

Transcriptome Analysis Console (TAC) Software 4.0.2 Release Notes

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

Transcriptome Analysis Console Software 4.0.2 addresses the following defect fixes:

1. The software has been updated to generate sources of variation data when there were few input genes or exon level data (<1,000).
2. The software has been updated to process arrays with low signals.
3. Wikipathways in the software has been updated to support all species that are supported in Wikipathways.org.
4. The software now supports more than one real covariate attribute.

Software and Hardware Requirements:

Transcriptome Analysis 4.0.2 is only supported on 64-bit systems with the following operating systems:

- Windows 7 Professional SP1 (64-bit)
- Windows 10 Professional (64-bit)

Memory and CPU Recommended Requirements

- Quad Core System, 2.83 GHz or above
- Minimum 8GB RAM, recommended 16GB RAM

The following are the known issues/differences that exist in Transcriptome Analysis Console Software 4.0.2:

1. For the Volcano Plot, it only displays up to 4 decimal places.
2. In some cases, clicking on Wikipathways may display an error message "Failed to load pathways". If this occurs, close the results and then reopen it.
3. In the Interactive miRNA and mRNA graph, if the nodes have been moved to new locations in the graph, using the navigational "back" and "forward" buttons will not preserve the new node locations. The nodes will appear in their original location when navigating.
4. Some of the QC metrics are not generated in TAC 4.0.2 anymore. For more information, please contact support.
5. When exporting histogram in Wikipathways, save the image and then print to get the histogram in the current view.
6. When running close to 1,000 samples, some select samples may be overlapped and to see them, resize the viewer window.