BaseSpace Core Apps Software Release Notes

TruSeq amplicon v1.0.0.0

For BaseSpace and BaseSpace Onsite

05/29/2014

Introduction

These Release Notes detail the key changes to software components for the BaseSpace Core Apps. This is the first release of the TruSeq amplicon 1.0.0.0 app. This app is based on the TruSeq amplicon workflow included in MiSeq Reporter version 2.4, with a minor filtering change to add compatibility with NextSeq 500 sequencers.

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 amplicon v1.0.0.0

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NEW FEATURES:

- Initial Release in BaseSpace
- V1.0.0.0 supports fixed panels based on Illumina TruSeq amplicon sample prep methodology, including the TruSeq Amplicon Cancer Panel, and the TruSight Myeloid Panel.
- V1.0.0.0 analysis pipeline uses a modified R8 filter for compatibility with NextSeq 500
- Aside from the previously noted R8 filter, the V1.0.0.0 analysis pipeline is identical to the TruSeq Amplicon workflow in MiSeq Reporter v2.4, which includes the following components (selectable via sample sheet in MiSeq Reporter):
    - Banded Smith-Waterman alignment algorithm to rapidly align reads vs. a manifest of target regions.
    - Users are able to select between three variant callers: GATK 1.6, the Illumina Isaac Variant Caller, and the Illumina Somatic Variant caller (recommended for tumor samples).
    - Users are able to select between two annotation sources: RefSeq and Ensembl.

DEFECT REPAIRS:

- None.

KNOWN ISSUES:

- None.