QIAseq® xHYB Custom Viral Analysis

Further information
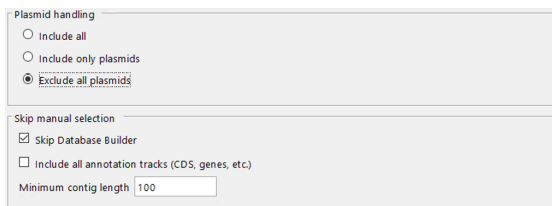
- QIAseq xHYB Microbial Panels: **qiagen.com/ngs/microbial**
- GeneGlobe: **geneglobe.qiagen.com**
- Technical assistance: **support.qiagen.com**

Important points before starting

- Download the custom viral panel Taxonomy List Excel® file from GeneGlobe® Custom Designer.
- Ensure that the latest version of CLC Genomics Workbench Microbial Genomics Module is installed.
- Ensure that the "Analyze QIAseq xHYB Viral Panel Data (Human Host)" workflow is installed.

Create custom taxonomic profiling index

1. Open "Download Custom Microbial Reference Database" tool through the following path: **Tool → Microbial Genomics Module → Databases → Taxonomic Analysis → Download Custom Microbial Reference Database**.

2. Select the following parameters.

3. Click **Next** and then select **Build database from accessions or TaxIDs**.

4. From the "Taxonomy List" Excel file downloaded from GeneGlobe Custom Builder, copy values from "Species Taxonomy" in column B. These are species level taxonomy IDs for the targets from the custom panel.

5. Paste the "Species Taxonomy" values in the "ID matching" field.

6. Click **Next** and then select **Save**.

7. After downloading sequences, select "Create Taxonomic Profiling Index" tool using the following pathway: **Tool → Microbial Genomics Module → Databases → Taxonomic Analysis → Create Taxonomic Profiling Index**.

8. Click **Next**. Select **Save**, then **Finish**.

Create "Find Best Reference Sequence" list

1. Open the "Search for Sequences at NCBI" tool.

2. Select **Nucleotide** as the database and **Accession** as the search parameter.

3. From the "Taxonomy List" Excel file downloaded from GeneGlobe Custom Builder, copy an accession number from "Reference" in column E.

4. Paste the accession number in the search field and start search.

5. Save sequence (suggest to make a new folder to store sequences) and then continue until all sequences from the Reference column are downloaded.

6. Select all downloaded sequences, and then click **New** → **Sequence List tool**.
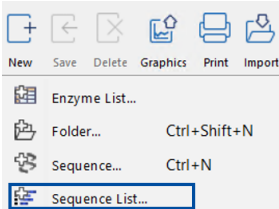
7. Select **Next** and then **Save**.

Viral analysis

1. Select Analyze QIAseq xHYB Viral Panel Data (Human host) workflow and select samples to be analyzed. Click **Next**.

2. Under "Specify reference data handling", select **Use specified data elements**.

3. The analysis is the same as cataloged panels but with the following 2 changes:

    a. In the Viral Taxonomic Profiling Index step, replace with the custom Taxonomic Profiling Index that was created under "Create Custom Taxonomic Profiling Index".
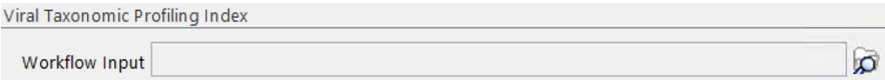
    b. In the Viral Reference Database step, replace with the Reference Sequence List that

was created under "Create Find Best Reference Sequence List".

Viral Reference Database	
Workflow Input	

Document Revision History

Date	Description
04/2025	Initial release

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