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Eureka™ Analysis Suite 1.0 Release Notes

(For research use only. Not for use in diagnostic procedures.)

Eureka Analysis Suite allows you to perform the following functions:

- Set up your Eureka™ Genotyping Assay plate
- Calculate amounts of each pooled library (wells of a single 384-plate pooled) that will be blended together on a single sequencing lane
- Run QC and Genotyping Algorithms
- View Cluster Graphs of genotype calls
- Export your data

The Suite contains three modules:

- **Eureka Genotyping Calculator** - Enables an end user to calculate the amount of each pooled library (one 384 plate pooled = one pooled library) to be mixed together & run on a single NextSeq lane. The calculator takes into account the control library from Illumina (PhiX), number of reads required, DNA concentration, read length, and SNP panel size.
- **Eureka Analysis** - Uses a genotyping algorithm to call genotypes.
- **Eureka Viewer**
  - View box plots, scatter plots and the 384-plate view to visualize QC data.
  - View Cluster Plots and to manually change calls.
  - Export data in text, PLINK and VCF format provided the appropriate annotation information is available.

Software and Hardware Requirements:

64-bit Operating System	Speed	Memory (RAM)	Available Disk Space*	Web browser
Microsoft Windows 7 (64 bit) Professional with Service Pack 1	2.83 GHz Intel Pentium Quad Core Processor	16 GB RAM	150 GB HD + data storage	IE 8.0 and above

*Minimum storage requirements are for a single run. Total storage space should include additional space for data storage of input and output files from current and previously completed analyses.

The following are known issues in Eureka Analysis Suite 1.0:

- Canceling an analysis during the binning process does not stop the analysis run until the binning is complete.
- The progress bar does not accurately reflect the true progress of the analysis.
- The lowest available resolution for display is 1280 x 720.
- When importing a tab delimited file for assigned user colors to samples, the column header listing the sample names must read cel_files. See Chapter 4 of the User Guide for details.
- When running in Genotyping mode, the pass/fail column should be ignored as there is not a QC check at this step.
- The analysis will not accept data paths containing characters that are non US English.

- Disconnecting from a network when working in Eureka Analysis Viewer may result in an error "Batch is currently in use by a remote application". If you receive this error under these circumstances, go to the \Users\Public\Documents\EurekaAnalysisSuite\Output\"name of the run" folder and deleted the "locked" file. This will allow you to re-open the analysis.

- When installing on a Windows 10 Spanish OS, the Indices library folder will not be automatically installed.

- During PLINK export, the sample_ped_info.txt won't be created if you browse to a new folder instead of using the default one.

- Changing the output folder to one that does not contain the sample_ped_info.txt file as well as selecting Sample Mapping when exporting genotyping data in Plink TPED format will result in an error stating 'Conversion of indexes to sample names was not performed. File may be locked by another application or a processing issue.' The workaround is to select the index mapping radio button or output folder that contains the sample_ped_info.txt.