MIA FORA NGS FLEX SOFTWARE v3.0

PART NUMBER: SR-790-00017 AND SR-850-00043 FOR USE WITH
MIA FORA NGS FLEX HLA TYPING KIT PART NUMBERS
SR-800-10433-24 (FLEX11), SR-800-10433-96 (FLEX11), SR-800-10441-24 (FLEX9), SR-800-10441-96
(FLEX9), SR-800-10440-24 (FLEX6), SR-800-10440-96 (FLEX6), SR-800-10439-24 (FLEX5) and SR-
800-10439-96 (FLEX5).

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MIA FORA NGS FLEX v3.0 introduces the following new features:

**COMPATIBILITY WITH MIA FORA NGS FLEX KITS**
User can select run mode for Flex 11, Flex 9, Flex 6 or Flex 5 kit. Also a custom run mode can be used for user defined gene set.

**UPDATED SIRONAQUANT**
SIRONAQUANT can now be used with variable sample number and each kit configuration.

**SEARCH ALLELE PAIR**
User can search for a sample by allele pair for each locus.

**FILTER FOR CANDIDATE ALLELE**
A user has the ability to use the regular expression filter box to quickly locate alleles of interest in the candidate table.

**LOOK AT ONE PLATE AT A TIME**
For runs with multiple plates, user can select to look at one plate at a time in the summary table.

**BATCH OPERATIONS FROM SUMMARY TABLE**
User can “approve all”, “unapprove all”, “confirm all”, or “unconfirm all” for all samples in a batch from the summary table. An XML report for multiple samples can be exported from the summary table.

**EXPORT PROJECT RESULTS IN HML FORMAT**
User can export project results using the HML format with contig block sequences.

**DATA REVIEW OF SAMPLES DURING ANALYSIS**
User can review the results for finished samples once the analysis for that sample is complete.

**SIMPLIFIED VIEW FOR DATA REVIEW**
Software provides a simplified view of the genotyping results and quality metrics.
MIA FORA NGS FLEX RELEASE NOTES

<table>
<thead>
<tr>
<th>FEATURE</th>
<th>FUNCTION</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AUTO START THE ANALYSIS WHEN SEQUENCING RUN IS DONE</strong></td>
<td>THE ANALYSIS CAN START AUTOMATICALLY AFTER THE SEQUENCING RUN IS FINISHED AND THE RAW DATA IS READY ON THE GLOBAL STORAGE.</td>
</tr>
<tr>
<td><strong>SAMPLE LEVEL QC IN REVIEW</strong></td>
<td>FOR DATA REVIEW PAGE, A SAMPLE QC BUTTON IS ADDED TO SHOW THE SAMPLE LEVEL QC METRICS AND CAN BE EXPORTED IN PDF FORMAT.</td>
</tr>
<tr>
<td><strong>AMBIGUITY IN THE SUMMARY TABLE</strong></td>
<td>AMBIGUITY IS SHOWN IN THE SUMMARY TABLE IN A SEPARATE COLUMN.</td>
</tr>
<tr>
<td><strong>NULL ALLELES INCLUDED IN CANDIDATE TABLE</strong></td>
<td>FOR ALLELES SHOWN IN THE CANDIDATE TABLE, CORRESPONDING NULL ALLELES ARE ALWAYS LISTED SO USERS CAN COMPARE AND CONFIRM THE CALL.</td>
</tr>
<tr>
<td><strong>OPTION TO VIEW SAMPLE QC IN REPORT</strong></td>
<td>LAB DIRECTOR CAN SET THE OPTION TO SHOW SAMPLE QC PAGE IN THE REPORT.</td>
</tr>
<tr>
<td><strong>OPTION FOR REPORTING 3 FIELDS</strong></td>
<td>LAB DIRECTOR CAN SET THE OPTION TO REPORT ALLELE WITH 3 FIELDS. THE DEFAULT IS 4 FIELDS.</td>
</tr>
<tr>
<td><strong>OPTION FOR INCLUDE COMMENTS IN THE REPORT</strong></td>
<td>LAB DIRECTOR CAN SET THE OPTION TO SHOW COMMENTS IN THE REPORT.</td>
</tr>
<tr>
<td><strong>LAB INFORMATION IN PREFERENCE</strong></td>
<td>LAB DIRECTOR CAN SPECIFY REPORTING CENTER CONTEXT, REPORTING CENTER ID AND NMDP HL7 ID.</td>
</tr>
<tr>
<td><strong>ANNOTATION TRACK FOR CONTIG BLOCKS</strong></td>
<td>ADDED ANNOTATION TRACK IN THE GENOMIC COVERAGE VIEW AND ASSEMBLY BROWSER TO INDICATE BOUNDARIES OF PHASED CONTIG BLOCKS.</td>
</tr>
</tbody>
</table>

MIA FORA NGS FLEX SOFTWARE V3.0 INTRODUCES THE FOLLOWING NEW FEATURES:

- Compatibility with **MIA FORA NGS FLEX kits**. The User can select run mode for FLEX 11, FLEX 9, FLEX 6, or FLEX 5 kit. Also a custom run mode can be used for user defined gene set.
A User can search for a sample by **Allele Pairs** for certain locus using the Search box.

A Regular Expression Filter Box provides a search tool for allele of interest on the candidate allele table as well as the Candidate Pair Table.
Data review of samples can begin for a sample when it is complete without having to wait for the entire batch to be completed. This is indicated when the third arrow is dark gray, and when all the samples are ready it becomes orange. Once the review has started, the arrow stays blue until all samples have been reviewed.

Users can process the data in **Batch Operations**. At the top of the table, users can click “Approve All”, “Unapprove All”, “Confirm All” and “UnConfirm All” buttons to process the data in a batch. In addition, users can click on the buttons to export the project in XML format.
The Review Window provides a **Simplified View** of the genotyping results and quality metrics.
Once configured correctly with the project name matching the Experiment name in the MiSeq or MiniSeq run, the FLEX software is designed to start **Data Analysis Automatically** once the sequencing run is done. The software will generate the FASTQ files from the sequencing raw data and launch the analysis pipeline after the generation of the FASTQ files. For configuration details to fetch the sequences from the Illumina instruments please contact Technical Support.

A **Sample QC button** has been added to the sample information block. The sample QC button will show the sample level QC metrics, which can be exported into PDF format.

If an **Ambiguity** exists it will be shown in a separate column in the summary table.
For alleles shown in the candidate table, corresponding **Null Alleles** are always listed so users can compare and confirm the call.

```
<table>
<thead>
<tr>
<th>Allele</th>
<th>Call</th>
<th>MME</th>
<th>MME</th>
<th>cRead</th>
<th>Cov</th>
<th>gRead</th>
<th>Cov</th>
<th>Cen</th>
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</thead>
<tbody>
<tr>
<td>A*23:01:01</td>
<td>✔</td>
<td>0</td>
<td>0</td>
<td>8902</td>
<td>100</td>
<td>18</td>
<td>20103</td>
<td>87</td>
</tr>
<tr>
<td>A*01:01:01</td>
<td>✔</td>
<td>0</td>
<td>0</td>
<td>9118</td>
<td>83</td>
<td>22</td>
<td>20439</td>
<td>69</td>
</tr>
<tr>
<td>A*01:188</td>
<td></td>
<td>1</td>
<td>N/A</td>
<td>1393</td>
<td>91</td>
<td>22</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A*01:01:02N</td>
<td></td>
<td>0</td>
<td>4</td>
<td>9118</td>
<td>83</td>
<td>22</td>
<td>20254</td>
<td>-3</td>
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<tr>
<td>A*01:01:03</td>
<td></td>
<td>0</td>
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<td>9118</td>
<td>83</td>
<td>22</td>
<td>19576</td>
<td>-6</td>
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<td>N/A</td>
<td>3246</td>
<td>81</td>
<td>18</td>
<td></td>
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<td>N/A</td>
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<td>75</td>
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<td>1</td>
<td>N/A</td>
<td>1241</td>
<td>52</td>
<td>9</td>
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<tr>
<td>A*23:03:02</td>
<td></td>
<td>1</td>
<td>N/A</td>
<td>1021</td>
<td>32</td>
<td>4</td>
<td></td>
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<tr>
<td>A*01:30</td>
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<td>3</td>
<td>N/A</td>
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<tr>
<td>A*01:89</td>
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<td>1</td>
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<td></td>
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<td>A*23:70</td>
<td></td>
<td>4</td>
<td>N/A</td>
<td>3130</td>
<td>15</td>
<td>3</td>
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<tr>
<td>A*01:14</td>
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<td>8989</td>
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<td>N/A</td>
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<td>14</td>
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<td></td>
<td></td>
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<td>3</td>
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<td>13</td>
<td>2</td>
<td>18977</td>
<td>-7</td>
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</tbody>
</table>
```
Additional **Reporting Options** have been added in Preferences for Lab Directors. Lab Directors can now set an option to show sample QC metrics, report allele with 3 fields (default is 4), and show comments in the report.

**Laboratory Information in Preferences** now allows a Lab Director to specify reporting center context, reporting center ID, and NMDP HL7 ID.
Instructions for Software Upgrade

REQUIRED:
- Update thumb drive provided by Immucor (SR-800-00467)
- Access to server with attached keyboard, mouse and monitor

1. Log in to the system directly as root and choose "KDE plasma workspace" (see screenshot to the right); Click on "not listed" at the bottom of the page, enter “root” as username, and sign in.

2. Connect the thumb drive provided by Immucor to the server, open dolphin file manager (RedHat start -> File Manager), and copy opeUpdate.tar.gz to your home folder (by dragging). Eject thumb drive after it's completely done copying.

3. Open a terminal window (RedHat start -> Terminal), uncompress the update file, execute the following command in the terminal:

   tar xzf opeUpdate.tar.gz

4. Run the update program, execute the following command in the terminal and follow the instructions in the screen.

   ./OnePassInstaller
5. If no errors are shown during any of the steps above, you have successfully updated your NGS system to the latest version. Let's clean up by executing the command below in one line in the terminal.

```bash
rm -rf opeUpdate.tar.gz OnePassInstaller modules/
```

6. Log out, you should not have to log in as root until the next update.

**Related Documents**


**Recommendations:**

MIA FORA NGS Software is used to deliver HLA Typing results. Follow MIA FORA Software User Guide for HLA typing data analysis. Due to the complex nature of HLA Testing, qualified laboratory personnel must review any result to ensure correctness.

*We welcome your comments and feedback for future product improvements.
If you have any questions or concerns please feel free to contact Technical Support at: 855-IMMUCOR: Select option #2 and then option #7.*