

Expression Console™ Software 1.4.1 Release Notes

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

Expression Console 1.4.1 includes the following changes and enhancements:

1. New SST-RMA algorithm to support Transcriptome arrays.
2. Reduced the required probeset annotation columns for WT exon and Transcriptome arrays.
3. Script feature removed.

The following are the known issues that also exist in the Expression Console™ Software version 1.4.1:

1. Only User-specified attributes are displayed in the Attribute Editor. Physical array attributes, such as information related to the array and fluidics used in the run, are not editable in attribute editor. They cannot be seen in EC study window or be used in PCA graph either.
2. The Lines view in Histogram graph may go beyond the x-axis of the graph when changing the scale range.
3. When adding a new attribute in Sample Attribute Editor, the new attribute may be added to the second to last position.
4. Clicking a point in the PCA graph will select the data in the Study window. Select the data in the Study window will not select the point in the PCA graph.
5. When opening the PCA graph in default view on a laptop, the PCA2 percentage may not be displayed.
6. In the IterPLIER and PLIER algorithms, some individual probe sets have differences in their output signal because of slight precision/rounding problems leading to convergence instability on what probes are chosen and how they are weighted. The differences simply “tilt” the magnitude of the estimated signal due to the shifting of the individual probe “weights”
7. In the MAS5 algorithm, we have observed changes in signal values between the 32 bit and 64 bit platforms where the changes are greater than 1%. The observation is with a very small number of probe sets (typically around 5) where each of the observed probe sets has low expression values. The Detection calls and p-values remain unchanged
8. Cannot Edit Metric in Report Thresholds before CHP File is created:
The user cannot change the Metrics in the Report Thresholds dialog without having a study open that contains at least one CHP file.
The workaround is to add at least one CHP file to the study and then modify the report thresholds.
9. ZIP utility does not always include library files for Exon arrays.

The ZIP utility includes library files for Exon arrays only when CHP files are analyzed as part of the study. If the user creates a study and adds existing CHP files then the library files will not be included in the ZIP archive. The workaround is to manually add the appropriate library files to the ZIP file. The library files can be found in the file properties for the CHP file.

10. Some memory intensive operations in the Expression Console software may run out of memory and provide an error message:
Expression analysis especially on Exon Arrays can generate large amounts of data. It is possible that while using Expression Console the application will run out of memory and provide an error message. Occasionally multiple error messages will be generated if there is not enough memory to complete a series of requested actions. For example, attempting to simultaneously open several 10's of CEL files (actually number will depend on the amount of RAM currently available to the Expression Console software) in the intensity viewer may cause the application to run out of memory. An error message will be displayed for each CEL file that was not able to be displayed. Closing other applications or requesting fewer items to be simultaneously displayed will minimize this issue.
11. Not all of the functions within the Expression Console software have Progress Meters: Exon arrays contain over 6 million probes organized into 1.4 million probe sets at the Exon level. Operations like Feature intensity box plots, and feature intensity views may take an extended amount of time to complete and they currently do not have progress meters. This will be addressed in a future release of Expression Console.
12. Renaming configuration files from the operating system causes errors:
Custom analysis configuration files are stored in the library file directory. Editing the name of the files outside of the application may cause the software to generate an error message when opening the configuration.
The workaround for this issue is to open the configuration within Expression Console and select "Save As" and give the configuration a new name.
13. Probe sets may have a signal value equal to 0:
Probe sets that fail to analyze with the PLIER and RMA workflows have their signal values reported as "0". For example, performing an Exon Analysis on all of the probe sets on the Exon array results in failed analyses for the background probes, thus they have a reported signal value=0. This will be addressed in a future release of Expression Console.
14. In the MvA Plot, the Y-Axis of the graph will not display the negative sign when the value is 10 or greater.
15. All library files must be in the active library file folder to be recognized by the Expression Console Software. For example, on the Advanced Exon/Gene configuration page entering the full path to a file will produce an error stating that the file is not found. The workaround is to place all of the library files for a particular analysis configuration in a single folder and identify that as the current library file folder in the Expression Console software.
16. No graph is displayed if CHP file names are more than 115 characters:
The workaround is to either enlarge the graph or user shorter CHP file names.