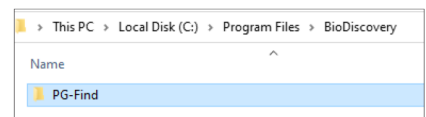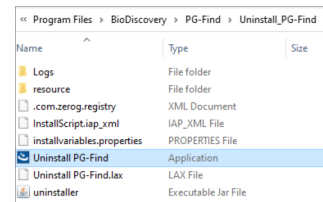# revvity

Transition guide to PG-Seq v3.0.

Quick and simple transition from PG-Find v2.0 to v3.0

Remove PG-Find™ v2.0

1. Navigate to the Uninstall PG-Find™ Folder, by default this is saved at the following location: C:\Program Files\BioDiscovery\PG-Find\Uninstall_PG-Find

2. Run the **Uninstall PG-Find.exe** application.

3. When complete, navigate to C:\Program Files\ BioDiscovery and delete the entire PG-Find folder.

Download PG-Find™ v3.0

4. Use the following links to download both the PG-Find™ Software and the PG-Find™ Reference builder.
   installers.biodiscovery.com/PG-Find/Windows64/VM/PG-Find.exe
   installers.biodiscovery.com/PG-Find/Windows64/VM/PG-Find Ref Builder.exe

Install PG-Find™ v3.0

5. Open each installer and follow the prompts to install the software. Please note you may need to right click on the installer and select "Run as administrator" to allow the program to save in the default location on the C: drive.

Request a License

6. Launch the PG-Find™ Software then select **Request activation key via email**.

7. Complete the **Activation request data** form.

For research use only. Not for use in diagnostic procedures.

8. Select **Launch Mail Client**. This should open your email client with a pre-filled request (if an email client is not launched, then click **Copy to Clipboard** and paste the pre-filled request in an email). **Please specify in the email that the request is for PG-Find v3.** Send the request email to **NGS@revvity.com**

9. Once you have received your license code (please allow 1-2 business days), open the PG-Find™ Software and select **Activate now**.

10. Copy and paste your license code into the **Enter activation code** field then click **OK**.
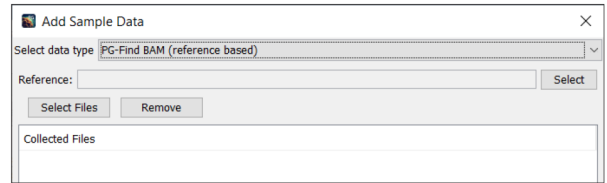
Use the New Features

1. Create a Reference file using the PG-Find™ Reference builder (See the PG-Find™ Software manual for more information).
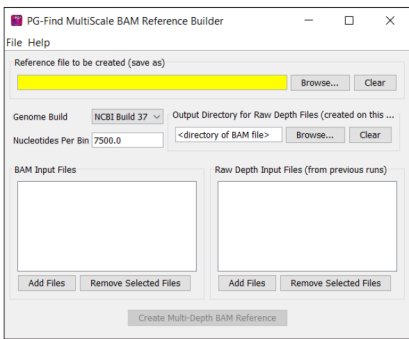
2. Check the settings for the reference-based algorithm and adjust if required.
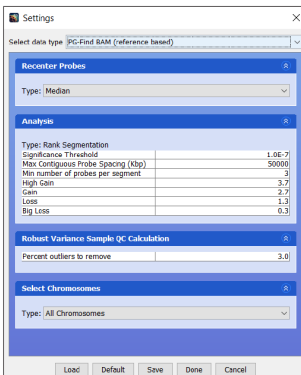
3. Load .BAM files and select the "PG-Find BAM (reference based)" option in the Add Sample Data window.

4. Select the reference file you made previously then press **Done** to queue processing.

Select Chromosomes

1. Open the settings menu

2. Under the Select Chromosomes option, change the type to Select Chromosomes

3. Uncheck the chromosomes you wish to remove from the visualization.
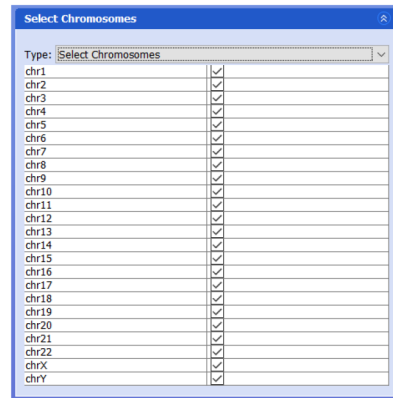
View the Raw Data

In the Whole Genome tab of the Sample Drill Down, check or uncheck the "Raw data (unsmoothed)" checkbox at the top of the window to toggle between the smooth and raw views.