

DEVA Software

Release Notes

May 2012

DEVA software automates the feature extraction, primary data analysis, and visualization processes for Roche NimbleGen arrays. The following describes the new features of DEVA v1.2 software and lists the known issues. Refer to [DEVA Software User's Guide v1.2](#) for more detailed information.

Software Updates v1.2

New Features

- Processes images with AccuSNP Workflows.
- Generates a SNP Quality Report.
- Enables automatic raw-data report generation.
- Enables users to define border width and to apply local alignment when running analyses and when extracting raw feature data.
- Allows custom analysis workflow and report workflow settings to be imported and exported.
- Provides faster analysis processing.

Known Software Issues

- When opening the *Image Workspace* to enable the user to manually adjust alignment, a status bar is initially displayed, but then disappears. For several seconds, the Alignment Details screen is unresponsive until the *Image Workspace* opens.
- When a DEVA project is upgraded to a DEVA v1.2 project, raw data analysis results that were available in the original project are not available for viewing in the upgraded project. To view raw data analysis, the analysis must be rerun or raw data reports must be regenerated for the project in DEVA v1.2 software.
- When viewing raw data, if two datapoints from different tracks reside in the same location, only the top-most datapoint is visible. Bringing the bottom-most datapoint forward has no effect. As a workaround, hide the track of the top-most datapoint.
- When viewing the Exported Files list while multiple reports are being generated, users will see a list of only those reports that DEVA software has finished generating at the time that the Exported Files list was opened. DEVA software will not update the list in real time. To view all generated reports, open the Exported Files list only after all reports have been generated.
- DEVA software places a product icon on the user's desktop regardless of the product-icon location selection made by the user during installation.
- When generating the Segmentation Table Report in the CGH workflow, the report file name will include the container name even if only one container is created
- Processed slides must be deleted before designs for those slides can be deleted.
- Cancelled and failed analyses cannot be opened. These analyses must be deleted and run again.

- n When printing tables using the “portrait” option, the table will be printed as landscape. If it is not acceptable to have a report in landscape, you can export the table and print from a spreadsheet management program.
- n CGH Consensus Segment plots include all analysis containers as part of the consensus calculation. Both displayed and hidden containers are included in this calculation and in the plot count.
- n When viewing annotation or data in the genomic viewer, you will be unable to see the point with the largest genomic position if it has the same start and end position. Note that this data point will still be used if you run “Map to Annotations” or “Export as GFF”.
- n Designs with more than 1,000 data tracks (sequence names) may result in slow analysis when running SegMNT in DEVA software. Designs with more than 10,000 data tracks (sequence names) will fail when segmentation is run on them in DEVA software.

Software Updates v1.2.1

New Features

- n Provides a “Transition Probability” slider in the CGH-LOH workflow, which enables customers to fine-tune the stringency of LOH calling. Lowering the Transition Probability value makes LOH calling more stringent, which can decrease the number of LOH calls. Raising the Transition Probability lowers the stringency of LOH calling and can increase the number of LOH calls.
- n Identifies LOH calling more robustly with an optimized LOH workflow.



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