

# **BaseSpace Core Apps Software Release Notes**

## **ISAAC Enrichment v2.0**

*For BaseSpace and BaseSpace Onsite*

**December 19, 2014**

## Introduction

These Release Notes detail the key changes to software components for the ISAAC Enrichment BaseSpace Core App since the release of the ISAAC Enrichment 1.0 app. This v2.0 release enables upload of custom manifest files (e.g., probes and targeted regions files) generated by Illumina DesignStudio upon ordering a custom enrichment panel.

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://illumina.com).

[http://support.illumina.com/sequencing/sequencing\\_software/basespace/documentation.ilmn](http://support.illumina.com/sequencing/sequencing_software/basespace/documentation.ilmn)

The software package includes:

- ISAAC Enrichment v2.0

## I. ISAAC Enrichment v2.0

### NEW FEATURES:

- Updated to a new version of the ISAAC aligner, version 02.14.08.06. The ISAAC Variant Caller version, 2.0.17, remains the same as the version used in the ISAAC Enrichment v1.0 App.
- Updated the following module and algorithm components:
  - Picard 1.79
  - SAMtools 0.1.19-isis-1.0.1
- Ability to use custom manifest files which have been imported to the BaseSpace project of interest.
- Updated to Illumina Annotation Service (IAS) version 3, which includes improved IAS annotation stability and robustness.
- Added tags to VCF header (e.g. annotator, variant caller version number).
- Improved logging and renamed workflow log files as WorkflowLog.txt and WorkflowError.txt.
- Improved reporting of software version numbers in PDF report.
- Adjusted Isaac aligner settings to avoid >1M bp indels in CIGAR string (resolves Picard warnings about BAM file).
- Only on-target variants are now reported.
- General stability and robustness improvements.
- Improved naming of workflow steps to provide greater consistency. (e.g. "Statistics generation" is now used instead of the previous "Generate statistics").

- Updated PDF report content (plots, notes, stats). See the User Guide for more details.
- Remove minimum depth threshold for variant calling to increase accuracy.

**DEFECT REPAIRS:**

- A fix was made to the calculation of fragment lengths. Now the TLEN column included in the bam file is used to derive fragment length, whereas previously fragment length was calculated from the mapping positions of the read pairs and the read length.
- A fix was made to the integration of IAS and the ISAAC Enrichment v2 app so that Deflate Stream errors will now longer occur.
- A fix was made to the reporting of adapter counts and resulting adapter trimming statistics. Trimming is now reported only for reads passing filter (PF) instead of all reads.
- A fix was made so that in the rare instance when a bam file containing no aligned reads is generated, this can be properly handled.
- A fix was made to the bam statistics generation to improve robustness of this operation by adding retry logic.

**KNOWN ISSUES:**

- None