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SoftGenetics Announces Release of New Version of its Mutation Surveyor Software

January 12, 2015 State College PA. SoftGenetics announced the release of version 5.0 of its market leading software for the analysis of Sanger Sequencing. The new version of the software includes new features designed to enhance and optimize the variant discovery in Sanger Sequence traces. Mutation Surveyor software is compatible with all major sequencing platforms and chemistries.

Included in version 5.0 is a new <u>variant knowledge database</u>, which allows users to track variants by chromosomal position, indicate false-positives and other chemistry/sequencing artifacts, and query the variant information from popular databases such as dbSNP, dbNSFP, and COSMIC.

Also incorporated in Mutation Surveyor software version 5.0 is a <u>user management</u> system, which enables administrators to set up password protected user names, control access rights, and generate a user audit trail for each analysis project. Access rights for each user are determined by the administrator, providing assurance that unauthorized individuals do not accidentally alter a project or change the analysis parameters established by the laboratory. User management also provides user ID and Organization in the header of the final reports. Each change to the project is captured by user and time stamped.

Additionally, Mutation Surveyor software analysis results can be saved in VCF format which allows Sanger confirmation to be easily uploaded into the company's Geneticist Assistant NGS workbench.

"The addition of the variant knowledge database", states Kevin LeVan, Product Manager, "provides users with a unique tool to indicate repetitive false positives and sequencing artifacts, areas of clinical significance as well as variant interpretation information. Taken together, these additions to the software should assist in optimizing the speed and quality of Sanger Sequence analysis."

The company offers no cost trials and training on Mutation Surveyor software which can be requested through its website: www.softgenetics.com