

# **DesignStudio Software Release Notes**

## **DesignStudio v1.7**

*For MiSeq, HiSeq and NextSeq systems*

**September 22, 2014**

## Introduction

These Release Notes detail the key changes to software components for the DesignStudio 1.7 since the v1.6 release.

As DesignStudio is an Illumina hosted web application, all customers will be impacted by the new release.

Projects created before this release will still be accessible through the new version of DesignStudio. Only new TruSeq Custom Amplicon projects will show the "Gaps" tab described in the following section.

## I. DesignStudio 1.7

### NEW FEATURES:

- TruSeq Custom Amplicon assay:
  - Added "Gaps" tab the grid with gap coordinates and hyperlinks to UCSC Genome Browser.
  - Changed the coverage % calculation to exclude probes themselves. Coverage is now specific to target sequence only.
  - Added the following labels to the project summary:
    - Targets Selected / Designed
    - Undesignable Targets
    - Amplicons Selected / Designed
- TruSeq Targeted RNA assay:
  - Added "Select Best Assay" option to target entry form and target grid. The option automatically selects the best assay based on the following logic from Bioinformatics:
    - 1) Choose validated assay if available. If multiple or none then:
    - 2) Choose assay that covers the most transcript isoforms. If multiple then:
    - 3) Choose 3' assay. If none then:
    - 4) Choose center assay. If none then:
    - 5) Choose 5' assay
  - Added a link to the available GeneFusions PDF document, on the target entry page.
  - Added Targets and Assays tabs; removed Targets and Assays hyperlinks.
  - Removed "Default Assays" selection from the Assays tab
  - "All Assays" is now the default view for the Assays tab
  - Added the following label to increase usability:
    - Targets tab: "Click target to view available assays"
- Nextera Rapid Capture assay:
  - Added the following label to the project summary:
    - Targets Selected / Designed

### DEFECT REPAIRS:

- TruSeq Custom Amplicon assay:

- Fixed an issue that showed incorrect start/stop coordinates in the grid and .bed files.
- Fixed an issue that showed inconsistent project summaries for the amplified region coordinate in some cases.
- TruSeq Targeted RNA assay:
  - Fixed an issue that resulted in omission of target sequences in some manifests.
- Platform level:
  - Fixed a compatibility issue between .bed file export and UCSC Genome Browser.
  - Fixed a timeout issue with some large fixed panels.
  - Design summaries now reflect all targets (previous versions did not reflect undesignable regions).
  - Added specific error messages and links to Technical Support.

**KNOWN ISSUES:**

- In rare cases, Nextera Rapid Capture will generate an error showing "FastA file not found during design." There is no actual error, and the design is unaffected.