DesignStudio Software Release Notes

DesignStudio v1.6.0

For MiSeq, HiSeq and NextSeq systems

June 10, 2014

Introduction

These Release Notes detail the key changes to software components for the DesignStudio 1.6.0 since the v1.5.1 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. TruSeq Custom Amplicon projects in progress will be submitted to the new, improved design algorithm. Customers interested in utilizing the new features (such as 1000 Genomes SNP Source) should consider restarting projects that have not been submitted yet.

I. DesignStudio 1.6.0

NEW FEATURES:

- TruSeq Custom Amplicon Assay:
    - Probe design algorithm optimized for both improved target coverage %, and performance.
    - TruSeq Custom Amplicon SNP sources updated:
        - dbSNP138 added to replace dbSNP131
        - 1000 Genomes added as SNP source for Homo sapiens designs; this SNP database contains subpopulations based on geographic origin (all populations selected by default). The available populations are Africa (AFR), Americas (AMR), Asia (ASN), and Europe (EUR)
    - New target selection types:
        - Coding Sequence Only (CDS ONLY) is now the default target selection type. CDS Only refers to only the protein coding portion of the gene, without Untranslated Regions (UTRs). Untranslated regions are included in the ALL EXONS target selection type.
        - When using Coding Sequence Only as the target selection type, users can choose to independently add 3’ and 5’ Untranslated Regions (UTRs) with the checkbox options.
        - Note: target selection options can be applied on a per target basis, enabling multiple selection types in a single project
    - Gene tab is now default target entry form for both assays
    - Target entry now includes a default padding per exon value of 5 base pairs.
    - Upload file format now supports CDS and UTRs
    - Updated target management grid including:
        - Updated UI to use Kendo grids (present in v1.5.1 for Nextera Rapid Capture)
        - Rearranged columns to place Design Warnings in the middle of the page

    - Removed SNP count, Amplicon, Score, coverage for pre-design state of project
    - Updated text for Avoid SNP buttons to enable "Yes/No" selection
  - Added project dashboard page (present in v1.5.1 for Nextera Rapid Capture)
    - Dashboard enables .bed file export
  - Highlighted *Start Design* button to increase visibility
- TruSeq Targeted RNA Assay:
  - Updated Gene Fusion list
  - Added ERCC targets
  - Renamed "No Filters" to "Show All Assays" during assay selection
  - Change the order of the user action on the assay selection page
  - Added project dashboard page (present in v1.5.1 for Nextera Rapid Capture)
- Nextera Rapid Capture Assay:
  - New target selection types:
    - Coding Sequence Only (CDS ONLY) is now the default target selection type. CDS Only refers to only the protein coding portion of the gene, without Untranslated Regions (UTRs). Untranslated regions are included in the ALL EXONS target selection type.
    - When using Coding Sequence Only as the target selection type, users can choose to independently add 3' and 5' Untranslated Regions (UTRs) with the checkbox options.
    - Note: target selection options can be applied on a per target basis, enabling multiple selection types in a single project
  - Upload file format now supports CDS and UTRs
  - Removed % GC content
- System Level Updates:
  - Help system updated to remove retired assays, and include new features introduced in v1.6.0
  - Removed embedded cost estimator feature and replaced with link to MyIllumina hosted estimator

DEFECT REPAIRS:

- TruSeq Custom Amplicon Assay:
  - Fixed merging issue related to merging multiple targets with multiple labels
- TruSeq Targeted RNA Assay:
  - Fixed "delete all" functionality to prevent deletion of fixed content for add-on designs

- Nextera Rapid Capture Assay:
    - Fixed an issue preventing add on design creation for up to 67,000bp
    - Fixed an issue preventing probe level errors from being copied
    - Fixed an issue preventing one pair base gaps that were not reported in the grid
    - Fixed "delete all" functionality to prevent deletion of fixed content for add-on designs

KNOWN ISSUES:

- TruSeq Custom Amplicon Assay:
    - Process wheels freeze occasionally (purely cosmetic; background processing still works)
    - Cannot target genes on the Y chromosome when they are also present on the X chromosome
    - When uploading a file with duplicate target names, the system does not provide a clear error message (but prevents the duplicate upload)
- TruSeq Targeted RNA Assay:
    - If a design contains Gene Fusions, the regions .bed file causes an error when uploading to the UCSC Genome Browser
    - Coordinate and Gene labels do not allow SPACES as part of the entry string