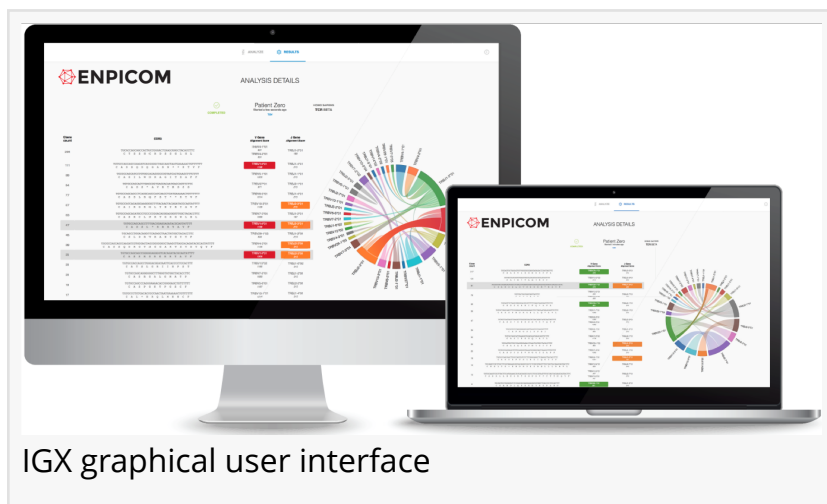


# ENPICOM Releases Immune Repertoire Sequencing Analysis Platform to Personalize Immunotherapies

*Dutch bioinformatics software engineering company finalizes development and releases the first version of their ImmunoGenomiX platform*

'S-HERTOGENBOSCH, NETHERLANDS, August 1, 2018 /EINPresswire.com/ -- Today [ENPICOM](#) announced that they have finalized development and released the first version of their ImmunoGenomiX (IGX) platform to support the development, patient stratification and treatment monitoring of immunotherapies.



The adaptive immune system, also known as the acquired immune system, is a subsystem of the overall immune system that is composed of T and B lymphocytes, which eliminate pathogens or prevent their growth. Moreover, the clinical relevance of T cells in the control of different human

cancers and autoimmune diseases is beyond doubt. Immunotherapies that boost the ability of T cells to destroy cancer cells have proven therapeutic efficacy in a variety of human malignancies.

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These results are very comforting, as highly accurate clonality analysis is the stepping stone towards successful application of this technology in the clinic at later stage”

*Dr. Nicola Bonzanni, CSO*

ENPICOM develops a T cell and B cell receptor (TCR/BCR) repertoire immunosequencing data analysis solution. This IGX platform will be modularly expanded to become a comprehensive end-to-end immunosequencing data analysis platform designed to analyze, monitor, and compare the immune repertoires in the context of immunotherapy development and at all stages of

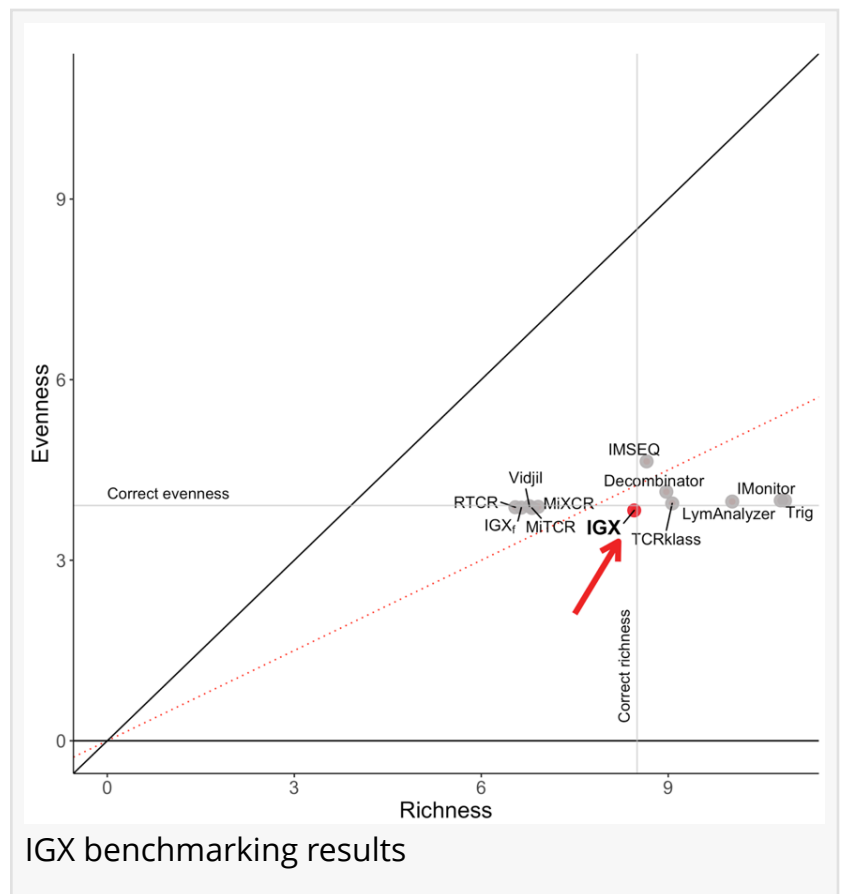
treatment and disease over time. Starting from high-throughput sequencing data, it will deliver an easy-to-read report depending on the specific application, be it research, diagnosis, patient stratification, or treatment monitoring. The IGX platform will allow customers to use their own sample preparation protocols and the next-generation sequencing technology of choice. It requires no programming skills as the interface is intuitive and flexible.

The first version is available as of today and consists of the base module, IGX Explore, to analyze TCR repertoires from raw sequencing data, report back the number of individual TCR clones and interactively visualize them in a user-friendly way. With IGX Explore (TCR) immunotherapy companies can boost their target discovery, research and drug development processes. In case they need TCR repertoire analysis for a specific application or results visualized in a different way, ENPICOM can custom-build it.

Using a recently published and independent benchmark, ENPICOM showed that IGX Explore offers superior accuracy. The independent benchmark was published in a recent paper by Afzal et al., in which the authors benchmarked ten state-of-the-art TCR repertoire analysis tools. More information about this benchmark study can be found at the company's [website](#).

Dr. Nicola Bonzanni, Chief Scientific Officer, explains: "An important step in repertoire analysis is the correction of sequencing errors. If sequencing errors were left uncorrected, the richness of a sample would be vastly overestimated; correcting too many errors would lead to under-estimating richness. A critical challenge in immune repertoire analysis is to correct the sequencing errors in the data without losing repertoire-specific information in the process. IGX Explore uses an Adaptive Error Correction algorithm that learns sample-specific mutation rates from the data. By using sample-specific error estimations, erroneous sequences can then be corrected to provide accurate clone sequences, sizes, and frequencies" and adds "These results are very comforting, as highly accurate clonality analysis is the stepping stone towards successful application of this technology in the clinic at later stage".

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