

## GeneMarkerMTP Changes and Risk Rank

### Revisions in v.2.7.0 – December 2016 changes from v.2.6.7

Feature	Description	Risk	Algorithm Change
Positive / negative control concordance	Automated display of positive and negative control concordance in main analysis screen and export control report table for long term monitoring.	Major	Yes
Contamination Check Tool	Linked tool to check for percent same genotype within a project for capillary-to-capillary contamination and against an elimination database of lab personnel	Major	Yes
Edit History Report	Export a single pdf of all edits/comments made to samples within a project.	Moderate	No
Project Comparison report	Export the entire project comparison spread sheet or save only the samples that are not concordant between the two projects.	Moderate	No
MLPA enhancement	Improved evaluation of Q fragments of MLPA data	Major	Yes
Relationship testing Database	Converted the previous Access database(GeneDB.mdb) to Sqlite database(GeneDB.db) resulting in faster searches	Minor	No
Additional Panels	Updated Additional Panels folder to include recent panels for analysis of MLPA (MRC® Holland), Cystic Fibrosis (Elucigene®) and Fragile X ( FastFraX™TMR Diagnostics)	Moderate	No

### Revisions in v.2.7.1 – February 2017 changes from v2.7.0

Feature	Description	Risk	Algorithm Change
<b>MLPA report table addition</b>	Automated display of F (samples that failed QC fragment evaluation) and N (samples with no detection of duplication/deletion) in the sample list and horizontal MLPA result table of the MLPA analysis application	Minor	No

#### Description of risk categories:

- Minor - cosmetic; such as changes to the graphic user interface and reporting options (no algorithm change)
- Moderate - includes additional parameters or functions that may affect the final report (no algorithm change)
- Major - includes algorithm change(s) and is evaluated by concordance testing.