Release Notes

DRAGEN Germline v3.8.4 for NextSeq 1000/2000

INTRODUCTION

These Release Notes detail the key changes to the DRAGEN Germline Pipeline on NextSeq 1000/2000 since the v3.7.4 release.

INSTALLATION INSTRUCTIONS

DRAGEN v3.8.4 is compatible with Control Software 1.2 and 1.3. For information regarding compatibility with other Control Software versions, please reference the NextSeq 1000/2000 Compatible Products page on the Illumina support site. If you would like to update the control software, please follow the steps detailed in 1000000160800 v00.

ONLINE INSTALLATION WITH V1.3 CONTROL SOFTWARE

* These instructions are intended for online installation of DRAGEN pipelines with v1.3 Control Software and beyond

Starting with v1.3 Control Software, cloud-based updates for DRAGEN are enabled.

1. Make sure that you have the password to the ilmnadmin account.
2. Log in to the ilmnadmin account:
   a. If you are already logged in as ilmnuser and in control software, select the control software menu, and then select **Exit Application** to access the desktop.
   b. Select the power button icon in the upper right corner and log out of ilmnuser.
   c. After you are on the login screen, select ilmnadmin, and then enter the password to log in.
   d. The control software automatically launches once you are logged in.
3. Select the **DRAGEN** screen in the control software.
4. Click on **check online** button in the DRAGEN workflows section.
5. A modal will pop up showing which workflows have an update available for installation.
6. Select which pipelines you would like to update.
   a. **NOTE: For Online Updates, DRAGEN BCL Convert must be installed before or with other workflows of the same DRAGEN Version**
7. Select download and install.
8. You will be prompted to enter the admin password once the download completes and proceeds to install
9. After installation is complete, you will be navigated back to the DRAGEN screen and can view the updated list of installed DRAGEN workflows.

OFFLINE INSTALLATION/ INSTALLATION WITH V1.2 CONTROL SOFTWARE

* These instructions are intended for offline installation of DRAGEN pipelines or installation with v1.2 Control Software (whether online or offline)

1. Make sure that you have the password to the ilmnadmin account.

2. Log in to the ilmnadmin account:
   a. If you are already logged in as ilmnuser and in control software, select the control software menu, and then select **Exit Application** to access the desktop.
   b. Select the power button icon in the upper right corner and log out of ilmnuser.
   c. After you are on the login screen, select ilmnadmin, and then enter the password to log in.
   d. The control software automatically launches once you are logged in.
3. The DRAGEN Germline installation requires up to 1 GB of free space on your desktop if DRAGEN BCL Convert is already installed. DRAGEN BCL Convert installation requires 8 GB of free space on your desktop.
   a. To access your desktop, select the control software menu in the control software, and then select **Minimize Application**.
   b. Delete or transfer files off the desktop that are not needed.
   c. Empty trash to free space from the drive.
      i. Select **Applications**, and then **Files** from the upper left corner of the desktop to launch the file explorer.
      ii. On the left panel of the file explorer, right click the Trash icon and select **Empty Trash**.
4. Launch Chromium to download the software upgrade installers from the Illumina Support Site.
   a. While in desktop view, open the Applications menu on the upper left corner. Select **Internet**, and then select **Chromium**.
      i. **Note: After launching Chromium, you may receive a prompt to unlock your login keyring. You can safely ignore and cancel out of the prompt.**
   b. Use Chromium to browse to the NextSeq 1000 and 2000 Software Downloads page on the Illumina Support Site.
5. Download the DRAGEN upgrade installers from the Illumina Support Site and save them to the desktop. **Do not extract these files; leave them as .tar.gz**
   a. **Note: at minimum, you must download and install the DRAGEN BCL Convert update.**
6. After the files have finished downloading to the desktop, maximize the control software by selecting it from the toolbar.
7. **Install DRAGEN workflows**
   a. Select the control software menu, then select **DRAGEN**.
   b. In the Version section, select **Browse for New Version**.
   c. In the browse window, navigate to the desktop and double-click the DRAGEN Germline workflow *.tar.gz package.
      i. **Note: DRAGEN BCL Convert must be installed before other workflows**
   d. In the control software DRAGEN window, select **Install**.
   e. At the login prompt, enter the ilmnadmin password.
   f. Confirm that DRAGEN Germline is updated to 3.8.4.

FEATURES

- Small Variant Calling Updates
  - Joint Detection of Overlapping Variants
    - A significant accuracy boost is achieved when variants at multiple loci in a single active region are detected jointly. Joint Detection alters the

variant caller algorithm in the area of localized haplotype assembly and genotyping under the appropriate conditions.
  - Enabled for SNP and INDEL
- CYP2D6 Genotyping
  - CYP2D6 genotyping is integrated in DRAGEN Germline on NextSeq 1000/2000 and is enabled by default.
  - Implementation is based on the open-source tool Cyrius and gives concordant results
  - The CYP2D6 caller outputs star allele diplotype for each sample e.g. '*1/*4+*68'
    - Over 120 CYP2D6 star alleles are supported, allowing DRAGEN to call a definitive genotype in nearly all samples
  - Includes a structural variant model to handle rare subtypes
  - Includes genotype likelihood model to select the most likely star allele diploid given:
    - Structural variant calls
    - Small variant calls
    - Population haplotype frequencies
- Two FASTQ files consolidated to one FASTQ file per Read if FASTQ files are saved
- Improved memory management in BCL conversion for large sample numbers
- Infrastructure upgrades (applicable to all v3.8.4 DRAGEN workflows on NextSeq 1000/2000):
  - FastQC report aggregation
  - New hg19, hg38, and hs37d5 reference genome available for download from the cloud (to be used with DRAGEN v3.8 and later)

RESOLVED ISSUES

N/A

KNOWN ISSUES

None