NextGENe®

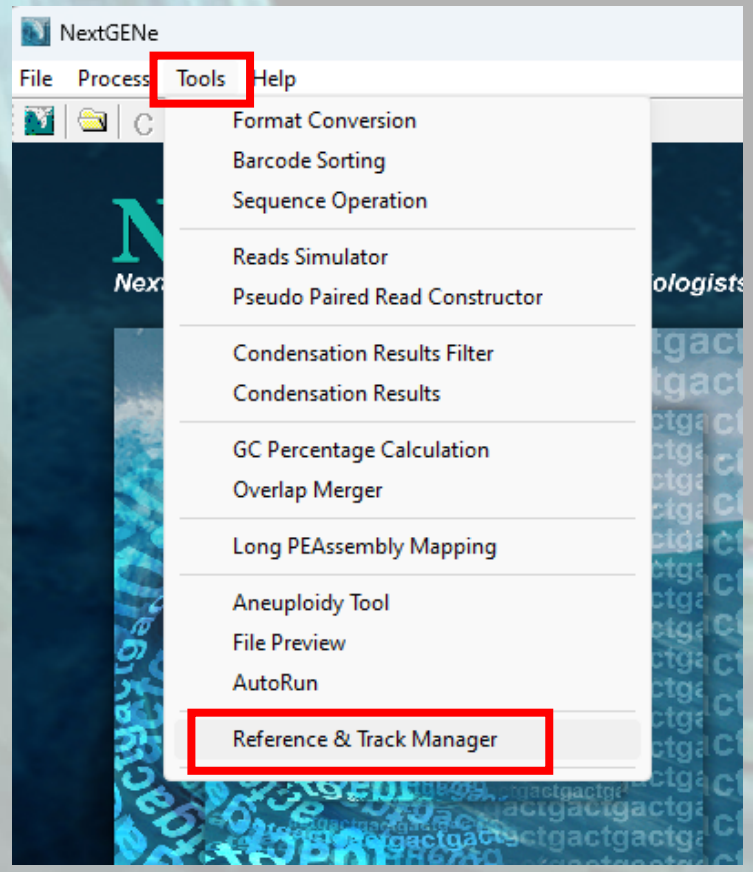
Next Generation Sequencing Software for Biologists

Importing References

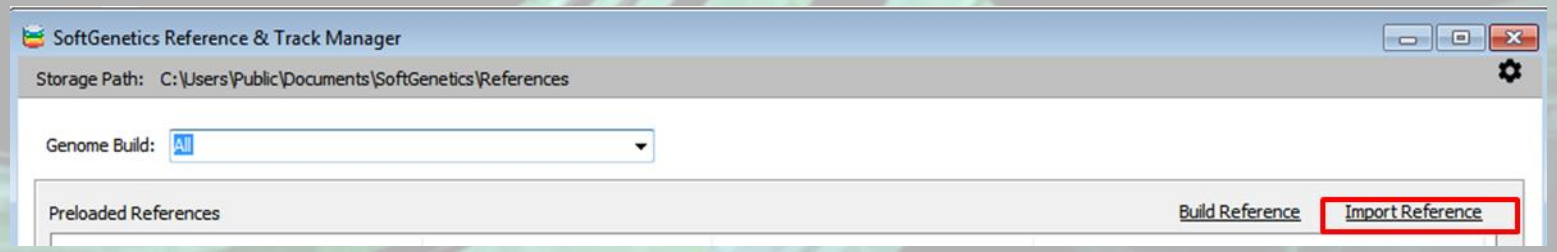
Depending upon your application you may need one of our Indexed references for NextGENe (for genomes larger than 250 Mbp), which may be downloaded and installed as follows.

The installation process of the reference is quite lengthy due to the data size.

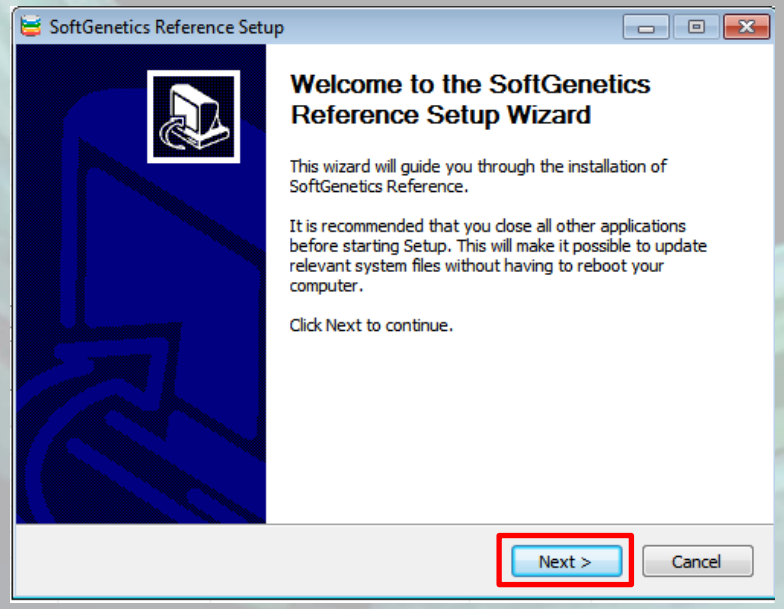
To obtain our pre-indexed reference genomes:

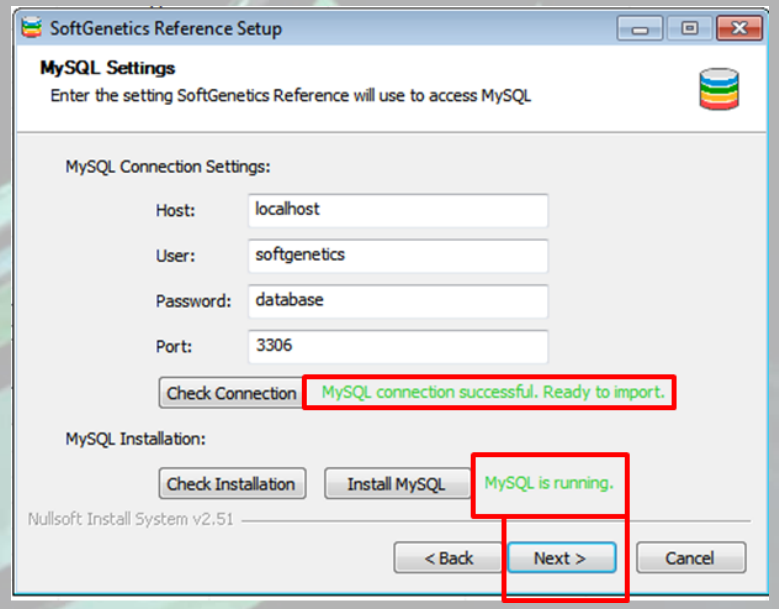


- **Right-click on NextGENe and choose “Run as Administrator.”**
- **Go to Tools > Reference and Track Manager**
- **Click "Import Reference.“**

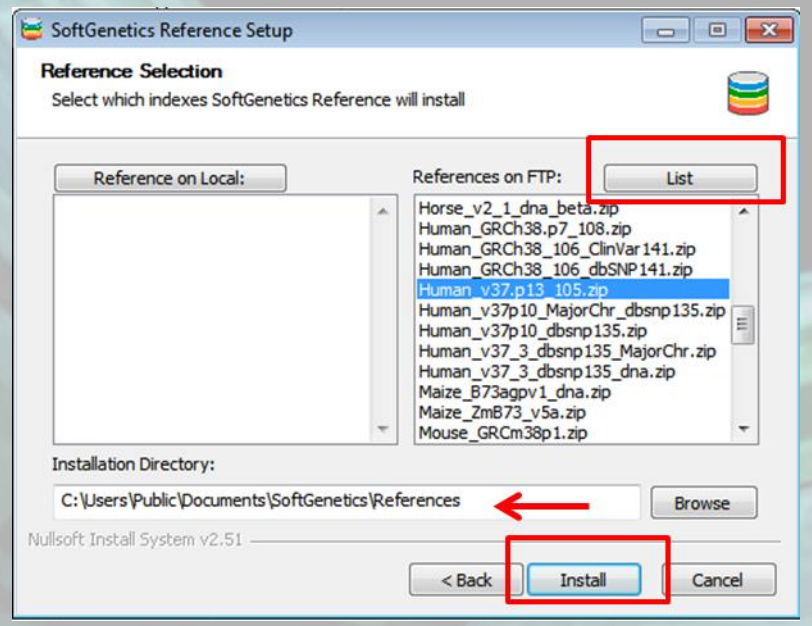


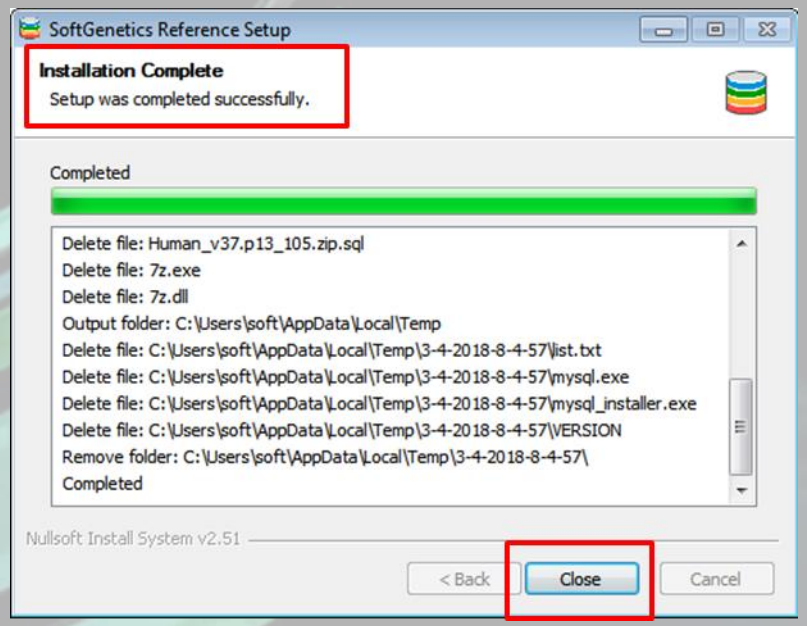
- The NextGENe Reference Setup Wizard Opens
- Click "Next" on Welcome screen.
- Ensure that MySQL is configured properly. Next to Check Connection, it will state that it is ready for import. If it is ready to import, click “Next” to proceed to next step.
  - If connection failed because MySQL is not installed, click Install MySQL. After this is complete, click Close.
  - Click Check Connection and if prompted with MySQL Connection Successful, then continue with importing of reference genomes. Otherwise, contact tech_support@softgenetics.com.



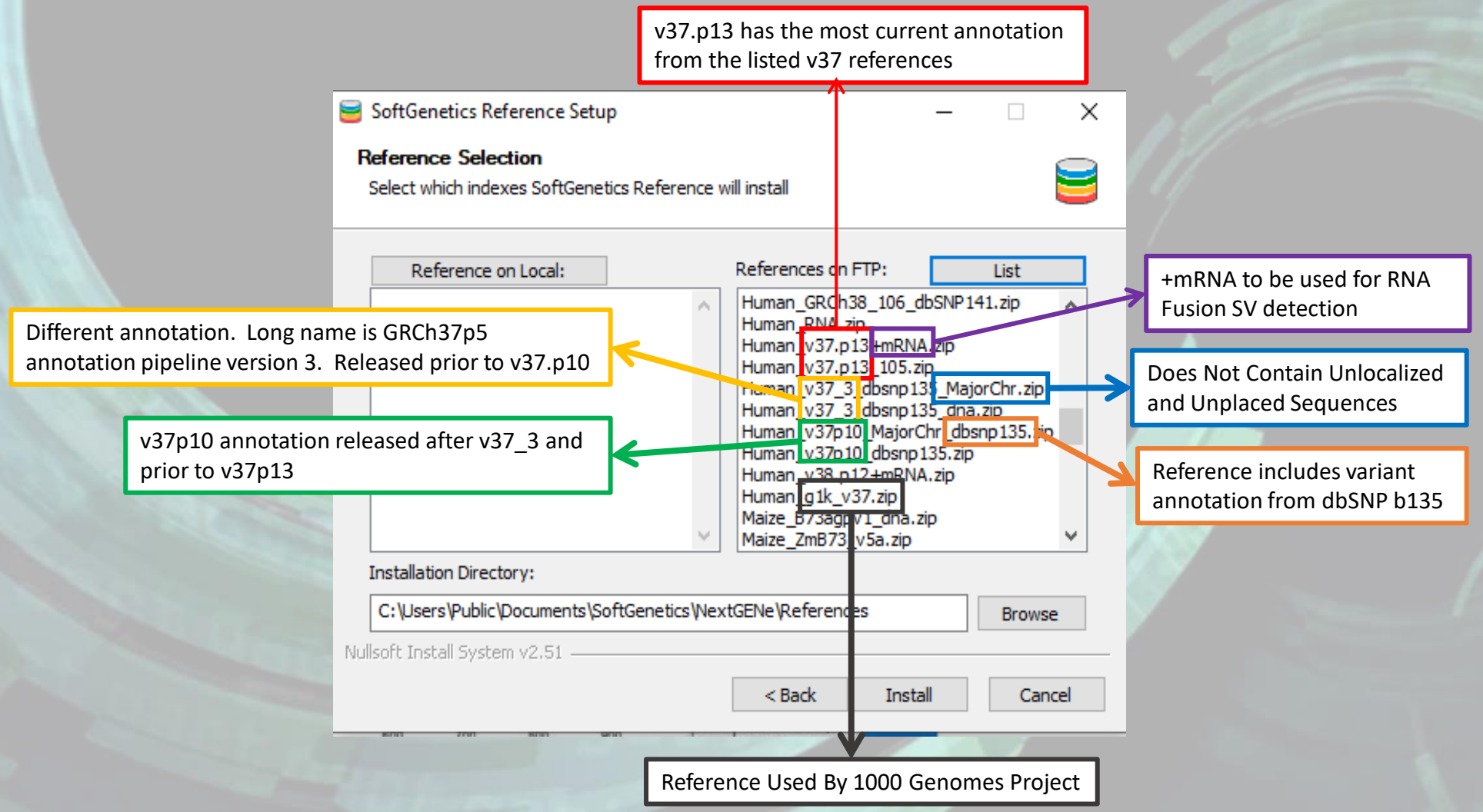


- To view all reference genomes on our FTP server, click "List".
- Highlight the genomes you would like to import.
- Click "Install". When reference and its database are downloaded and imported properly, you will see "Completed".



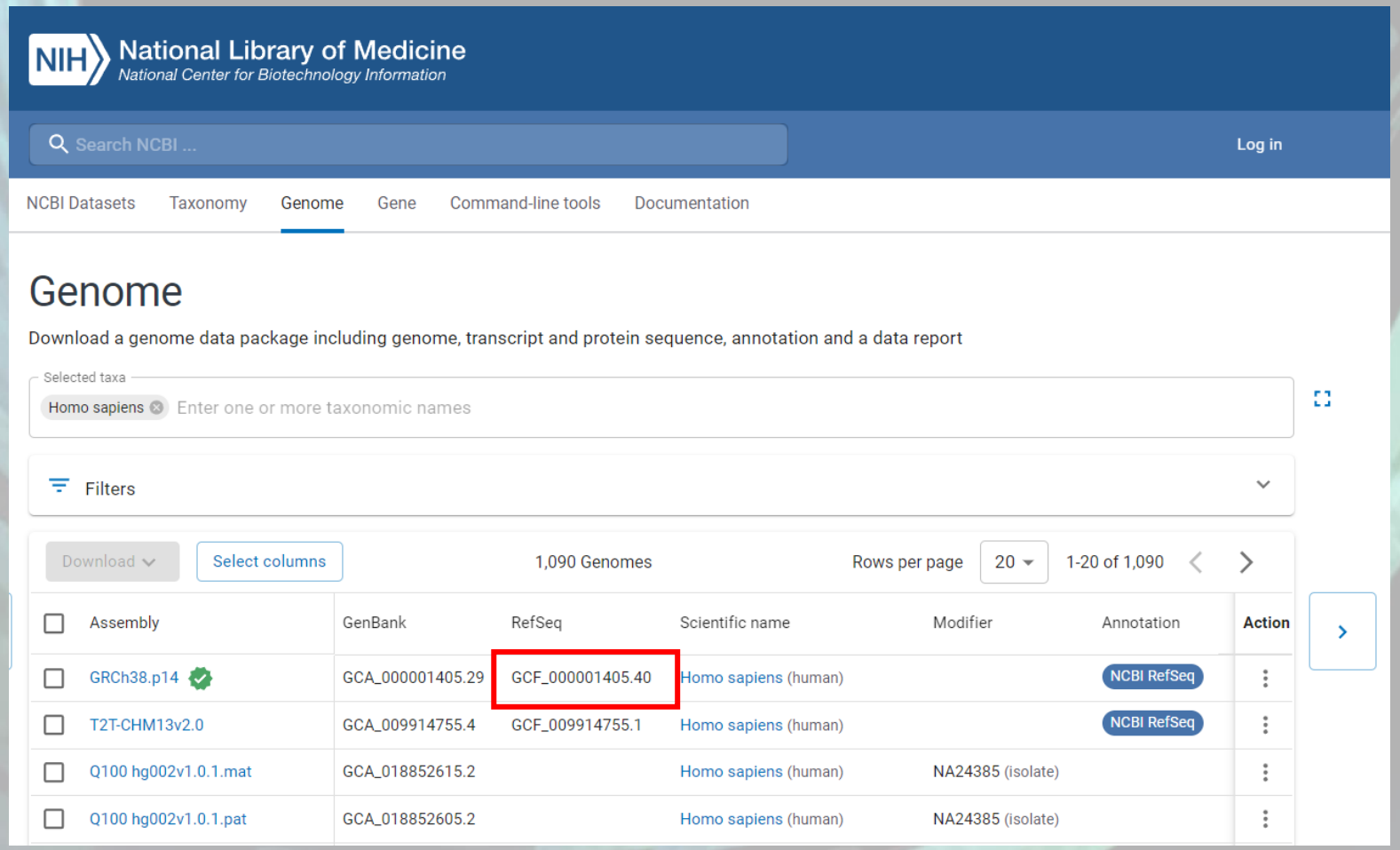


Not sure which Human Genome Reference to Import?



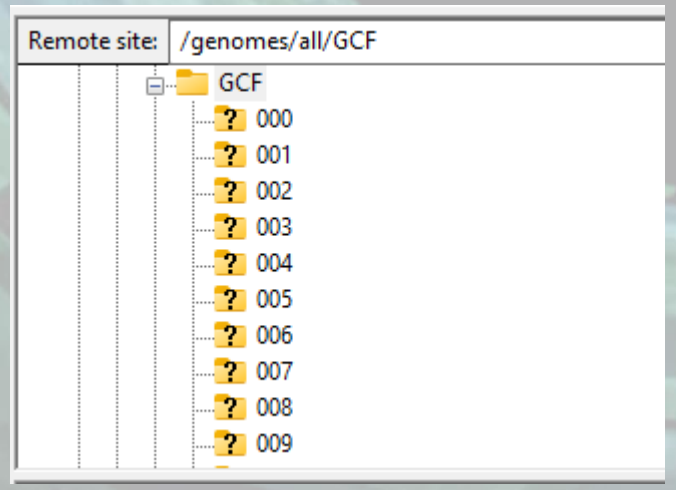
Do not see the genome you need listed?

1. Get the GCF Accession Number for the genome from NCBI

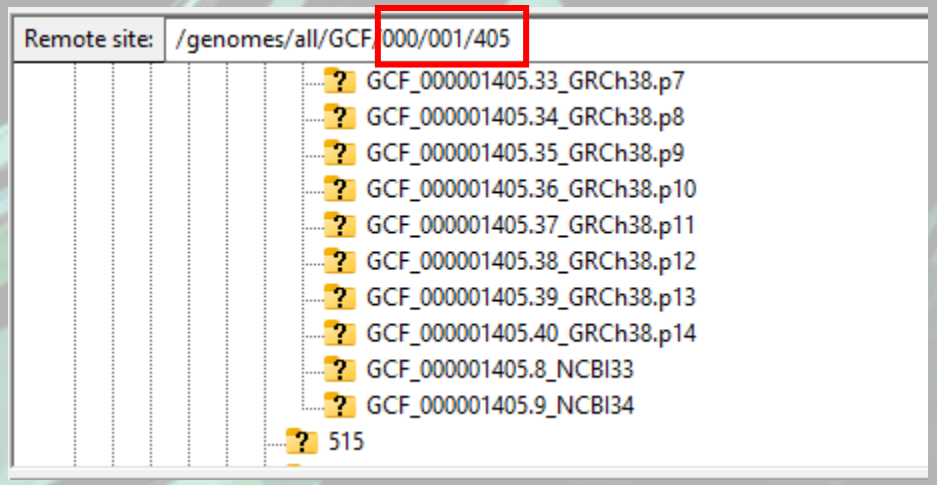


2. Use FTP client such as [FileZilla] to connect to NCBI's FTP

3. Navigate to genomes/all/GCF

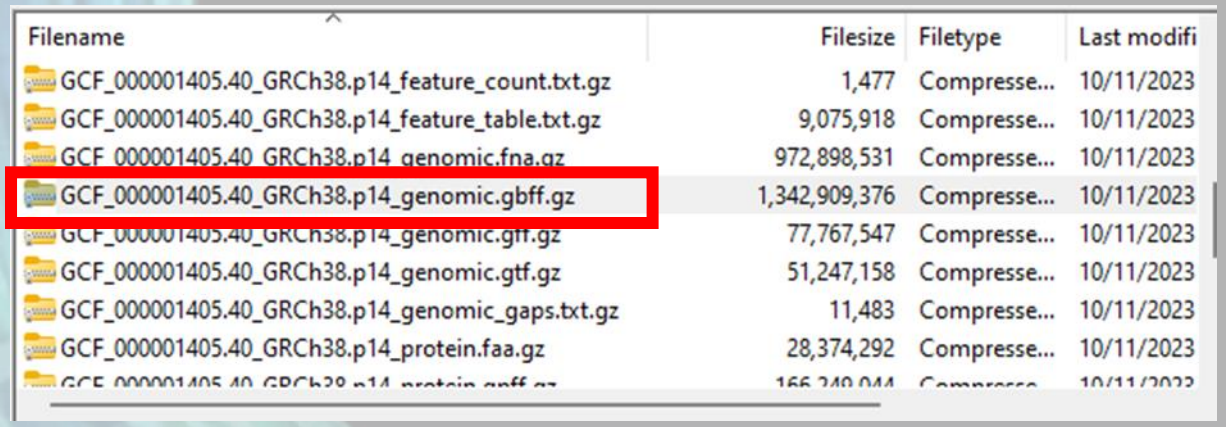


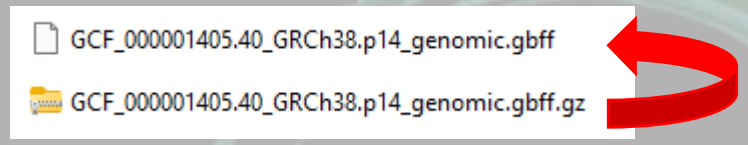
4. Navigate through the numbered folders according to the GCF accession number



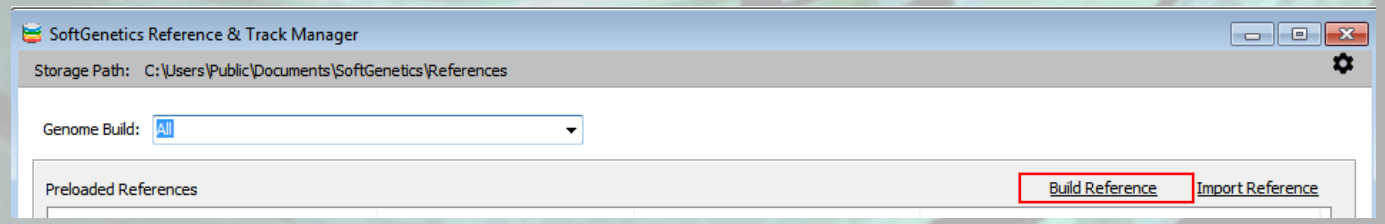
If you do not have an FTP client, open a web browser and go to https://ftp.ncbi.nih.gov/genomes/all/GCF/ and proceed with step 4.

5. Download the *_genomic.gbff.gz file and extract (can use 7-zip)

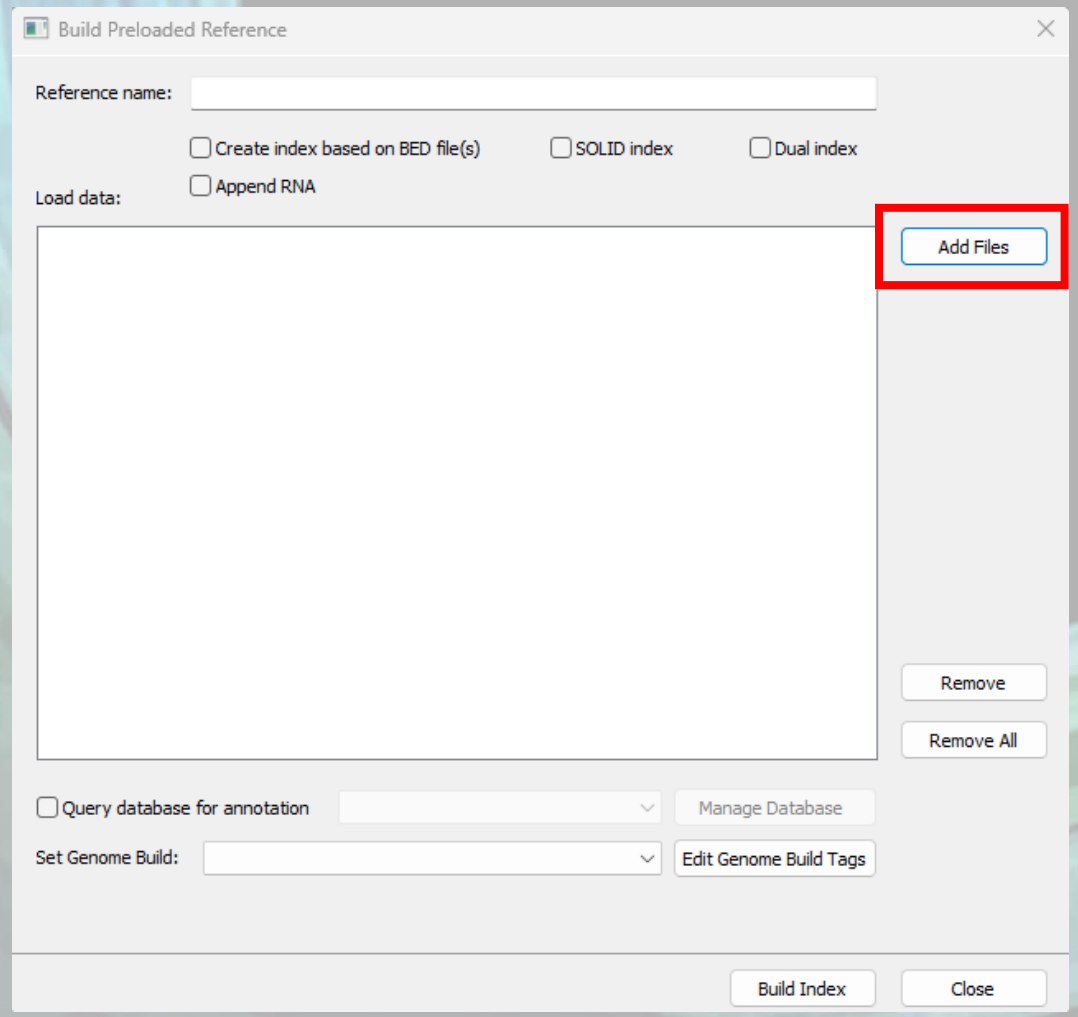




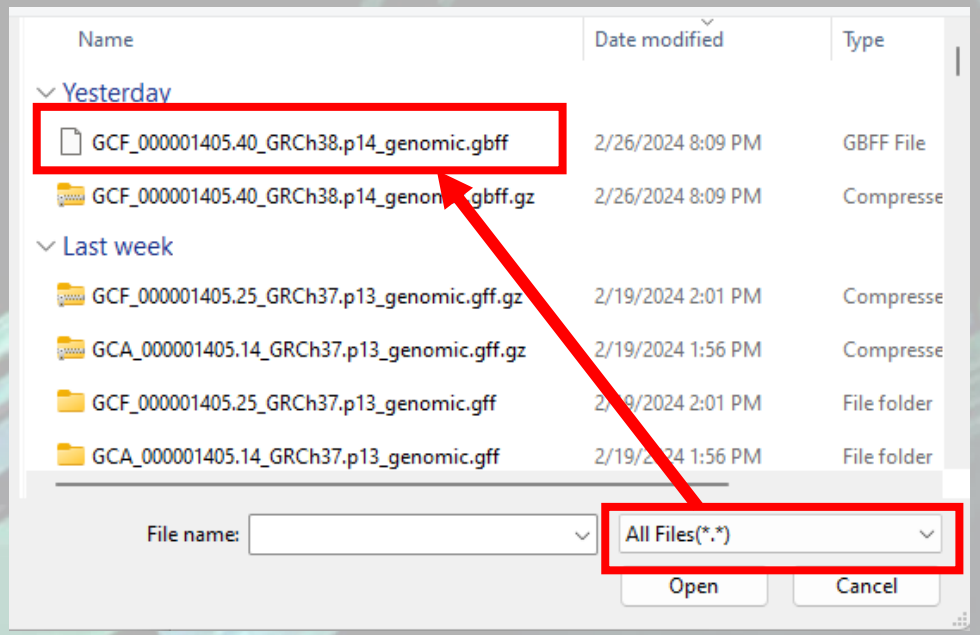
6. Open the Reference and Track Manager Tool (see page 2) and click “Build Reference”



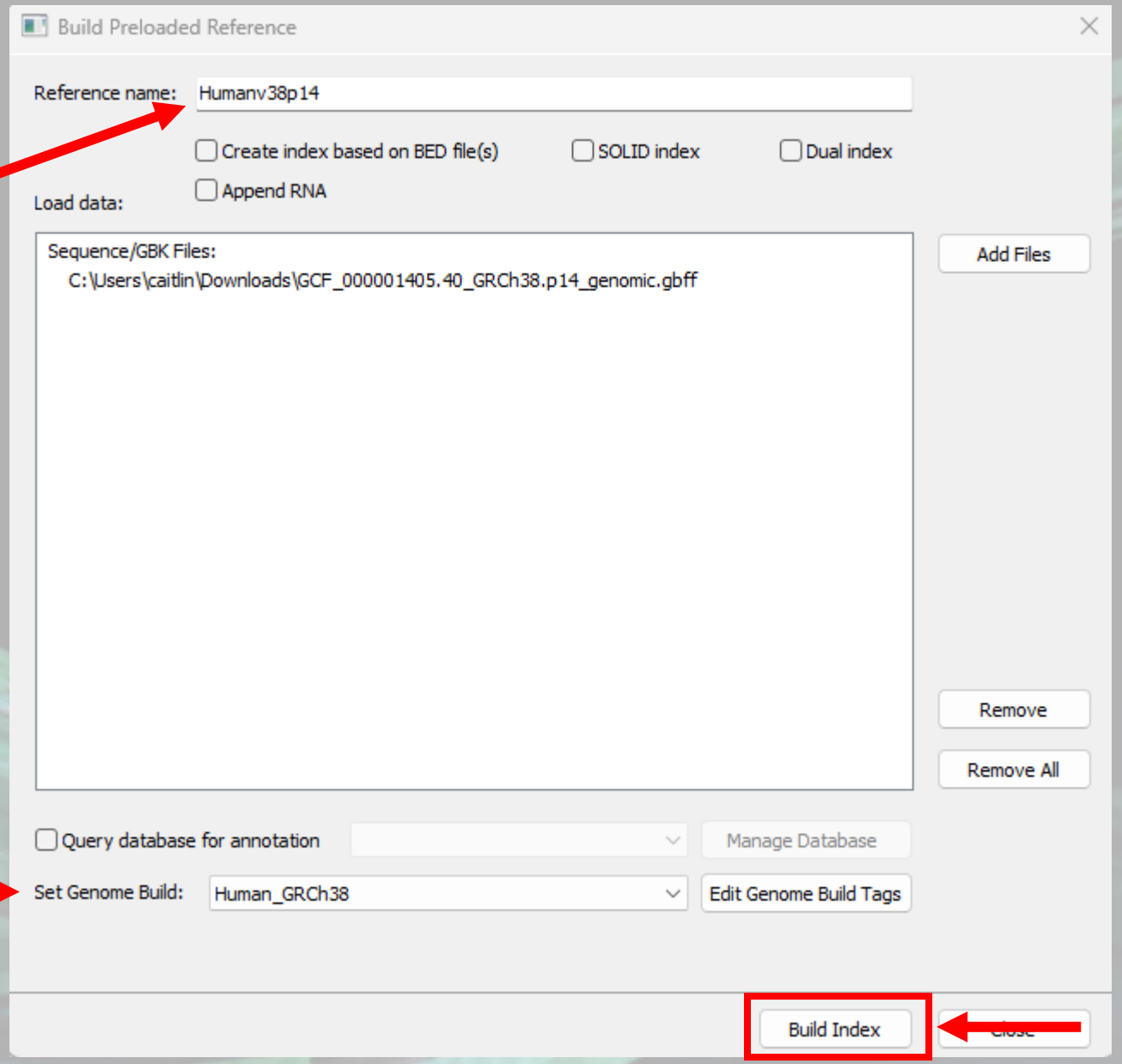
7. Click Add Files



8. Use the file type dropdown to select “All Files” and then select the extracted .gbff file



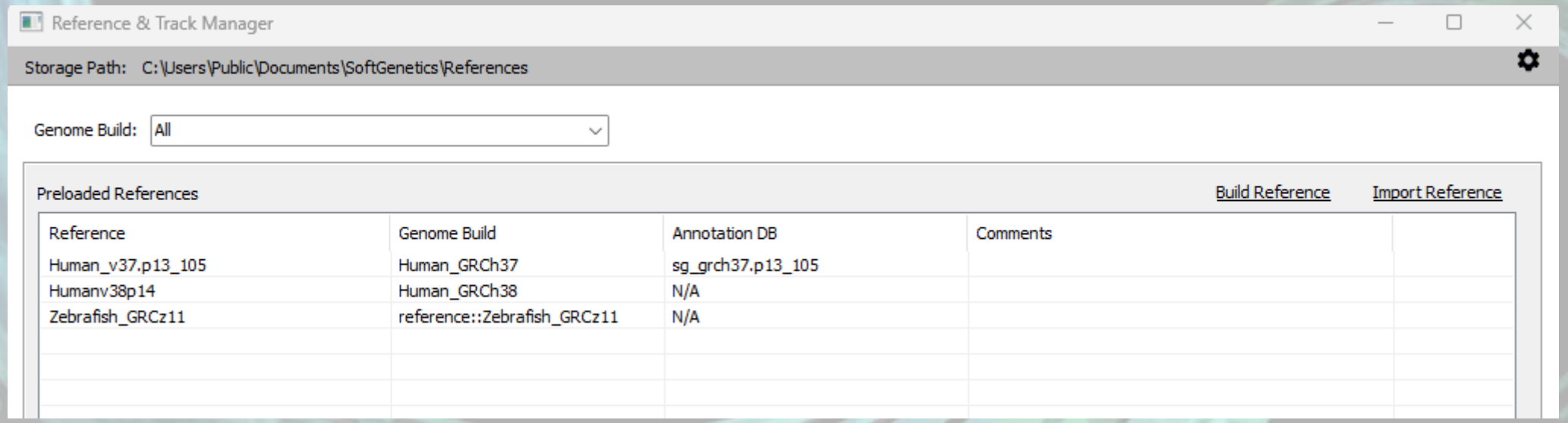
9. **Give your reference a name**



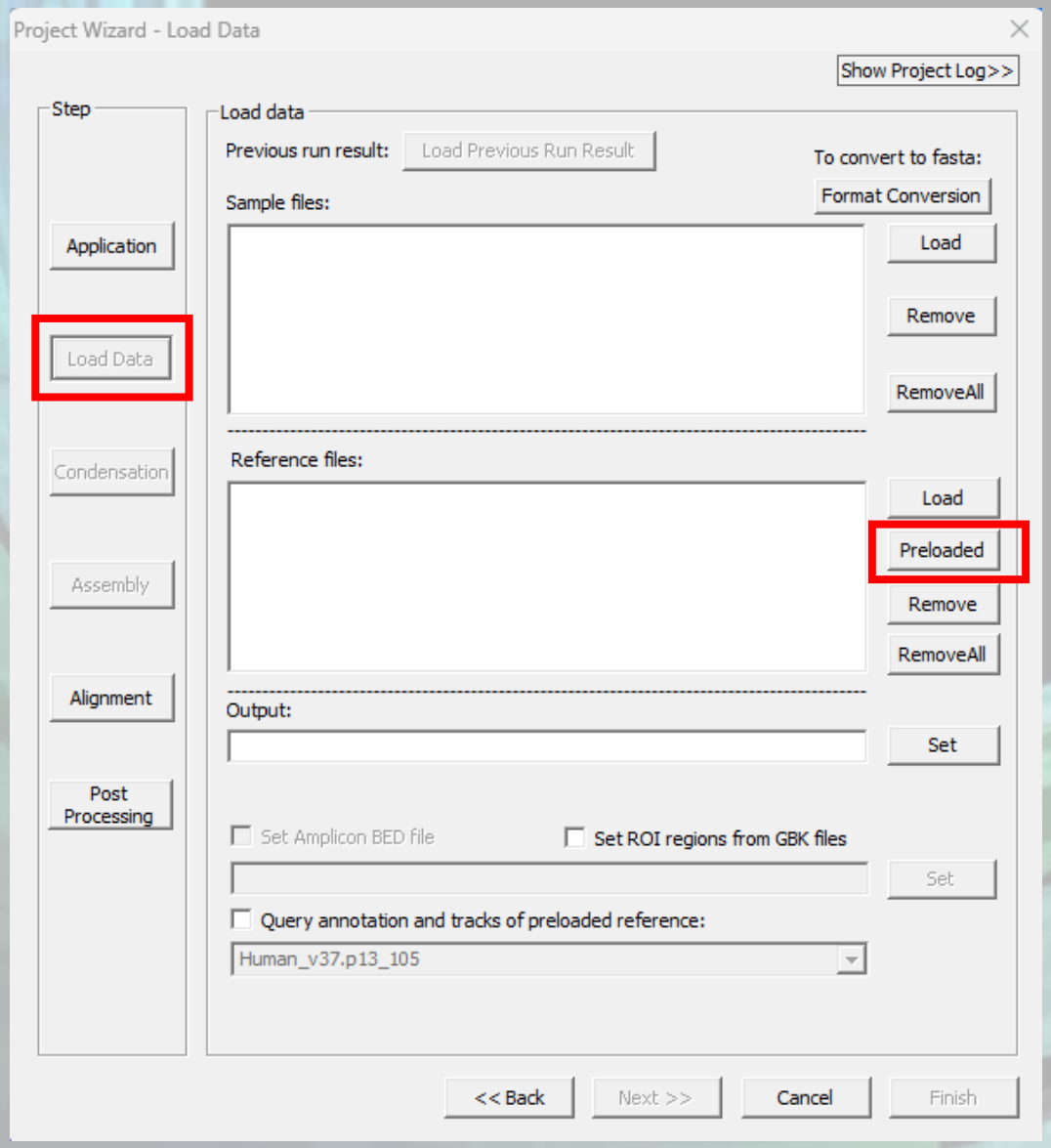
10. **If applicable, select a genome build**

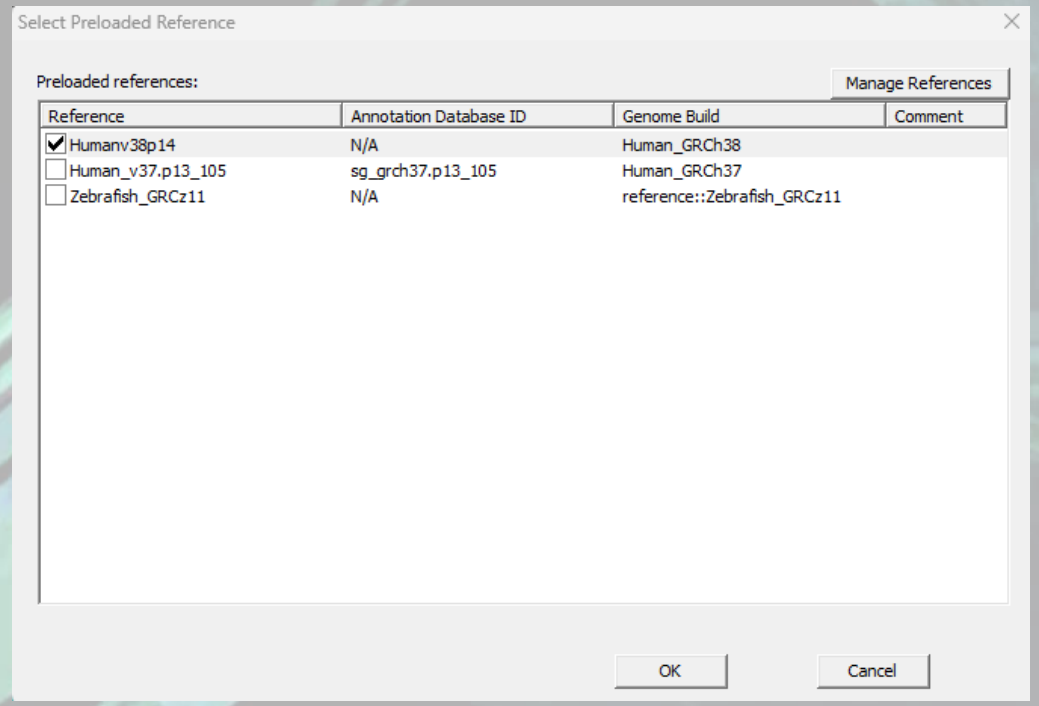
11. **Click “Build Index”**

In the Reference & Track Manager Tool, set the Genome Build to “All” to display all imported references

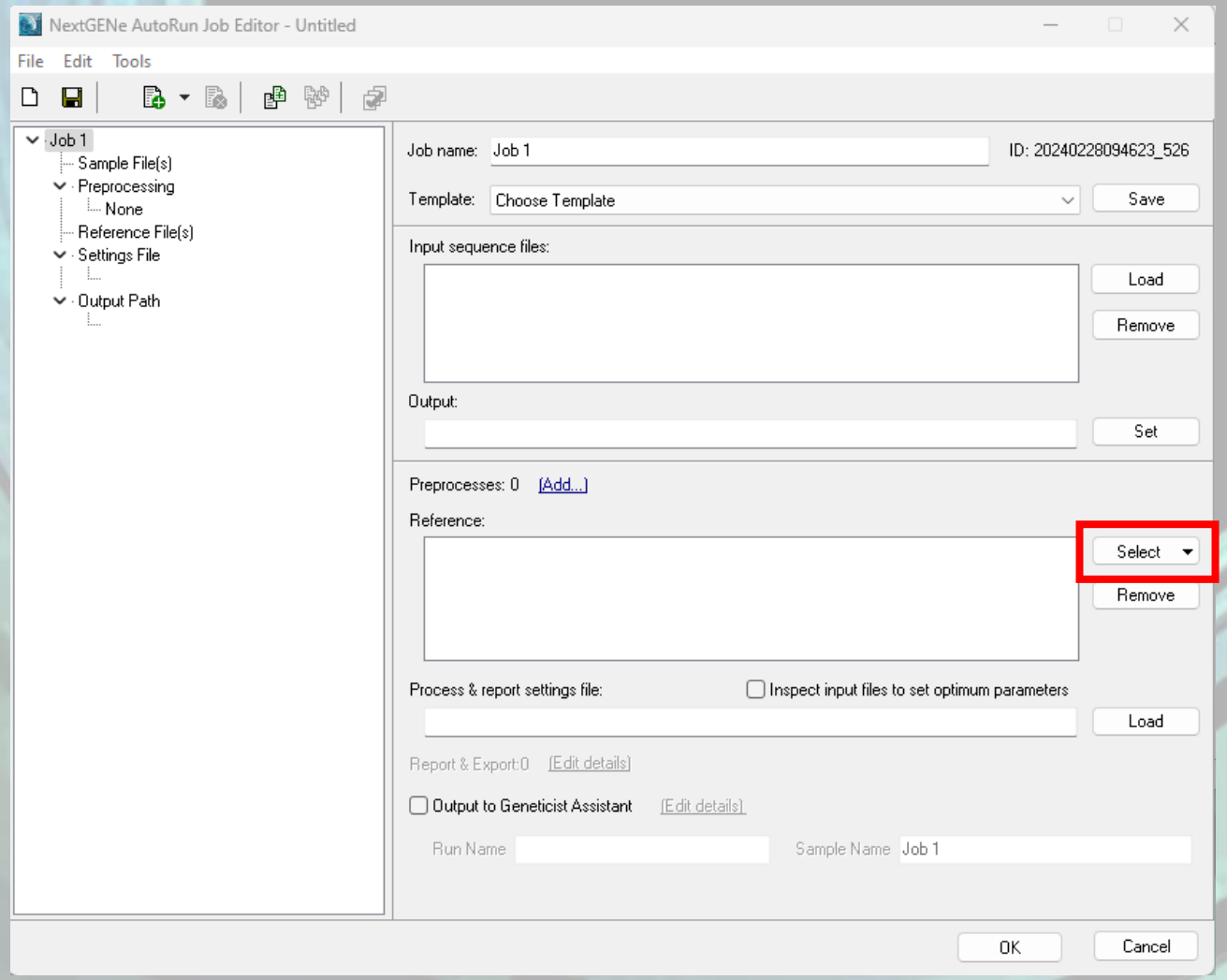


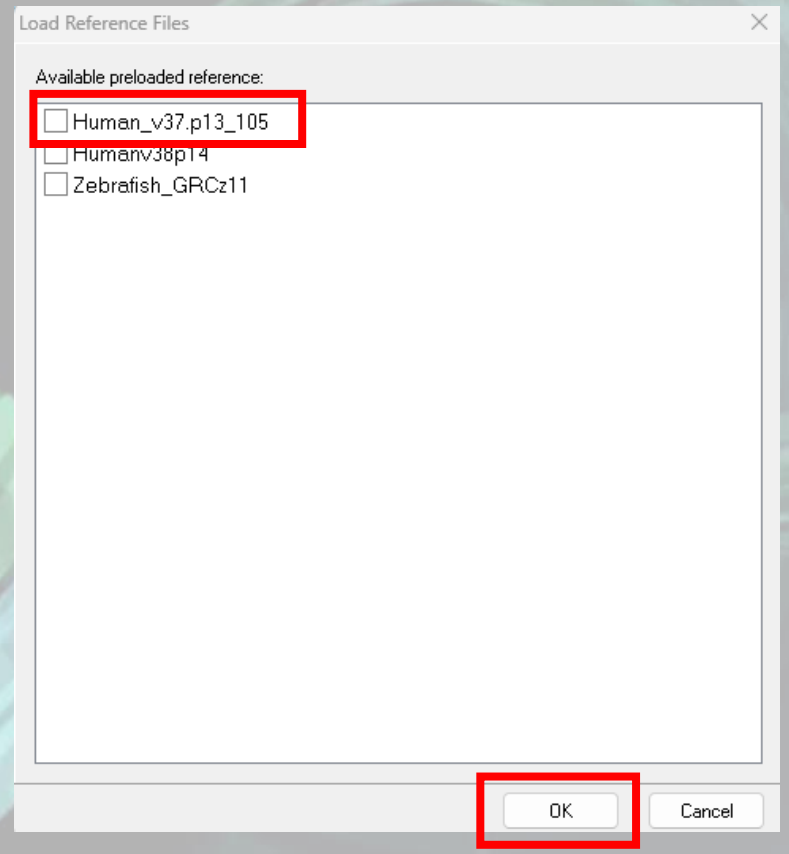
Apply your imported reference for a project run using the Preloaded button on the Load Data step of the Project Wizard





If using the AutoRun Tool, click the Select button to the right of the Reference field to open the list imported references. Select the preferred reference and click OK





Difficulty accessing our FTP or importing your needed reference?

Please email us at tech_support@softgenetics.com and let us know what reference you are trying to import and the difficulties being experienced and we will be happy to help.