

# Release Notes

To install or upgrade to the latest version of Partek Flow software, follow the directions outlined in the [Installation Guide](#).

## 11.0.24.0414

- Added CellphoneDB task to analyze cell-cell communication process
- Added display transcripts location ability on 10X Genomics Xenium data visualization
- Improved trim adaptor task to be more memory efficient
- Improved file browser when specify a location and click go button, it will scroll to the location on the left panel
- Moved all tasks in Peak analysis section to Region analysis section
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0414.55](https://registry.partek.com/r/w:24.0414.55)*

## 11.0.24.0325

- Added more options for variant filter by fields
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0325.52](https://registry.partek.com/r/w:24.0325.52)*

## 11.0.24.0317

- Added hierarchical cluster analysis task to similarity matrix data node
- Added statistical analysis task to cell descriptive stats
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0317.49](https://registry.partek.com/r/w:24.0317.49)*

## 11.0.24.0311

- Improved convert Seurat to matrix dialog to allow to configure meta data
- Added more options in filter annotated peaks dialog
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0311.45](https://registry.partek.com/r/w:24.0311.45)*

## 11.0.24.0226

- Improved differential analysis report filter option on log2 ratio to allow user to specify a range to filter
- Improved Normalize to housekeeping genes dialog to display both gene ID and gene name
- Added data repository management on Settings page
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0301.39](https://registry.partek.com/r/w:24.0301.39)*

## 11.0.24.0204

- Added long reads aligner minimap2 and pbmm2
- Simplified the Data Viewer configuration dialogs
- Added Scree plot and component loadings table to the PCA report by default
- Added Poisson regression and Negative binomial regression as options in the Differential analysis task
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0204.33](https://registry.partek.com/r/w:24.0204.33)*

## 11.0.24.0102

- Automatically generate spatial report on analysis tab after spatial data import
- Added alt-splicing task option on Salmon's transcript count data node
- Added STARsolo task for 10x Genomics scRNA-seq data
- Updated FreeBayes to v1.3.6
- PCA task default feature filter method is changed to variance from vst
- Filter peaks task is moved to Filtering section from Peak analysis section on the menu
- Make the enable/disable user account as separate privilege from add user account for admin
- Minor bug fixes

*Latest docker image: [registry.partek.com/r/w:24.0102.29](https://registry.partek.com/r/w:24.0102.29)*

## 11.0.23.1204

- Enabled MACS peak detection report visualizations in the Data viewer
- Improved the algorithm for the normalize to housekeeping genes task
- Added more gene annotation options in SNV task report
- Fixed the Venn diagram issue on some of the browsers
- Minor bug fixes

*Latest docker image: [registry.partek.com/rtw:23.1204.23](https://registry.partek.com/rtw:23.1204.23)*

## 11.0.23.1105

- Added search function in Help menu to directly search the content in documentation page
- Added option to choose a number of features to use in PCA computation
- Minor bug fixes

*Latest docker image: [registry.partek.com/rtw:23.1105.16](https://registry.partek.com/rtw:23.1105.16)*

## 11.0.23.1023

- Improved differential analysis report layout
- Add impute missing value task
- Minor bug fixes

*Latest docker image: [registry.partek.com/rtw:23.1023.14](https://registry.partek.com/rtw:23.1023.14)*

## 11.0.23.1009

- Improved pre-alignment QC report
- Fixed differential analysis report table download issue
- Minor bug fixes

*Latest docker image: [registry.partek.com/rtw:23.1009.11](https://registry.partek.com/rtw:23.1009.11)*

## 11.0.23.0918

- The user interface now boasts a modern appearance
- Enhanced the import wizard for greater intuitiveness and user-friendliness
- Added support for SomaLogic ADAT bulk protein data
- Improved the file browser for fast access to recent server uploads
- Bolstered file protection to prevent accidental deletions when used by other projects
- Added support for the 10x Genomics Xenium platform
- Introduced support for the Nanostring CosMx platform
- Added a new task for Correlation analysis between different assays
- Improved scatterplot selection with a handy painting mode
- Added the ability to display a high resolution Visium image with a new Spatial imaging report task for quick viewing
- Added a manual alignment option for tissue image visualization
- Streamlined the import process for multiple files per sample, e.g. import all 3 sparse matrix (feature-barcode-matrix) files per sample for all samples at one time
- Added more available information on the Annotated region report
- Improved the Seurat object conversion to be more intuitive
- Added a more detailed report to the Adapter trimming task
- Creating pseudobulk data by pooling single cells has been made easier with increased functionality
- Optimized the differential analysis dialogs for improved usability
- Changed the default normalization method for bulk RNA-Seq data to Median ratio (DESeq2)
- Improved the Detect fusions and Trim bases tasks to be more intuitive
- Allowed the Single-cell QA/QC task to be performed on individual samples
- Minor bug fixes

*Latest docker image: [registry.partek.com/rtw:23.0918.1](https://registry.partek.com/rtw:23.0918.1)*

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## Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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