

## eMap Software Release Notes: 16Sep2024

UI Release Version	Analysis Version	Update
1.0.0	1.42.8 (Unchanged)	Minor language updates.
		Updated button icons (autofill)
		Updated Default Settings values
		Added feature to view and download software Release Notes within the eMap application.
		Added feature to enable Brute Force Protection for Group accounts.
		Added feature to enable Multi-Factor Authentication for Group accounts.
		Introduced a feature allowing users to organise sample displays and SampleSheet lists by plate row or column for improved usability.
		Increased character limit for accessioned Subject Information fields to 60.
		Introduced a feature to mark all samples as "Default" or "Excluded" during pooling with a single click for faster workflow management.
		Added feature to allow direct entry of a final pool concentration into eMap, instead of using individual sample concentrations to inform the 1 nM dilution instructions.
		Improved the process when deleting a Pool ID to maintain the connection between samples and associated Plate ID(s).
		Added the Plate ID to the Experimental Details table and global search function.
		Karyotype formats have been expanded to include "sseq" notation, genome builds and optional cytoband and molecular position for abnormal regions. "Shorthand" format unchanged.
		New icons to signify when samples are Locked or Signed-Off from Run View and Cycle View lists.
Added feature to select sub-sets of samples within a run for re-analysis with modified settings (e.g. different normalisation protocol), including option to remove protections and re-analyse Locked or Signed-Off samples (User-Level dependent, with warning).		

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1.0.0	1.42.8 (Unchanged)	<p>Improved validation of smoothing value input.</p> <p>Hovering the mouse cursor over a CNV chart bin data-point, will display the copy-number value of the bin making data interpretation more intuitive.</p> <p>Added CNV chart configuration settings for axis ranges, and visualisation of guidelines. Chart settings can also be saved for reporting.</p> <p>Updated language referring to creating/deleting regions on the CNV chart to “manually annotated” or “manual annotation”.</p> <p>Revised CNV chart and Circos plot image format, to include a sample details footer.</p> <p>Added feature to view the sample sign-off history logs without needing to open the Sign-Off action dialogue.</p> <p>A new Cycle Summary Report PDF tool has been added, listing abnormalities by chromosome and the CNV chart image for all samples in a Cycle.</p> <p>Enhanced the eMap Cycle Report PDF to support multiple lines for the User's disclaimer statement, allowing for clearer communication.</p> <p>Samples with “FAIL” QC Status shall be reported as “No Result” on PDF reports, and “NA” for reported Karyotype, Sex, and Result Icon.</p> <p>Updated &lt;Pool ID&gt;_export.tsv file contents to include additional sample metadata and results.</p> <ul style="list-style-type: none"> <li>• (Re)quantification value of the final sequencing pool (if applicable).</li> <li>• Notes added on the Sample View page</li> <li>• Sign-Off Comment and Sign-Off History</li> <li>• Mosaic_Calling renamed Custom_CN_Thresholds</li> <li>• Manual_Changes renamed Manual_Annotation</li> <li>• Display of whole chromosome count value</li> <li>• Chromosome-specific region results columns 1-22,X,Y</li> </ul> <p>Karyotype reporting format settings</p> <p>Added the ability to download all CNV charts and Circos plots from a run in a single .zip folder for increased efficiency.</p>

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1.0.0	1.42.8 (Unchanged)	Sort Cycles by "created date" and Samples by alphanumeric "Sample ID", when adding to PDF reports.
		Fix for sample result icon not displayed correctly following analysis pipeline failure due to insufficient data in the BAM file.
		Minor user interface styling updates.
		Improved rules for refresh rate of "Waiting" samples in runs that are in "Processing" status.