

OhmX™ Platform Quick Start Guide

This guide can be used as a reference for experienced users of the OhmX Platform.
For complete instructions and more details, please refer to the **OhmX Analyzer Guide**.

Note: The software will prompt you to complete an action during several steps in the process. Make sure to read the software prompts and complete the described action(s) before continuing.

Start a Sample Run

- ☐ 1. **Select Abort**
 - Selecting **Abort** stops any protocol currently running on the analyzer, including **Sleep** mode.
- ☐ 2. **Select Empty Waste**
 - Empty all four waste tubes.
- ☐ 3. **Select Load Reagent Cartridge**
 - Ensure a used or storage detector is installed.
 - If you are using a newly received reagent cartridge, ensure it has been stored at room temperature for 24 hours prior to use.
 - Insert a new reagent cartridge (orange label).
 - Properly dispose of the used reagent cartridge (if flush cartridge, put aside for later use).
- ☐ 4. **Select Load Detector**
 - Load a new OhmX Detector
- ☐ 5. **Select Initial Clean**
 - Initial Clean** begins the detector cleaning protocol and takes approximately 45 minutes.
- ☐ 6. **Select Start Sample Run**
 - The analyzer exchanges the detector into the sample run reagent and prepares the detector for sample injection. This protocol takes approximately 15 minutes.
- ☐ 7. **Dilute Sample in OhmX Sample Injection Diluent:**

Tagged & Coated DNA Sample (µL)	Sample Running Buffer (µL)
33	150

- Add 150 µL of the Sample Injection Diluent to a 1.5 mL tube.
 - The tagged and coated DNA sample is transferred to the tube containing the Sample Injection Diluent using the INTEGRA electronic pipette custom program **SAMPLE DILUTION** with a wide-bore tip. This is a 3-step program that (1) aspirates 33 µL of tagged & coated sample (2) dispenses the sample into the tube containing the Sample Injection Diluent (3) mixes the diluted sample 20x at the appropriate speed; total mix time is ~4 min.
- ☐ 8. **Enter Sample Information**
 - Select **Yes**, and then enter the sample information.
 - Select **OK** to continue.
- ☐ 9. **Inject Sample**
 - Using the INTEGRA pipette **INJECTION** custom program, press **RUN** to aspirate 165 µL of the diluted sample into a standard bore 300 µL pipette tip (this should take ~35 seconds).
 - Holding the pipette vertically, insert the pipette tip into the sample injection port and press the **RUN** button on the INTEGRA pipette a second time to inject the sample into the analyzer. Injection takes ~30 s, and the pipette will beep once it is complete. Remove the pipette tip from the injection port and dispose of the tip containing the residual sample.
 - Press the **RUN** button on the INTEGRA pipette to reset it.

☐ 10. Select Start

- View real-time results in the OhmX Software user interface.
- The sample run ends automatically if the waste containers are full, the remaining reagent volume is too low, or there are no viable channels on the detector. You can end the run manually using **Stop Sample Run**.

End a Sample Run

Note: A sample run should be stopped by selecting **Stop Sample Run** after 16–18 hours have elapsed and Molecules Rate has decreased to less than 60 mol/s.

☐ 1. Select Stop Sample Run

- Following the **Water Flush** from Step 1 above, select **Sleep Mode**.

☐ 2. Complete Signal Processing

- Confirm that signal processing has completed and that the **Data Processing Status** box says **Idle** before transferring data.

☐ 3. Start Sleep Mode

- Following the **Water Flush**, select **Sleep Mode** to start the protocol for temporary analyzer storage (up to 1 week) with the reagent cartridge installed.
- If the system won't be used for > 1 week, insert a flush cartridge using the **Load Reagent Cartridge** protocol. After the purge completes, select **Sleep Mode**.
- If the system will be idle for more than 4 weeks, contact Nabsys Technical Support (support@nabsys.com) for further guidance.

Upload Your Run to Human Chromosome Explorer (HCE)

☐ 1. Compress Analyzer Sample Output Folder into a Zip File using Nabsys Data Selector

- Open **Nabsys Data Selector** software
- Select the **D:\SharedData\Samples** folder as the input and output folders.
- Select the sample you want to zip.
- Select **Exclude Raw Data**.
- Select **Run**.

☐ 2. Upload the File to HCE

- Open **HCE** (<https://hce.structuralvariation.bio>) and log in.
- Select the **Injections** tab.
- Select the reference genome for pre-processing (t2t, hg38, hg19).
- Select **Upload New Data**.
- Select **Choose File** and select the zipped file from **Step 1**.
- Select **Upload**.
- When the upload has completed, select **OK**.

Technical Support

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