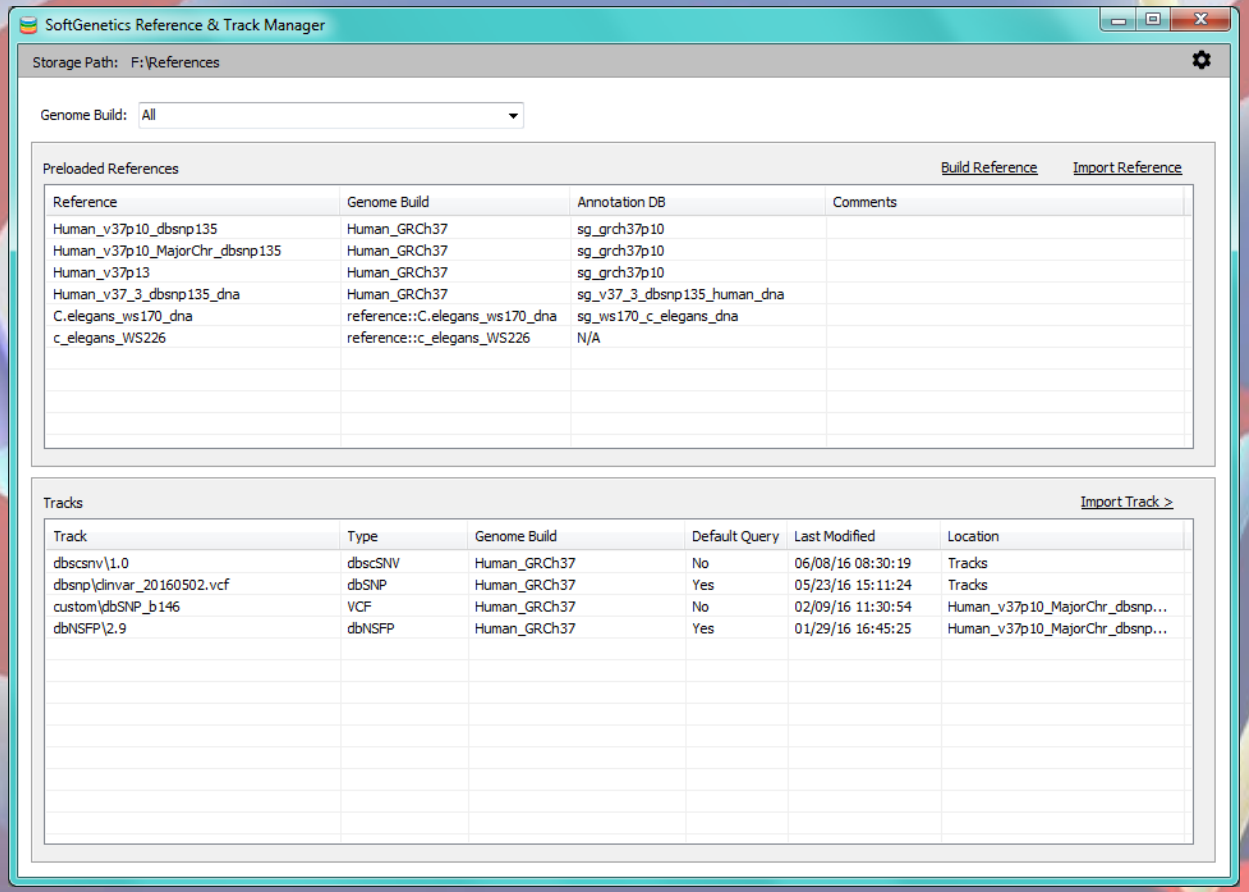
- After download is complete, select Group from dropdown and click “Add” to add database
  - Select ClinVar for clinically relevant SNPs (if downloaded)
  - Select dbSNP for common SNPs (and for 00-All.vcf.gz)
- Enter dbSNP build number in name field
- Click “OK”



Importing a Custom Variant Database

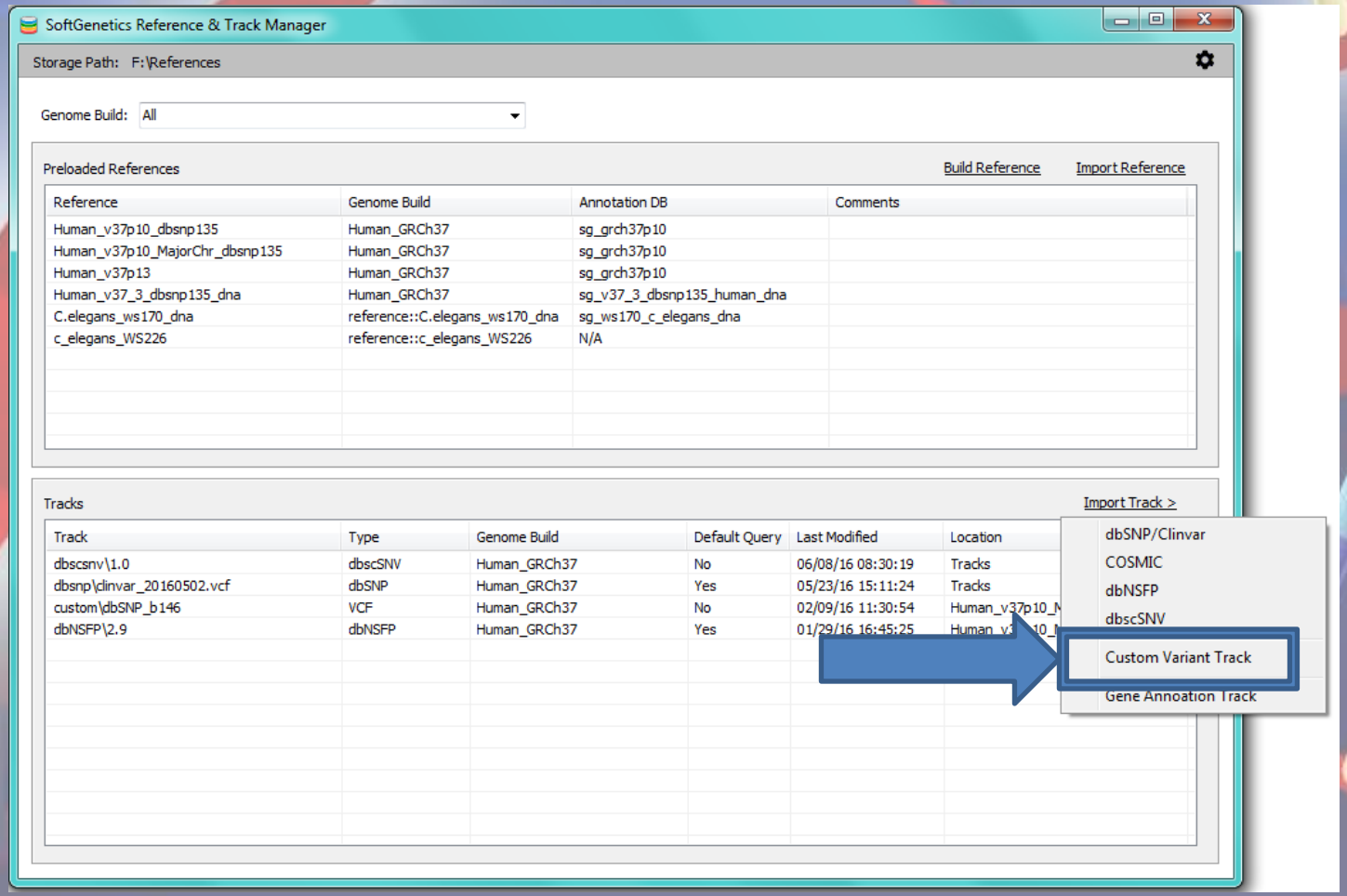
The Track Manager Tool includes specialized support for the dbNSFP, dbscSNV, COSMIC and ClinVar/dbSNP databases.

To import a custom database, database files should first be downloaded outside of Mutation Surveyor



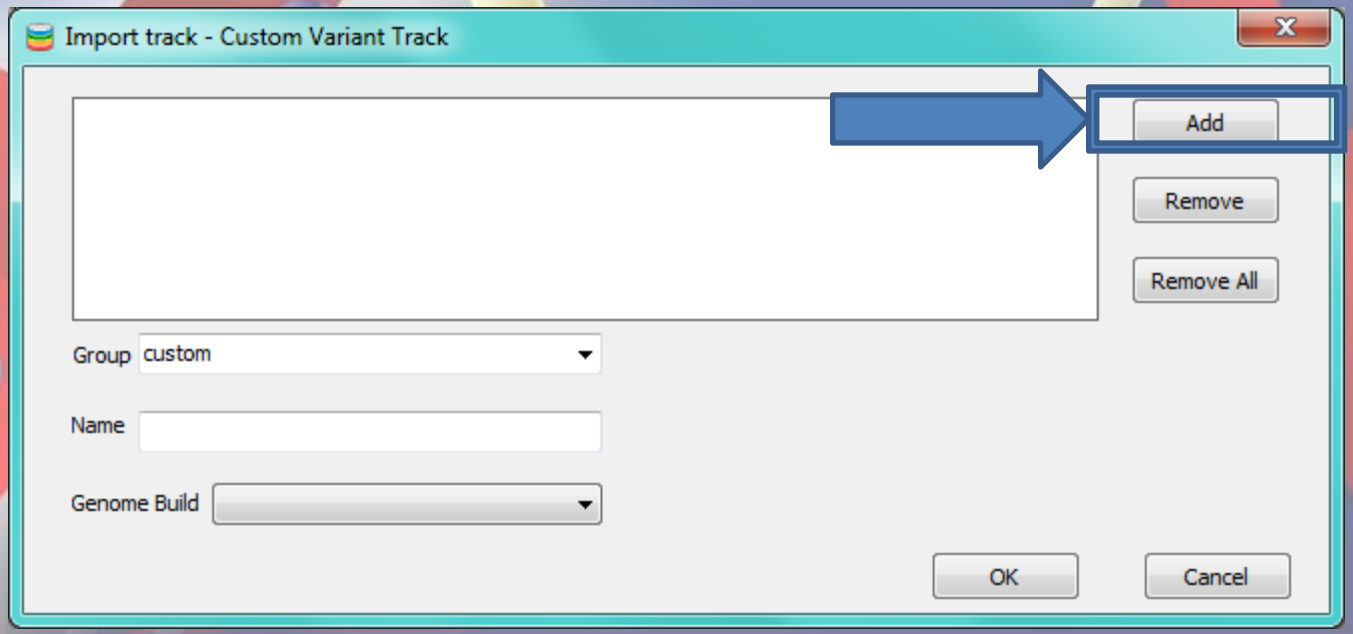
Importing a Custom Variant Database

Click “Import Track” > “Custom Variant Track”



Importing a Custom Variant Database

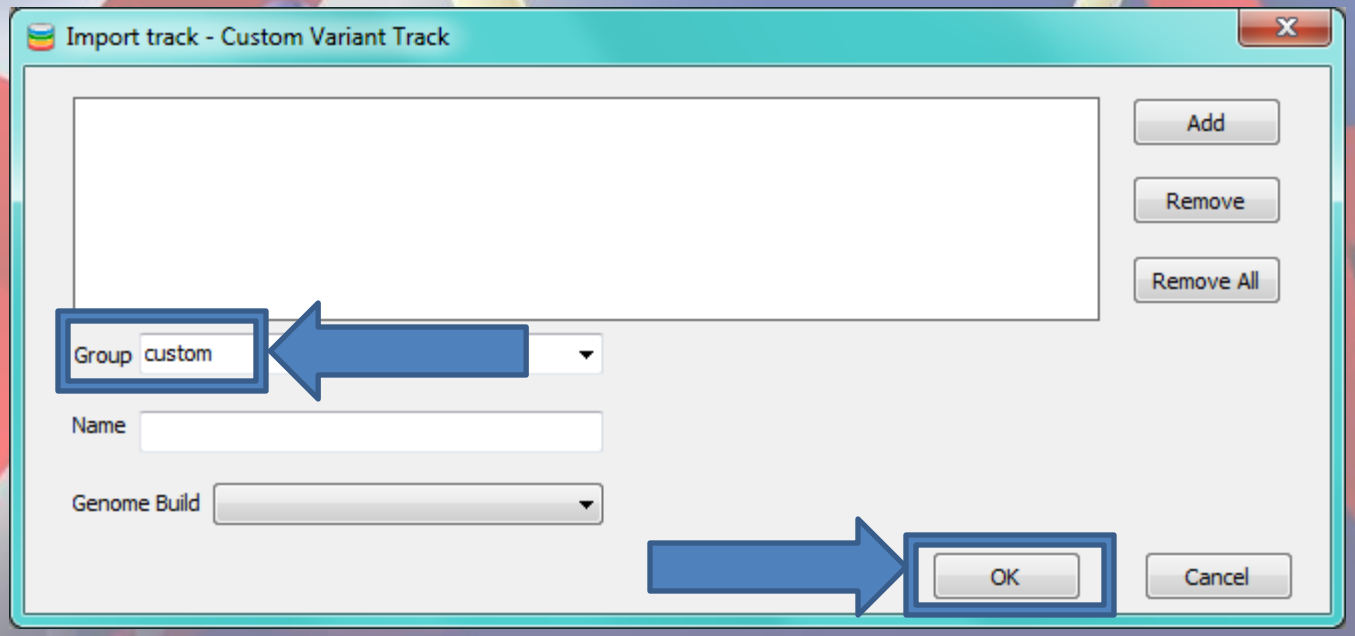
Click “Add” to browse to and select the downloaded database file



Note: To import a custom database, database files should first be downloaded outside of Mutation Surveyor

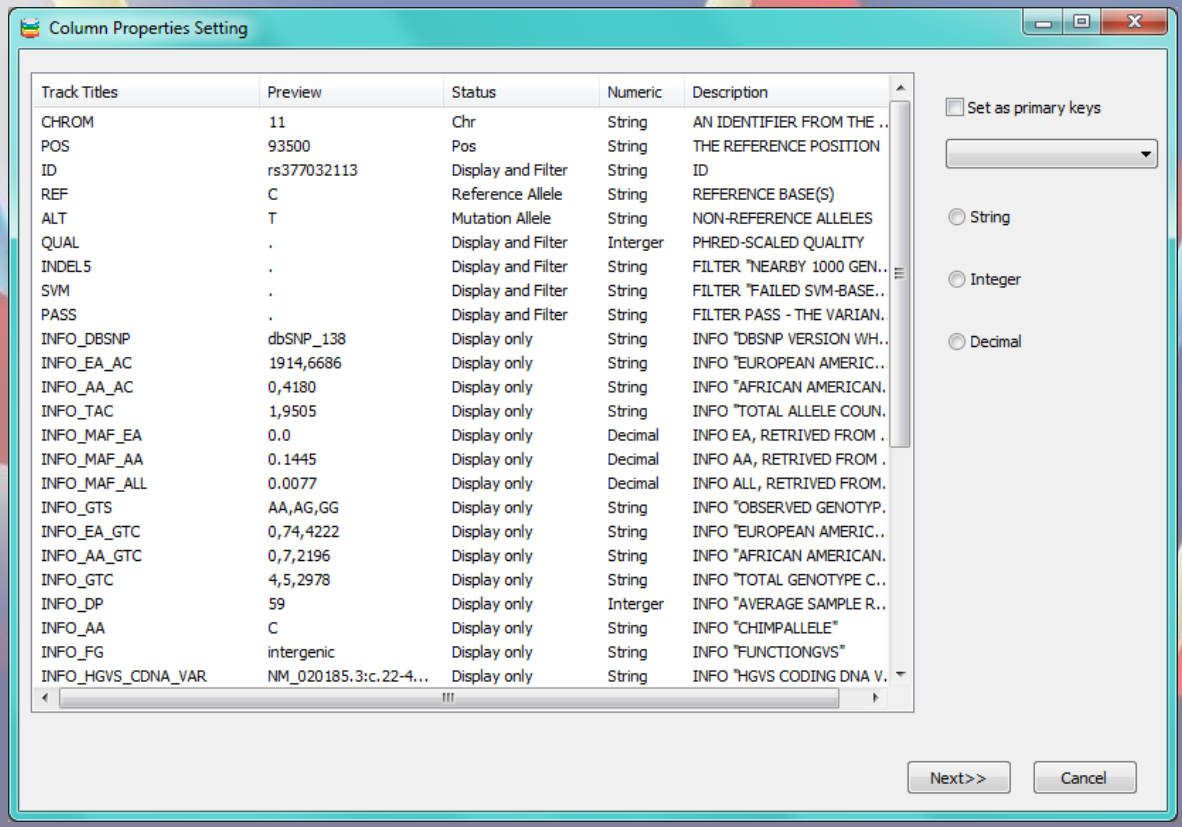
Importing a Custom Variant Database

Group can be renamed from Custom. Enter a name including version for the database track and select the appropriate genome build from the dropdown list. Then click “OK”.



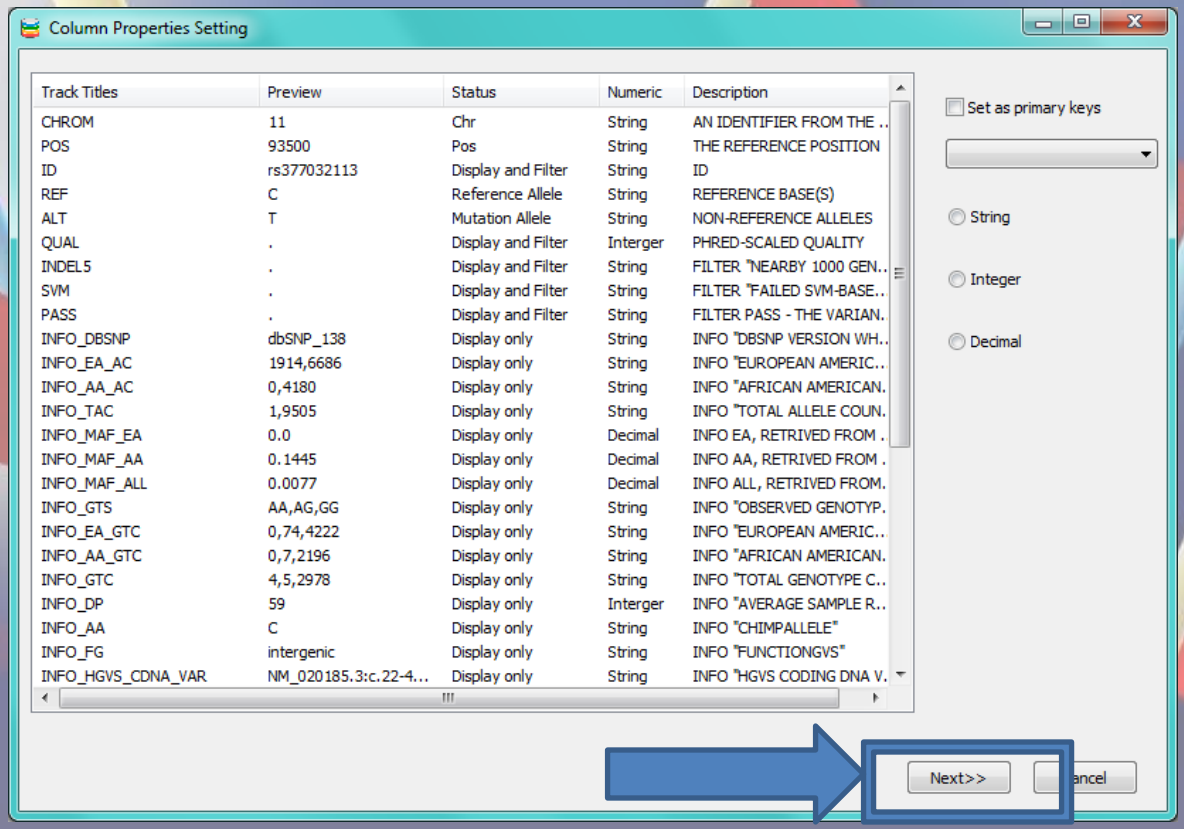
Importing a Custom Variant Database

Custom Database Import – Exome Variant Server used for example
Choose how to handle all fields in the database. Highlight any field and choose “Skip”, “Display Only”, or “Display and Filtering”.



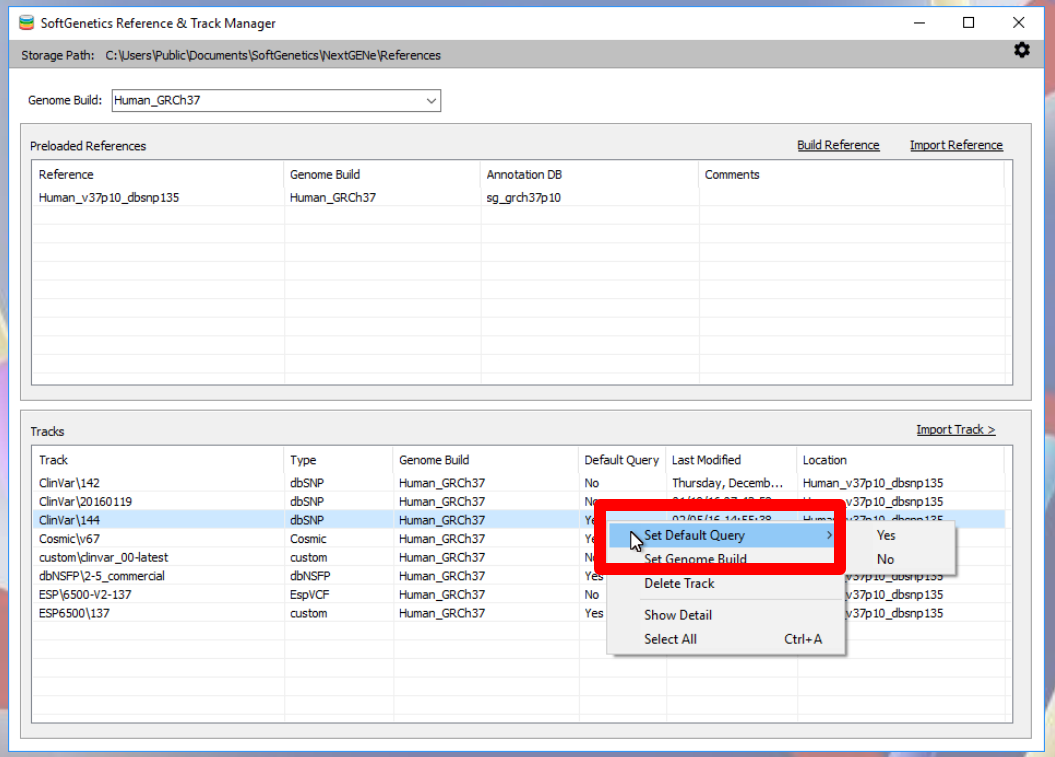
Importing a Custom Variant Database

Custom Database Import – Exome Variant Server used for example
After modifying the Import Settings as needed, click “Next” to begin import



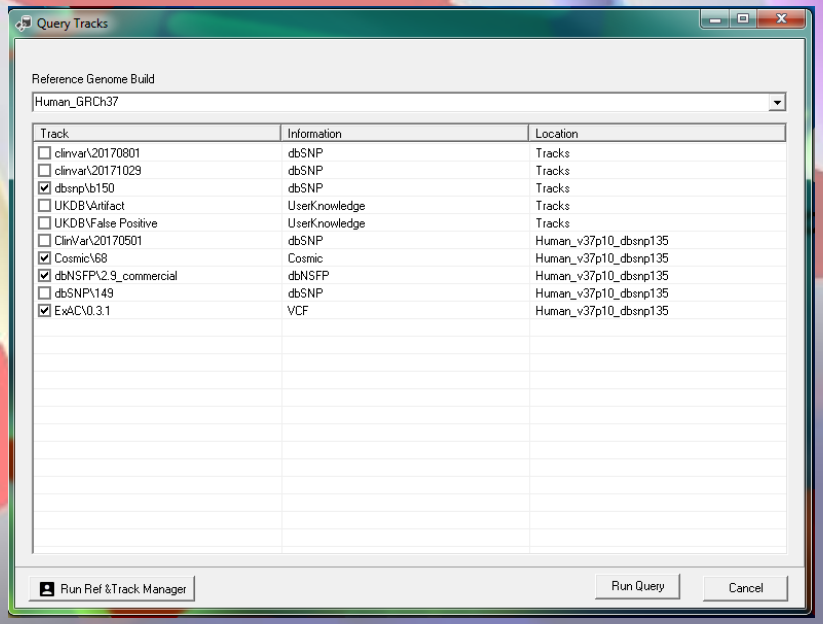
Querying Databases

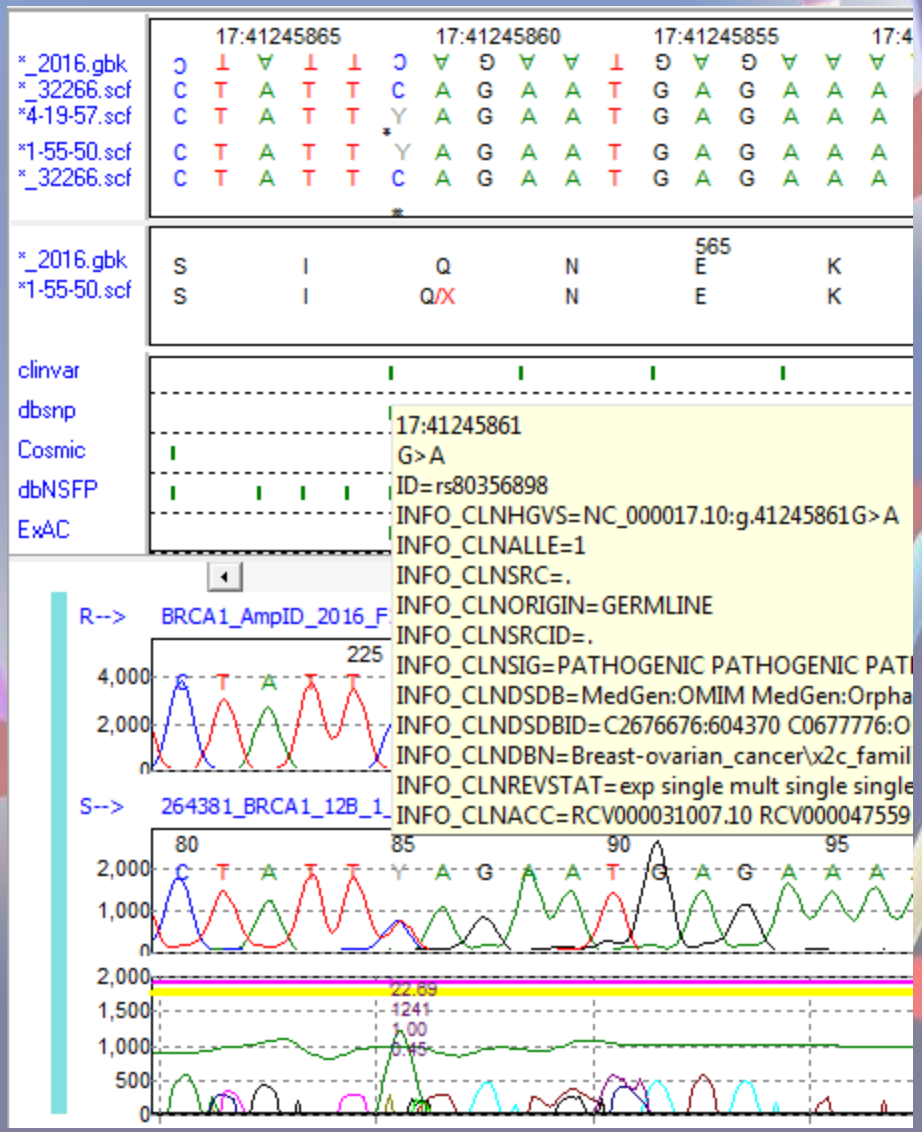
- Following import, each database can be queried for Mutation Surveyor projects.
- To automatically query a database for projects, right click the database and set “Default Query” value to “Yes”



Querying Databases

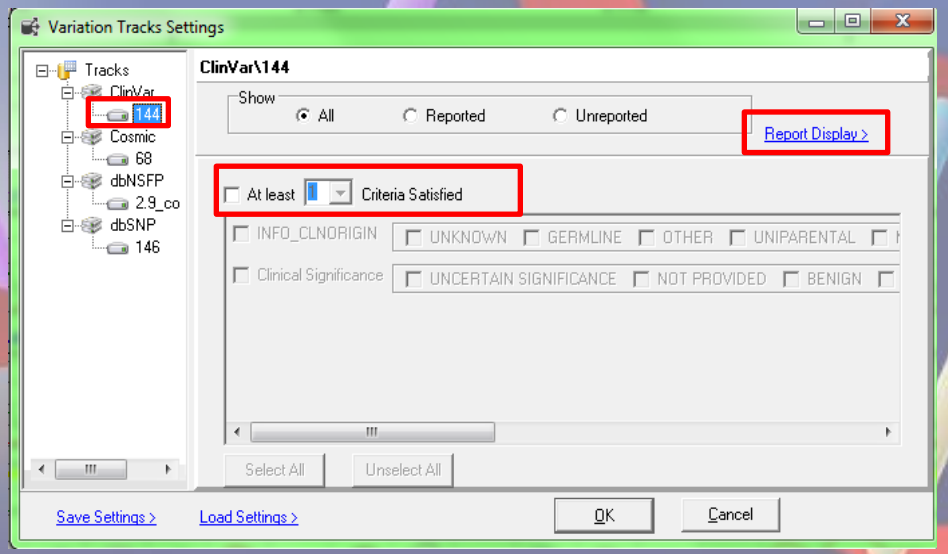
- Select Process / Query Reference Tracks to customize the displayed tracks within each project





Adjust Track Settings

- Select the Tracks Settings icon on the GAD toolbar
- Click on the track name of interest
- Set filters based on track criteria
  - Check box next to “At least” and select the minimum number of criteria a variant must meet to pass filter
  - Specify required criteria
- Set filters based on track inclusion
  - Variants must first pass all other filters
  - Select to Show All variants, only variants Reported in track, or only variants Unreported in track



- Open Report Display dialog for annotation display options

Report Display Settings

- Select the information to be displayed for variant annotation
- After all selections have been made, click “OK” to return to the Variation Tracks Settings dialog