

BaseSpace Onsite Platform

Release Notes

For BaseSpace Onsite v1.1

June 25, 2014

Revision History

Revision	Date	Description of Change
A	June 25, 2014	Initial Release.

Introduction

These Release Notes detail key changes to software components for BaseSpace Onsite between the specific versions listed in the following table.

Software Application	Prior Version	New Version
BaseSpace Onsite	1.0	1.1

I. BaseSpace Onsite v1.1 – New Features Overview

Primary New Features:

- Upgrade to BaseSpace Platform v3.7
 - Prep Tab Enhancements:
 - Import Libraries
 - Imports data from a spreadsheet in .CSV file format
 - Customer Prep Kits
 - Configure custom library kits in “My Account ” > “Library Prep Kits”
 - VCF Import Tool
 - Used to upload VCF and gVCF files read by VariantStudio and others apps
 - Downloader App for both Windows & Mac upgraded to latest released version
- VariantStudio v2.2 (Integrated App Download, Launch, Data Access)
- Integrative Genome Viewer (IGV) update to v2.2.1

Secondary New Features:

- Upgraded the following Apps to latest released version.
 - FASTQ / Isis
 - RNA-Seq
- When rerunning any analysis on a sample, the old analyses can now be stored under a subfolder.
 - The user can view all analysis results for a sample.
 - The user is No longer limited to viewing only new analyses.
- Support for externally hosted SMTP servers for email notifications.

II. BaseSpace Onsite v1.1 – New Features in Detail

Primary New Features in Detail:

- Upgrade to the BaseSpace Platform v3.7, including the following:
 - Prep tab now supports the ability to import libraries from a .csv file. A template for the import file is available for download when “Import Sample Libraries” has been selected.
 - Prep tab now offers support for custom library prep kits. When prepping libraries, select, “Custom Library Prep Kit” to enter information for the index set to use. After it is created, the custom kit is saved and can be reused for subsequent libraries.
 - Mac support has been added to the Import tool, allowing the upload of VCF and gVCF files.
 - The Downloader app has been upgraded to the latest version for both Windows and Mac.
- The VariantStudio™ app has been added to BaseSpace Onsite. This app accepts a VCF or gVCF file as input, provides variant annotations, and contains a comprehensive set of customizable variant filters. For more information, visit the following link:
www.illumina.com/clinical/clinical_informatics/illumina-variantstudio.ilmn
- The Integrative Genome Viewer (IGV) app has been upgraded to v2.3. For more information, visit the following link:
www.broadinstitute.org/software/igv/node/250

Secondary New Features in Detail:

- We have also updated the GenerateFASTQ and RNA-Seq apps to match the latest released version in BaseSpace Cloud. Release notes for these apps can be found at the following link:
support.illumina.com/sequencing/sequencing_software/basespace/documentation.ilmn
- When rerunning any analysis on a sample, the old analyses are now stored in a subfolder and viewable from the Samples page.
- Added support for an externally hosted SMTP server for email notifications.

III. Defects repaired in this release:

- The End-User License Agreement can now be viewed and accepted.
- Projects no longer disappear when the "Share By" link is clicked.
- The GenerateFASTQ analysis now correctly sets the number of reads for a sample. Previously, this information was not pulled correctly from the FASTQ files and would display as 0.
- App result files from the Isaac v2 app are now displayed in the sample page. Previously, they did not display at all.

IV. Known Issues:

- The BaseSpace Onsite web-based user interface does not support Internet Explorer 9.x or 10.x when browsers are in compatibility mode.