

# **Local Run Manager**

## **DNA Amplicon Analysis Module v2.1.0**

### **Release Notes**

## Introduction

This release notes capture notable changes for the DNA Amplicon Analysis Module v2.1.0 release relative to the DNA Amplicon Analysis Module v1.1.0.

DNA Amplicon Analysis Module v2.1.0 requires Local Run Manager Framework v2.0.0 or higher and is not compatible with Local Run Manager Framework v1.3.1 or lower. The DNA Amplicon Analysis Module replaces the Amplicon Analysis Module.

For more information about this analysis module and how to use it, refer to the Local Run Manager DNA Amplicon Analysis Module Workflow Guide, available from the Local Run Manager support page under Documentation & Literature section, on illumina.com.

[http://support.illumina.com/sequencing/sequencing\\_software/local-run-manager/documentation.html](http://support.illumina.com/sequencing/sequencing_software/local-run-manager/documentation.html)

Performing variant annotation on human data using the latest version of the Nirvana Annotation Software requires a new set of annotation files, which can be downloaded from the Local Run Manager support site:

[https://support.illumina.com/sequencing/sequencing\\_software/local-run-manager/downloads.html](https://support.illumina.com/sequencing/sequencing_software/local-run-manager/downloads.html)

### NEW FEATURES:

- Added support for GRCh38 Decoy reference genome.

### IMPROVEMENTS:

- Adjusted variant frequency emit cutoff based on the input of somatic variant frequency threshold. This increases the number of true positive calls and reduces the number of false positive calls.

### KNOWN ISSUES:

- Unnecessary warning messages indicating invalid values appear when hovering the mouse cursor over any of the numerical input fields with up/down arrows, when the entered value is not divisible by the step of the up/down arrows.
- When importing a run, if the path of the run folder is greater than 100 characters, some of the intermediate files created will have paths that exceed the Windows path character limit of 260 characters.
- On MiSeq and Off Instrument Local Run Manager Configurations, the following special characters are accepted in the UI for the Sample Description field, but will trigger an error when attempting to save the Run: `~!@#%\$\_-\_{}
- In rare instances, the Sample Sheet file generated during analysis may not reflect the same ordering of samples as what was entered on the "Run Setup" page.