MRC Holland Support

Coffalyser.Net v.210604.1451 and v.210226.1433 release notes

This article lists the most important changes made in Coffalyser.Net v.210604.1451 and v.210226.1433.

Important

These are not the latest versions of Coffalyser.Net. See the version history for information about other (newer) versions.
Read more about updating. We recommend creating new worksheets after installing the new version to benefit from the latest probe(mix) information from MRC Holland.

Note

Coffalyser.Net v.210604.1451 and v.210226.1433 only differ in the installation procedure. There is no need to update to v.210604.1451 if you already have v.210226.1433 installed.

Coffalyser.Net v.210226.1433

The sections below list the changes as compared to the previous version, v.140721.1958.

Improvements

Most prominently visible improvements

- Improved workflow for manual bin set creation.
- Adjusted probe counter to make a clear distinction between expected probe signals and unexpected probe signals. More details.
- Added probe colours in the genomic profile tab of the fragment analysis and electropherograms tab of the comparative analysis for improved visualisation and identification of unexpected results. More details.
- Added purple colours to binning profiles to identify probes that deviate too much from the center of a bin. More details.
- Added support for the Applied Biosystems SeqStudio Genetic Analyzer and the Promega Spectrum Compact capillary electrophoresis devices. More details about using the Promega Spectrum Compact device.

Technical improvements

- Updated default Microsoft SQL Server from 2008 R2 to 2014 SP3 to help prevent possible future security issues with SQL Server and to increase compatibility with modern systems.
- Improved support for Windows 10 (32- and 64-bit). View all system requirements.

Improvements to quality scores

- Added a max probe length deviation quality check to the FMRS score to provide warning if a probe fragment length is too far removed from the center of a bin. More details.
- Added FMRS score penalties if the 92 nt benchmark fragment is not within an appropriate signal range. This includes a heavy FMRS score penalty if the benchmark fragment is absent but expected, to avoid a potential overestimation of quality because some quality checks cannot be calculated without the benchmark fragment.
- Added the possibility for the PSLP score to become red/bad and lead to an increased penalty for the CAS score if there are large differences in sloping.
- Added an FMRS score penalty for undetected probes in undigested reference samples in MS-MLPA.
- Added a CAS score penalty for test samples when signals in the experiment's dedicated reference samples are out of range.

Other improvements

- Adjusted the way that results for probes with a signal ≤ 10% of the median signal of the reference probes are displayed. Results for these probes are now displayed as intra-normalised ratio (as percentage) in all tables to enhance the visibility of unexpectedly low signals. Results for probes with a higher signal (> 10%) are still displayed as final ratios.
- Improved automatic bin boundaries for mutation-specific probes that are not identified in the experiment. These bins now become wider by default to increase the chance of detection of positive signals. A manual bin set and SALSA Binning DNA should be used to avoid this situation.
- Adjusted minimum signal height for filtering from 5,000 to 3,000 for Beckman devices.
- Adjusted mapview locations to display the approximate location of probes.
- Adjusted default region analysis method, which will be set to StaticMRCData if available. When not available, this option is no longer shown in menus.
- Improved fit of information displayed in tooltips to the screen.
- Improved visibility of information about mutations in PDF reports.
- Improved consistency in available zoom options throughout the software.
- Improved layout of the sample information displayed at the top of PDF reports.
- Removed outdated, non-functional links to the reference manual and YouTube channel.
- Removed comparison of samples to the overall sample population and to the positive sample population throughout the software.
- Removed intra-normalisation ratios throughout the software.
- Removed two unused, non-functional conditional format options from menus: PeakDeltaNucleotideExpectedLength and PeakWidthInDataPoints.

- Removed normal range from PDF reports as they did not apply to all situations.
- Removed "DNA" check for no-DNA reactions as it had limited value.
- Updated information in the About dialog.
- Added support for a potential future alternative approach to MS-MLPA (referred to as unpaired MS-MLPA in the software).

(Bug) fixes

- Fixed inconsistent display of results for mutation-specific probes. Previously, results in the Sample report tab of the Comparative Analysis Sample Results Explorer could be displayed differently than in other places in the software in certain situations.
- Fixed sex determination in the absence of the 92 nt benchmark fragment in the fragment analysis tab.
- Fixed inconsistent display of PSLP warnings in dialogs and PDF reports.
- Fixed inconsistent display of FRSS scores in some situations.
- Fixed an exception and inability to view all results when a digested sample had a signal for a probe without signal in the undigested reaction in MS-MLPA.
- Fixed an exception and inability to generate PDF reports when the length of text describing the reference samples on PDF reports was exactly 91 characters.
- Fixed rare conditions in which peaks could be assigned a negative area.
- Fixed rare situations in which changes to the fragment analysis configuration did not reset the comparative analysis.
- Fixed incorrect slope correction warning when no slope correction was applied.
- Fixed incorrect warning for incomplete digestion for experiments not analysed as MS-MLPA experiment.
- Fixed incorrect last modified date for experiments.
- Fixed absence of altered formatting to warn for large probe fragment length deviations from the center of a bin in PDF reports and tables in certain situations.
- Fixed layout of PDF reports in the absence of chromosomal band information for probes (only relevant for custom probemixes).
- Fixed inconsistent rounding rules for result ratio calling and displayed values.

Coffalyser.Net v.210604.1451

As compared to v.210226.1433, two changes were made to improve the installation procedure. No other changes were made.

- Improved handling of aborted or interrupted installation of Microsoft SQL Server.
- Fixed an issue with computer names containing Unicode (UTF-8) characters.

Note

Coffalyser.Net v.210226.1433 was made available on our website on 26 May 2021.
Coffalyser.Net v.210604.1451 was made available on our website on 10 June 2021.
Coffalyser.Net version history.

Tags

Coffalyser.Net

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