BaseSpace Core Apps Software Release Notes

TruSeq Long-Read Assembly v1.1

For BaseSpace

February 23, 2015

Introduction

These Release Notes detail the key changes to software components for the TruSeq Long-Read Assembly v1.1 App. This v1.1 release consists mainly of modifications to underlying code for error handling and FASTQ file parsing.

This app is deployed on BaseSpace Cloud.

For more information about this app and how to use it, refer to the app User Guides, available from the details page of each app, and the BaseSpace Support Page, Documentation and Literature, on illumina.com.

http://support.illumina.com/sequencing/sequencing_software/basespace/documentation.ilmn

The software package includes:

- TruSeq Phasing Analysis v1.1

I. TruSeq Long Read Assembly v1.1

NEW FEATURES:

- General stability and robustness improvements.
- Faster start-up time of the app without having to pre-download input files.
- Better handling of missing data/empty wells, particularly for plot generation.
- Improved app logging. Please see user guide for description of log file contents.

DEFECT REPAIRS:

- Extended the stack size limit during barcode assembly to allow for more complicated data sets to be assembled. This only effects combined samples, and which result in 1000 or more FASTQ files being processed.

KNOWN ISSUES:

- TruSeq Synthetic Long-Read Samples that were previously merged in BaseSpace incorrectly due to a platform level bug (i.e. the flowcell numbers in the FASTQ file name kept incrementing per barcode instead of per constituent sample) are no longer compatible with the app. To get around this issue, please re-merge the Samples in BaseSpace.