Sequence Analysis Viewer Software Release Notes

SAV 1.8.37

For all Illumina sequencing systems

Revision History

Revision	Date	Description of Change
A	April 2014	Original release
B	May 2014	Added known issue and fixed minor typographical errors

Introduction

These Release Notes detail the key changes to Sequence Analysis Viewer (SAV) Software since the release of SAV version 1.8.36. This new version supports the display and analysis of run data from all Illumina Sequencing platforms.

For more information on using SAV, refer to the SAV User Guide, available for download from illumina.com.

If you are upgrading from a version before SAV v1.8.36, review the release notes for SAV v1.8.36 for a list of features and bug fixes introduced in that version.

The software package includes:
- Sequence Analysis Viewer (SAV) Software v1.8.37

I.   Sequence Analysis Viewer 1.8.37

NEW FEATURES:

- Added support for HiSeq X**™** run folders and output. SAV 1.8.37 is compatible with all Illumina sequencers.

   - Note: On NextSeq**™** 500 and HiSeq X systems, the Index tab is not populated unless FASTQ conversion and demultiplexing are completed via the bcl2fastq v2 converter. For more information on performing demultiplexing and BCL to FASTQ conversion of NextSeq and HiSeq X Ten data, please refer to the NextSeq 500 System User Guide, the HiSeq X Ten System User Guide and the appropriate bcl2fastq v2 User Guide.

DEFECT REPAIRS:

- On HiSeq**®** 1000, 1500, 2000 and 2500 systems, if a sample sheet created by Illumina Experiment Manager version 1.5 or above is used, the Index tab information is now properly populated.

KNOWN ISSUES:

- Windows Control Panel, Programs and Features can show entries for previously installed version after updating.