BaseSpace Core Apps Software Release Notes

Small RNA v1.0

For BaseSpace

April 14, 2015

Introduction

These Release Notes detail notable items for the Small RNA BaseSpace Core App v1.0 release.

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:

- Small RNA v1.0

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KNOWN ISSUES:

- Adapter trimming for the Small RNA v1.0 app is not supported by the Illumina Experiment Manager (IEM) or the BaseSpace Prep tab.
    - A workaround is to use the FASTQ Toolkit v1.0 app to trim the adapters. For read filtering, the minimum read length should be set to 20 or a reasonable length for small RNA.
    - For the TruSeq Small RNA Sample Prep Kit the adapter sequence is 5′ TGGAATTCTCGGGTGCCAAGG.
    - The FastQC app in BaseSpace can be used to determine if adapter sequence is present.
- Users may be unable to find the Novel output folder when downloading the entire set of app output files from BaseSpace.
    - A workaround is to download the individual files manually.
- Users may cause the app to abort when using some (3 total) non-alphanumeric characters (/ \ and “) to name merged samples on BaseSpace.
    - A workaround is to not use the problematic characters when created merged samples on BaseSpace.
- Users may experience slight display issues when viewing in-browser reports using the Safari Browser on a Mac.
    - A workaround is to use the Chrome browser, also available on a Mac.
- Users may experience trivial display issues when viewing in-browser reports using the Firefox and Internet Explorer browsers.
    - A workaround is to use the Chrome browser.
- Users may not be able to find a Small RNA public dataset available to use for testing the app.

    - A workaround is for the user to upload their own dataset, or import one from SRA using the SRA Import BaseSpace Labs app.