

Sequencing Analysis Viewer

Software Release Notes

SAV 2.4.5

13-FEB-2018

Introduction

These Release Notes detail the key changes to the Sequencing Analysis Viewer (SAV) Software since the release of SAV version 2.1.8.

Software Application	Prior Version	New Version
<i>Sequencing Analysis Viewer</i>	2.1.8	2.4.5

Sequencing Analysis Viewer version 2.4.4 is used to visualize sequencing run data from MiniSeq, MiSeq, NextSeq, HiScanSQ, all HiSeq (2000, 2500, 3000, 4000, and HiSeq X), and NovaSeq. For data generated on Illumina GAIIX sequencing instruments, continue using SAV 1.8.37.

This SAV version requires Windows .NET Framework 4.5.1 and Visual C++ Redistributable for Visual Studio 2015. If your system is using Windows .NET Framework 4 or you are running a MiSeq with MiSeq Control Software v2.5 and lower, continue using SAV 1.8.37.

IMPROVEMENTS:

- Added "Occupied Count (k)" and "% Occupied" metrics representing the amount of patterned flowcell wells occupied by DNA sequences to the "Analysis" and "Imaging" tabs
- Added option to view data across all lanes on the "Indexing" tab
- Improved performance of loading data when importing a run folder
- "Analysis" tab now hides metrics in the drop-down menus that have been deprecated or are not calculated for the sequencing platform used to generate the run folder
- Set a restriction on the minimum Y-axis range of plots on the "Analysis" tab to 0.01. Previously, the Y-axis range could be set to any value, but setting a value that was too small would make the plots unreadable
- Standardized phasing-related terminology across all tabs. For phasing (and similarly for prephasing), the slope calculated from 25 cycles is listed as "Legacy Phasing Rate", the per-cycle weights are listed as "Phasing Weight", and the full-read best-fit line is listed as "Phasing Slope" and "Phasing Offset"
- Changed the sorting on rows on the "Indexing" tab to be based off of the order provided by the IndexMetrics.bin file to more closely align with the ordering on samples as they are specified in the Sample Sheet. Previously the rows were sorted alphabetically based on the index sequences
- The installer now includes the Microsoft Visual C++ 2015 Redistributable package as part of the installation process if it doesn't already exist on the system

DEFECT REPAIRS:

- Fixed issue on the "Indexing" tab where the wrong bar on the "% Reads Identified (PF)" barchart would be highlighted after selecting a row in the samples table. For example, previously the second bar in the barchart would be highlighted red if the

second row in the samples table were selected, even if the index number was a number other than "2" after sorting the table on one of the columns. This has been resolved and now the correct bar in the barchart will be highlighted based on the "Index Number" column in the samples table

- Fixed issue where the software would crash upon loading malformed or corrupt data. Instead, an error message describing the issue with the data is now displayed

KNOWN ISSUES:

- Loading NovaSeq runs from a network location may be slow
- Using Copy to Clipboard or Zip My Run features on Novaseq run may be taxing on computer resources