GENALICE
TECHNOLOGY FOR PEOPLE & SCIENCE

Press Release

GENALICE EXPANDS ITS NGS SECONDARY DATA ANALYSIS SUITE WITH IMPORTANT FUNCTIONALITY FOR BETTER DIAGNOSIS OF ONCOLOGY PATIENTS

October 18, 2016 – Vancouver, Canada – Today, at the opening of the Annual Meeting of the American Society of Human Genetics, GENALICE announced the release of a new version (V2.4.0) of its Next-Generation Sequencing (NGS) secondary data analysis suite, GENALICE MAP. The key component of this release is the Somatic Calling module, with impressive performance and best-in-class quality results. Somatic Calling is used for molecular diagnosis of oncology patients. It concerns a technology to distinct variants found in normal tissue from variants in a tumor sample, in order to identify tumor specific DNA mutations.

In a head-to-head comparison the GENALICE MAP Somatic Calling module outperforms the combination of four commonly used pipelines (MuTect, Strelka, FreeBayes, VarScan), by being 190 times faster and producing better results. None of the individual pipeline results came even close to the results of GENALICE MAP.

Hans Karten, CEO/CTO, explains: “With the addition of the Somatic Calling module, our NGS secondary analysis solution immediately becomes more relevant for clinical application. The exceptional validation results clearly show our added value in this field. This is an important step forward in realizing the mission of our company to save lives and improve the quality of life of patients with complex DNA diseases, such as cancer.”

Other important additions to this new software version are:

1. *Profiles*: While other tools rely on generic training sets to improve the outcome of known variants in a patient sample, MAP allows for the creation of specific profiles for any defined cohort from no matter what species. Such a profile allows for very targeted call amplification and suppression and thus boosts accuracy of detecting known variants.
2. *Copy Number Variation (CNV)*: CNV detection, as a first and important element of Structural Variant detection, is now available in GENALICE MAP.
3. *HIPAA compliance*: To be able to run HIPAA compliant, hooks to encrypt data in transit and data at rest are provided.
4. *GRCh38 support*: Specific support of the ‘alternative sections’ as used in GRCh38 has been added.

“Another important milestone for our company," Hans continues, “is the announcement of the first version of our workflow manager. With growing data sets and increasing functionality the need for an excellent system to support smooth big data processing and

management in complex environments is clear. The workflow manager delivers full version control and provides a unified view of all samples stored anywhere. The scheduler can work in flex-compute environments and all functionality is accessible through API or Graphical User Interface. We expect this to be an important addition to our product to further reduce the complexity of NGS data processing."

About GENALICE

GENALICE is a highly innovative biomedical big data solutions company, with global headquarters in the Netherlands. GENALICE designs and builds groundbreaking software solutions for ultra-fast, highly accurate and cost-effective DNA data processing and analysis. The software is deployed on general-purpose hardware or flexible cloud. With GENALICE MAP, the company has introduced the first Next-Generation Sequencing (NGS) secondary data analysis pipeline with true population power. By partnering with world-renowned research institutes and healthcare companies, GENALICE is committed to unlocking the potential of whole genome, exome and transcriptome sequencing for biomarker discovery and clinical application.

More information on GENALICE can be found at www.genalice.com.

For more information, please contact:

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Supportive Infographics:

GENALICE MAP in a nutshell

Somatic Calling module

Population Calling module