

# Biomark/EP1 Software

To download the latest version of the software for Biomark™ HD, Biomark, and EP1™, go to [fluidigm.com/software](http://fluidigm.com/software). For more information about updating the software, see the Updating the Biomark/EP1 Software Quick Reference (101-6793).

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## Data Collection Software Release Notes

For more information, see the Biomark HD Data Collection User Guide (100-2451) and the Biomark/EP1 Data Collection User Guide (68000127).

### v4.7.1 Data Collection Release Notes

- Biomark Data Collection software v4.7.1 is not compatible with Windows® XP. Contact Fluidigm Technical Support to upgrade your operating system from Windows XP to Windows 10.
- Biomark Data Collection software v4.7.1 requires Microsoft® .NET Framework v4.7.2. The Microsoft .NET Framework is updated when you install the Biomark Data Collection software. Updating the Microsoft .Net Framework on your computer can take up to 15–20 min.

#### v4.7.1 Biomark, Biomark HD, and EP1 Data Collection Enhancements

- Adds support for the FAM-DBQ probe type.
- Adds a new chamber-finding algorithm and median intensity calculation method for 96.96 IFCs to support gene expression assays with bright reagent chambers. Contact Fluidigm Technical Support for assistance.
- Allows calibration images to be saved in JPEG 2000 format (.j2k), which compresses the image files to save disk space.
- Includes the Biomark Image Viewer for viewing compressed calibration images (.j2k).
- Prevents the user from exceeding Windows filename length limitation during the data acquisition. The file path length is limited to 180 characters or less.

- Alerts the user when the firmware is being updated. After the firmware update is complete, the user is prompted to restart the Biomark Data Collection software.
- Updates company branding.

#### **v4.7.1 Biomark Data Collection Bug Fixes**

When a vacuum error occurs, the chiprun.bml file is saved when the IFC run is completed.

## **v4.5.2 Data Collection Release Notes**

### **v4.5.2 Biomark and Biomark HD Data Collection Enhancements**

If the Windows automatic backup utility runs during an integrated fluidic circuit (IFC) run, the available storage could be reduced to below the amount required to save all data from the IFC run. To ensure that the instrument has sufficient storage to complete the run, the software now requires at least 2 GB of free storage beyond the expected amount of storage required for an IFC run.

### **v4.5.2 Biomark HD Data Collection Bug Fixes**

Under rare circumstances during instrument startup, the instrument would incorrectly report a problem with the thermal cycler heat sink fan. This has now been corrected.

### **v4.5.2 Biomark Data Collection Bug Fixes**

Prevents the IFC run from being aborted if communication with the lamp module fails during an IFC run.

## **v4.5.1 Data Collection Release Notes**

### **v4.5.1 Biomark and Biomark HD Data Collection Enhancements**

Adds support for the 24.192 Dynamic Array™ IFC for gene expression.

### **v4.5.1 Biomark and Biomark HD Data Collection Bug Fixes**

- Protocol Editor adds .pcl extension to thermal protocol filenames.
- Loads predefined IFC runs from v4 analysis software.
- Improves focusing for endpoint reads on Biomark.
- Improves auto-focusing for GE 192.24, GE 24.192, and all Digital Array™ IFCs.

## **v4.2.2 Data Collection Release Notes**

### **v4.2.2 Biomark, Biomark HD, and EP1 Data Collection Enhancements**

None.

### **v4.2.2 Biomark, Biomark HD, and EP1 Data Collection Bug Fixes**

Data Collection software is compatible with Microsoft® .NET Framework 4.5.1.

## **v4.2.1 Data Collection Release Notes**

### **v4.2.1 Biomark, Biomark HD, and EP1 Data Collection Enhancements**

Adds support for the Juno™ 96.96 Genotyping IFC.

### **v4.2.1 Biomark Data Collection Bug Fixes**

The lamp idle time is corrected.

## **v4.1.3 Data Collection Release Notes**

### **v4.1.3 Biomark, Biomark HD, and EP1 Data Collection Enhancements**

None.

### **v4.1.3 Biomark, Biomark HD, and EP1 Data Collection Bug Fixes**

- Data Collection software is compatible with Windows 7 and supports v3 analysis software.
- The instrument idle timer no longer starts during IFC runs.

## **v4.1.2 Data Collection Release Notes**

### **v4.1.2 Biomark, Biomark HD, and EP1 Data Collection Enhancements**

- Adds compatibility with the Microsoft Windows 7 operating system.
- Contact Technical Support for Windows upgrade information.

### **v4.1.2 Biomark, Biomark HD, and EP1 Data Collection Bug Fixes**

None.

## v4.1.1 Data Collection Release Notes

### v4.1.1 Biomark and Biomark HD Data Collection Enhancements

- Adds an installer wizard for updating the drivers.
- Updates three protocols on the Biomark HD system to improve thermal uniformity across the IFC: Standard and Fast TaqMan® for the 96.96 Gene Expression IFC, and Standard TaqMan for the 48.48 Gene Expression IFC.

**NOTE** The three v1 protocols can still be accessed from the new Legacy subdirectory.

- Adds Biomark HD thermal protocol for EvaGreen® gene expression for the 192.24 Gene Expression IFC: 192x24 Fast PCR + Melt v2.
- Adds new protocols and other files to support the Flex Six™ Genotyping IFC.
- Replaces the embedded user guide with a link to the most current user guide on the Fluidigm website.

### v4.1.1 EP1 Data Collection Enhancements

Adds support for the Flex Six Genotyping IFC. Replaces the embedded user guide with a link to the most current user guide on the Fluidigm website.

### v4.1.1 Data Collection Bug Fixes

Enables installation of the software on computers that have Internet Explorer® 10 installed. Internet Explorer 10 users need to perform a full installation of Microsoft .NET Framework 4 using the installation wizard.

## v4.0.1 Data Collection Release Notes

### v4.0.1 Biomark and Biomark HD Data Collection Enhancements

- Adds support for the 192.24 Gene Expression IFC.
- Adds support for the Flex Six Gene Expression IFC.
  - Allows the user to choose partitions to scan.
  - Provides a mechanism to track partition usage.
- Adds support for the High-Precision 96.96 Genotyping™ IFC and the qdPCR 37K™ IFC.
- Adds support for Access Array™ 48.48 PCR and melting curve analysis.

### v4.0.1 Biomark and Biomark HD Data Collection Bug Fixes

None.

# Real-Time PCR Analysis Software Release Notes

For more information, see the Real-Time PCR Analysis User Guide (68000088).

## v4.7.1 Real-Time PCR Analysis Release Notes

- Real-Time PCR Analysis software v4.7.1 requires Microsoft .NET Framework v4.7.2. The Microsoft .NET Framework is updated when you install the Real-Time PCR Analysis software. Updating the Microsoft .Net Framework on your computer can take up to 15–20 min. The .NET Framework v4.7.2 is not compatible with Windows XP.

### v4.7.1 Real-Time PCR Analysis Enhancements

- Adds support for two new detector types: Blank and Control.
  - Adds a new Ct threshold method that only uses the Control detector assay (with Control type) to determine the Ct threshold.
  - Does not use Blank and NTC samples and NRC assays when calculating Auto Ct Threshold.
- Adds a new chamber-finding algorithm and median intensity calculation method for 96.96 IFCs to support gene expression assays with bright reagent chambers. Contact Fluidigm Technical Support for assistance.
- Allows export of inlet-to-well position mapping.
- Applies median filter boundary handling for all of the chambers if more than 50% of the chambers have a larger intensity variation between first and second cycles.
- Includes the Biomark Image Viewer for reviewing focus and exposure images (**Tools > Biomark Image Viewer**).
- Changes the grid color to green for manual grid-finding.
- Improves chamber-finding algorithm for 96.96 IFCs.
- Updates company branding.

### v4.7.1 Real-Time PCR Analysis Bug Fixes

- Standard curve can be enabled for 24.192 IFCs.
- Heat map results can be exported from a command line.
- 192.24 Gene Expression IFC runs can be converted to more sample chip runs.
- Ct values for the last cycle are reported (they were reported as 999).
- Melting curve analysis (MCA) peak is identified even when there is an abnormal signal.

## v4.5.2 Real-Time PCR Analysis Release Notes

### v4.5.2 Real-Time PCR Analysis Enhancements

None.

### v4.5.2 Real-Time PCR Analysis Bug Fixes

- Exported data correctly shows if  $\Delta C_t$  or  $\Delta\Delta C_t$  was calculated using two-color real-time data collection with Export Reagent Reference Count deselected.
- Installs the required C++ redistributables for new Windows 10 installations.
- Corrects the fold change when the  $\Delta\Delta C_t$  is 999 ( -1 instead of 999).

## v4.5.1 Real-Time PCR Analysis Release Notes

### v4.5.1 Real-Time PCR Analysis Enhancements

- Support is added for the 24.192 Dynamic Array IFC for gene expression, including:
  - Support for importing multiple 96-well assay plates for the GE 24.192 IFC.
  - Support for annotation of reagents for two 96-well assay plates for the GE 24.192 IFC.
- An IFC run is protected from being overwritten by a second user if a user is analyzing it.
- Export options are updated:
  - Exporting Table Results with Raw Data includes amplification and MCA curve data.
  - An export option is added to enable user to exclude sample and reagent plate information for compatibility with previous versions.
- Options in the Details Views pane are updated:
  - The label “Fail” is replaced with “Flag” for  $C_t$  calls.
  - The manual No Call option is removed to avoid confusion with the new Flag label.
  - Clicking Log Graph only affects the amplification curve plot.

**NOTE** You can continue to export the label “Fail” by selecting **Substitute “Flag” with “Fail”** in the Tools Menu Options under Results Export. If you desire to continue using the No Call option, contact Technical Support for assistance to enable it.

- When calculating the quality score for  $\Delta C_t$  and  $\Delta\Delta C_t$ ,  $C_t$  values manually marked Pass are changed to 1 and  $C_t$  values manually marked Flag are changed to 0.
- The user can select multiple inlets and designate them as reference using the Sample Editor or Detector Editor in the Sample and Detector Setup Views.
- The time needed to perform the  $\Delta\Delta C_t$  calculation is reduced.
- An IFC map is added to display the inlet locations for the samples and assays/detectors.
- The dispense map selection button is relabeled “Map...”

- The calibration chart displays the linear equation parameters with three digits.
- When an assay is annotated “NRC,” the Auto (Detectors) Ct Threshold Method uses the lowest Ct threshold from other assays as the Ct threshold for the NRC assay.

#### v4.5.1 Real-Time PCR Analysis Bug Fixes

- Updates the Installer to support Windows 10.
- When using two 96-well sample plates for the 192.24 IFC, designating a sample as reference in one plate does not change the reference designated in the other plate.
- The estimated background intensity and the smoothness of the amplification curve are improved when the signal intensity is low and the background is high.
- For closed T<sub>m</sub> peaks that have the same whole-number value but different decimal values (for example, 86.4 and 86.9), if the T<sub>m</sub> maximum threshold is placed between the two peaks, the Range column for the higher T<sub>m</sub> peak is 999 and the Out Range column is the peak value.
- When two 96-well plates are used for samples or detectors, the IFC name and barcode information are displayed in exported data.
- The Summary View correctly displays the sample plate information when annotating samples from two 96-well plates.
- The equation for the calibration curve updates after the standard concentration is updated.

### v4.3.1 Real-Time PCR Analysis Release Notes

#### v4.3.1 Real-Time PCR Analysis Enhancements

- Provides support for multiple reference detectors:
  - Allows multiple reference detectors (assays) to be used for  $\Delta\text{Ct}$  and  $\Delta\Delta\text{Ct}$  calculation.
  - Adds a new group of Reagent Reference Count columns in the Details Views for additional detector reference information. To export data from the Reagent Reference Count columns, you must enable this feature in the Tools Menu Options under Results Export.
- Adds options for Results Export in Tools > Options. Each of these options must be enabled before it can be used.
  - **Export comments:** When enabled, includes the user-defined comments in the exported data.
  - **Mark User Calls in Table Results:** When enabled, indicates manually changed calls as “mPass” or “mFail.”

- **Export Reagent Reference Count:** When enabled, includes the Reagent Reference Count columns.
- When finding corners manually, the software performs an alignment quality check and alerts the user if the corners are not positioned correctly.
- Allows the user to export table results with raw data.
- Renames Analysis Views to Details Views.

#### v4.3.1 Real-Time PCR Analysis Bug Fixes

- Improves the automatic chamber finding for 192.24 IFCs.
- The  $T_m$  Peak Detection Range is not limited to the acquisition temperature steps.
- Add Comments and Accelerator Key Definitions can be saved as default when using any level of Windows operating system user account settings.
- Quality Calls for  $\Delta Ct$  and  $\Delta\Delta Ct$  calculations are determined from both the target and reference samples and detectors (not just the target sample and detector).
- In the Heat Map view, the Clear All command updates the display for all the chambers with user calls.

## v4.1.3 Real-Time PCR Analysis Release Notes

### v4.1.3 Real-Time PCR Analysis Enhancements

None.

### v4.1.3 Real-Time PCR Analysis Bug Fixes

When running two 192.24 IFCs, the non-annotated inlets on the second plate are no longer labeled with the annotations from the first IFC.

## v4.1.2 Real-Time PCR Analysis Release Notes

### v4.1.2 Real-Time PCR Analysis Enhancements

None.

### v4.1.2 Real-Time PCR Analysis Bug Fixes

In the Ct Thresholds tab and the MCA tab in the Analysis Settings section of the Tasks pane:

- Enables sorting for the Detector column.



- Selecting an assay displays the corresponding amplification curve plot and melting curve (for EvaGreen assays) plot in the Graph Viewer pane.

## v4.1.1 Real-Time PCR Analysis Release Notes

### v4.1.1 Real-Time PCR Analysis Enhancements

- Allows user to customize default analysis parameters:
  - **For Ct Analysis:** Quality Threshold, Baseline Correction Method, and Ct Threshold Method
  - **For Melt Curve Analysis:** Peak Sensitivity and Peak Ratio Threshold
- Replaces the embedded user guide with a link to the most current user guide on the Fluidigm website.

### v4.1.1 Real-Time PCR Analysis Bug Fixes

- Enables installation of the software on computers that have Internet Explorer 10 installed. Internet Explorer 10 users need to perform a full installation of Microsoft .NET Framework 4 using the installation wizard.
- IFC runs with different assay sets can now be combined as long as the runs have the same sample names.
- Makes chamber alignment corrections.

## v4.0.1 Real-Time PCR Analysis Release Notes

### v4.0.1 Real-Time PCR Analysis Enhancements

- Adds support for the 192.24 Gene Expression IFC.
- Adds support for the Flex Six Gene Expression IFC.  
Allows the user to combine partitions into a single analysis.
- Allows the user to change the  $T_m$  range in melting curve analysis using decimal points.
- Updates the Ct quality score algorithm for the Linear (Derivative) method.  
Using the new algorithm, the quality score is calculated based on slope and linearity of the data around the point at which the curve crosses the threshold for Ct determination using five neighboring datapoints ( $\pm 2$ ). Additional filtering helps determine if there is no amplification. Since the score is primarily focused on the Ct threshold region, more consistent scores are produced.

- Changes the default baseline method for new IFC runs to Linear (Derivative). Data remains unchanged if the user stays with the Linear method.
- To change the baseline correction: Click **Analysis Views**. Under Analysis Settings, select a different option in the Baseline Correction field.
- Adds support for two modes of image contrast adjustment (All vs. Individual).
  - Clicking Auto Contrast performs an auto contrast of the entire image. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
  - Dragging the left or right bars in the contrast range selection changes image contrast. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
- Enables display of two or three fused images in the image view. If the contrast mode is All, the user can adjust the contrast of the fused images. If the mode is Individual, the user must display and adjust individual dye images and then reselect image fusion.
- Permits a dual primary view so the user can view a table and a heat map concurrently.
- Allows the user to set up predefined comments using a set of accelerator keys. Associating comments with accelerator keys (like function keys—F2, F3, etc.) ensures that the user does not have to type comments repeatedly.
- Adds the ability to create custom sample or reagent dispense maps for the Access Array 48.48 IFC.
- For Real-Time Gene Expression Analysis IFC runs, permits combined IFC runs if the user annotates the IFC runs with matching annotations.
- Adds a shortcut to email IFC run information to Fluidigm Technical Support. The extracted IFC run information includes ChipRun.bml, first and last cycle images, and analysis software screenshots.

#### v4.0.1 Real-Time PCR Analysis Bug Fixes

Sample name is now displayed correctly in Image view.

# SNP Genotyping Analysis Software Release Notes

For more information, see the SNP Genotyping User Guide (68000098).

## v4.5.1 SNP Genotyping Analysis Release Notes

### v4.5.1 SNP Genotyping Analysis Enhancements

- Adds support for the 24.192 Dynamic Array IFC for genotyping, including:
  - Support for importing multiple 96-well assay plates for the GT 24.192 IFC.
  - Support for annotation of reagents for two 96-well assay plates for the GT 24.192 IFC.
- Adds an export option to enable users to exclude sample and reagent plate information for compatibility with previous versions.
- Updates to the Assay Reference Library (ARL) and/or Adaptive Assay Reference Library (AARL):
  - By default, the cluster center is displayed.
  - The Align NTC (no template control) feature is disabled for SNP Type™ assays.
  - Ellipses created with one or two datapoints are visible.
  - Assay reference database checks the axis setting when adding IFC run data.
- Right-clicking the points in the scatter plot view performs consistently with right-clicking points in the other views.
  - Right-clicking a point highlights it and opens the context-sensitive menu.
  - Pressing Ctrl while clicking adds points to the selection.
- Updates to marking samples “Invalid”:
  - Samples that are named “Invalid” are marked invalid automatically to exclude them from being used in clustering. These unused samples can then be hidden by selecting **Hide Invalid**.
  - The user can mark all samples for a specific assay “Invalid” by annotating the assay as “Invalid.”
  - Bad chambers are marked “Invalid” (instead of No Call) so they can then be hidden by selecting **Hide Invalid**.
- The Allele X and Allele Y annotations can be switched in the final call by adding “>” at the beginning of the allele name.
- An IFC map is added to display the inlet locations for the samples and assays/detectors.
- The dispense map selection button is relabeled “Map...”

### v4.5.1 SNP Genotyping Analysis Bug Fixes

- The Installer is updated to support Windows 10.

- When assay names in an IFC run are changed, the embedded Assay Reference Library will no longer be in use.
- All selected IFC run data is added to the Assay Reference Library.
- Combined IFC runs with labels that set the first probe type to the Y axis and the second probe type to the X axis can be used with the Assay Reference Library.
- When two 96-well plates are used for samples or detectors, the IFC name and barcode information are displayed in exported data.
- The Summary View correctly displays the sample plate information when annotating samples from two 96-well plates.
- Circling of multiple points in the scatter plot is not affected when the text size of the Windows operating system is set higher than 100%.
- SNP Trace™ no longer crashes when the sample name field is empty.
- The entire IFC run name is shown in the Assay Reference Library Manager Remove Chip Run dialog box.
- In the Assay Reference Library Manager, cluster information is displayed correctly when the user adds an IFC run when the Align NTC option is on.
- For 192.24 IFCs, annotations made in one sample container update the annotations in the other sample container.
- Changes to the Allele X and Allele Y annotation also result in updates in the replicated assays.
- Installs the required C++ redistributables for new Windows 10 installations (Installer update, August 2018).

## v4.4.1 SNP Genotyping Analysis Release Notes

### SNP Genotyping Analysis v4.4.1 Enhancements

- Adds enhancements to the Assay Reference Library:
  - Adds a new Adaptive Assay Reference Library option for analyzing IFC runs that use assay panels. When analyzing an IFC run with the Adaptive Assay Reference Library, the run will be analyzed with the library that matches the panel, IFC type, and system.
  - Adds a matching score for the Adaptive Assay Reference Library. The score is calculated for assays containing three autocalled clusters.
  - For all runs analyzed with an Assay Reference Library or an Adaptive Assay Reference Library, shows the assay reference center in the Assay Summary View cluster plots.

- Allows users to manage the Assay Reference Libraries and Adaptive Assay Reference Libraries from the Options window.
- Adds an option to use raw intensity only to combine multiple IFC runs from the same system.
- High ROX™ Reference Dye values are no longer called as No Calls.
- Protects an IFC run from being overwritten by a second user if a user is analyzing it.
- Allows the user to select a specific cycle for endpoint conversion.
- Allows the user to export table results with raw data.

### SNP Genotyping Analysis v4.4.1 Bug Fixes

- A single cluster is no longer labeled No Call.
- The Options window correctly shows the Analysis Parameter setting as unchecked when not using a customized confidence threshold value.
- The Analysis Views link in the Chip Run Summary pane is renamed Detail Views and opens the Detail Views pane when clicked.
- A single datapoint cluster is correctly labeled when analyzing data with the Assay Reference Library.

## v4.3.2 SNP Genotyping Analysis Release Notes

### SNP Genotyping Analysis v4.3.2 Enhancements

When finding corners manually, the software performs an alignment quality check and alerts the user if the corners are not positioned correctly.

### SNP Genotyping Analysis v4.3.2 Bug Fixes

- Changing the Microsoft Windows operating system font size has no effect on the Allele Settings window.
- For 192.24 IFC runs, identifies misloaded samples as no-calls.
- Add Comments and Accelerator Key Definitions can be saved as default when using any level of Windows operating system user account settings.
- Modified allele settings can be saved as default for an IFC run.
- Genotyping assay plates from SNP Genotyping Analysis software v3 can be imported.
- The Assay Reference Library properly aligns to the cluster when no NTC is defined for SNP Type™ assays.

## v4.3.1 SNP Genotyping Analysis Release Notes

### v4.3.1 SNP Genotyping Analysis Enhancements

- Allows the user to convert a real-time run to an endpoint run.
- Allows the user to perform genotyping clustering analysis on different cycles for individual assays.
- Allows the user to open a two-color real-time gene expression run in read-only mode.
- Adds an optional ID column for samples. This feature can be enabled in the Tools Menu Options under Annotation.

### v4.3.1 SNP Genotyping Analysis Bug Fixes

- In the SNP Trace Panel Analysis tool, the no-call count is calculated correctly when the required number of no-calls for Y-chromosome SNPs is changed from the default value for the female rule.
- Assay Reference cluster ellipses align properly when using the SNP Type normalization method with Assay Reference Libraries.
- Comments per chamber works with all runs in a combined IFC run.
- The user can create 2D combined IFC runs.

## v4.2.1 SNP Genotyping Analysis Release Notes

### v4.2.1 SNP Genotyping Analysis Enhancements

Adds support for the Juno 96.96 Genotyping IFC.

### v4.2.1 SNP Genotyping Analysis Bug Fixes

Comments and summary results export properly.

## v4.1.3 SNP Genotyping Analysis Release Notes

### v4.1.3 SNP Genotyping Analysis Enhancements

None.

### v4.1.3 SNP Genotyping Analysis Bug Fixes

- When running two 192.24 IFCs, the non-annotated inlets on the second plate are no longer labeled with the annotations from the first IFC.
- 96.96 IFC endpoint runs on the EP1 reader no longer fail due to no-calls.

## v4.1.2 SNP Genotyping Analysis Release Notes

### v4.1.2 SNP Genotyping Analysis Enhancements

Allows the user to rename assays in the Assay Reference Library.

### v4.1.2 SNP Genotyping Analysis Bug Fixes

The Chip Run Analysis Report now displays the correct call rate for the 192.24 IFC in the Sample Summary.

## v4.1.1 SNP Genotyping Analysis Release Notes

### v4.1.1 SNP Genotyping Analysis Enhancements

- Renames the RUID QC Panel to SNP Trace Panel.
  - Requires only the 6 gender assays and 10 quality assays to perform the SNP Trace Panel analysis on each sample.
  - For more information about using the SNP Trace Panel, see to the Fluidigm SNP Trace Panel User Guide (PN 100-7282).
- Adds support for the Flex Six Genotyping IFC.
- Allows the user to customize default analysis parameters for Confidence Threshold.
- Replaces the embedded user guide with a link to the most current user guide on the Fluidigm website.

### v4.1.1 SNP Genotyping Analysis Bug Fixes

- Enables installation of the software on computers that have Internet Explorer 10 installed. Internet Explorer 10 users need to perform a full installation of Microsoft .NET Framework 4 using the installation wizard.
- The user can combine IFC runs with different assay sets, as long as the runs have the same sample names.
- The call rate for 192.24 Genotyping IFCs now displays correctly in Summary View.
- Makes chamber alignment corrections.
- Genotyping Email Chip Run Information no longer produces an error and shuts down the application.
- Genotyping Allele naming is now consistent with the naming conventions in version 3.

## v4.0.1 SNP Genotyping Analysis Release Notes

### v4.0.1 SNP Genotyping Analysis Enhancements

- Adds support for the High-Precision 96.96 Genotyping IFC.
- Adds the SNP Type Normalization method as the default analysis method for SNP Type assays.
- In cases where an assay design forms nonspecific amplicons and no template control (NTC) data are invalid, SNP Type Normalization uses NTCs from other assays in the same IFC to normalize the data.
- Adds support for two modes of image contrast adjustment (All vs. Individual).
  - Clicking Auto Contrast performs an auto contrast of the image. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
  - Dragging the left or right bars in the contrast range selection changes image contrast. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
  - Enables display of two or three fused images in the image view. If the image contrast mode is All, the user can adjust the contrast of the fused images. If the mode is Individual, the user must display and adjust individual dye images and then reselect image fusion.
- Permits a dual primary view so the user can view a table and a heat map concurrently.
- Allows users to set up predefined comments using a set of accelerator keys. Associating comments with accelerator keys (like function keys—F2, F3, etc.) ensures that the user does not have to type comments repeatedly.
- Adds the ability to analyze the SNP Trace Panel.
- Permits the user to customize analysis parameters and save them as a default setting or a file for subsequent use.
- Enables the user to write comments at the chamber level in the detailed table.
- Adds a shortcut to email IFC run information to Fluidigm Technical Support. The extracted IFC run information includes ChipRun.bml, first and last cycle images, and analysis software screenshots.

### v4.0.1 SNP Genotyping Analysis Bug Fixes

- Convert To More Sample Chip Run is no longer enabled for an IFC run that has already been converted to more samples.
- Sample name is now displayed correctly in Image view.
- Sample names and formats are now correctly displayed for combined IFC runs on the 192.24 Genotyping IFC.



- The Assay Reference icon is no longer displayed for assays that were not part of the assay library, with all datapoints as invalid or no-calls.
- The 192.24 assay dispense map matches the instructions in the Genotyping with the 192.24 IFC Using Fast TaqMan Assays Quick Reference (PN 100-3184) and the Genotyping with the 192.24 IFC Using SNP Type Assays Quick Reference (PN 100-3913).

# Digital PCR Analysis Software Release Notes

For more information, see the Digital PCR Analysis User Guide (68000100).

## v4.1.2 Digital PCR Analysis Release Notes

### v4.1.2 Digital PCR Analysis Enhancements

None.

### v4.1.2 Digital PCR Analysis Bug Fixes

- In the Ct Thresholds tab in the Analysis Settings section of the Tasks pane:
  - Sorting is now enabled for the Detector column.
  - Selecting an assay now displays the corresponding amplification curve plot in the Graph Viewer pane.
- Installs the required C++ redistributables for new Windows 10 installations (Installer update, August 2018).

## v4.1.1 Digital PCR Analysis Release Notes

### v4.1.1 Digital PCR Analysis Enhancements

- Allows the user to customize default analysis parameters for Ct Analysis and End Point Analysis:
  - **For Ct Analysis:** Quality Threshold, Baseline Correction Method, Ct Threshold Method, and Ct Range
  - **For End Point Analysis:** Quality Threshold and Intensity Threshold Method
- Replaces the embedded user guide with a link to the most current user guide on the Fluidigm website.

### v4.1.1 Digital PCR Analysis Bug Fixes

- Enables installation of the software on computers that have Internet Explorer 10 installed. Internet Explorer 10 users need to perform a full installation of Microsoft .NET Framework 4 using the installation wizard.
- Makes chamber alignment corrections.

## v4.0.1 Digital PCR Analysis Release Notes

### v4.0.1 Digital PCR Analysis Enhancements

- Adds support for the qdPCR 37K IFC.
- Adds functionality that combines PCR and melting curve analysis protocols for using Delta Gene™ assays and digital IFCs.
- Allows the user to specify the Ct detection range by probe type or panel.  
Changes the default baseline method for new IFC runs to Linear (Derivative).
- To change the baseline correction: Click **Analysis Views**. Under Analysis Settings, select a different option in the Baseline Correction field.
- Adds support for two modes of image contrast adjustment (All vs. Individual).
  - Clicking Auto Contrast performs an auto contrast of the image. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
  - Dragging the left or right bars in the contrast range selection changes image contrast. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
- Enables display of two or three fused images in the image view. If the image contrast mode is All, the user can adjust the contrast of the fused images. If the mode is Individual, the user must display and adjust individual dye images and then reselect image fusion.
- Permits a dual primary view so the user can view a table and a heat map concurrently.
- Allows the user to set up predefined comments using a set of accelerator keys. Associating comments with accelerator keys (like function keys—F2, F3, etc.) ensures that the user does not have to type comments repeatedly.
- Adds a shortcut to email IFC run information to Fluidigm Technical Support. The extracted IFC run information includes ChipRun.bml, first and last cycle images, and analysis software screenshots.

### v4.0.1 Digital PCR Analysis Bug Fixes

None.

# Melting Curve Analysis Software Release Notes

For more information, see the Melting Curve Analysis User Guide (68000118).

## v4.1.3 Melting Curve Analysis Release Notes

### v4.1.3 Melting Curve Analysis Enhancements

None.

### v4.1.3 Melting Curve Analysis Bug Fixes

- When running two 192.24 IFCs, the non-annotated inlets on the second plate are no longer labeled with the annotations from the first IFC.
- Installs the required C++ redistributables for new Windows 10 installations (Installer update, August 2018).

## v4.1.2 Melting Curve Analysis Release Notes

### v4.1.2 Melting Curve Analysis Enhancements

None.

### v4.1.2 Melting Curve Analysis Bug Fixes

In the Peak Detection Range section of the Tasks pane:

- Enables sorting for the Detector column.
- Selecting an assay now displays the corresponding melting curve plot in the Graph Viewer pane.

## v4.1.1 Melting Curve Analysis Release Notes

### v4.1.1 Melting Curve Analysis Enhancements

Replaces the embedded user guide with a link to the most current user guide on the Fluidigm website.

### v4.1.1 Melting Curve Analysis Bug Fixes

- Enables installation of the software on computers that have Internet Explorer 10 installed. Internet Explorer 10 users need to perform a full installation of Microsoft .NET Framework 4 using the installation wizard.

- The user can combine IFC runs with different assay sets, as long as the runs have the same sample names.
- Makes chamber alignment corrections.

## v4.0.1 Melting Curve Analysis Release Notes

### v4.0.1 Melting Curve Analysis Enhancements

- Adds support for the 192.24 Gene Expression IFC.
- Adds support for two image contrast adjustments (All vs. Individual).
  - Clicking Auto Contrast performs an auto contrast of the image. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
  - Dragging the left or right bars in the contrast range selection changes image contrast. If the contrast mode is All, contrast values apply to all colors. If the mode is Individual, values apply to the selected color only.
- Enables display of two or three fused images in the image view. If the image contrast mode is All, the user can adjust the contrast of the fused images. If the mode is Individual, the user must display and adjust individual dye images and then reselect image fusion.
- Permits a dual primary view so the user can view a table and heat map concurrently.
- Allows the user to set up predefined comments using a set of accelerator keys.
- Permits multiple simultaneous IFC runs for melting curve analysis.
- Adds a shortcut to email IFC run information to Fluidigm Technical Support. The extracted IFC run information includes ChipRun.bml, first and last cycle images, and analysis software screenshots.

### v4.0.1 Melting Curve Analysis Bug Fixes

Sample name is now displayed correctly in Image view.

### For technical support visit [fluidigm.com/support](https://fluidigm.com/support).

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