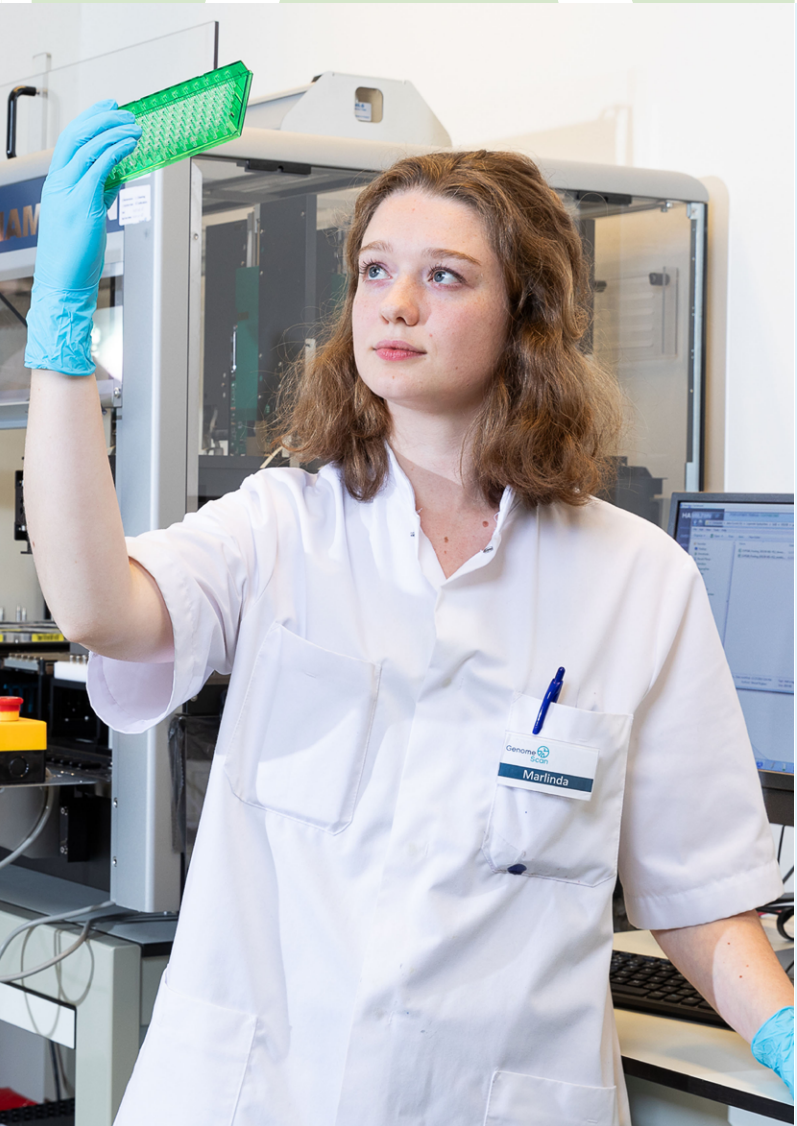
Revolutionizing cancer treatment: a case study of personalized vaccine development



A case study performed by GenomeScan in collaboration with myNEO Therapeutics.

Introduction

Cancer stands as one of the leading causes of death globally, posing significant challenges to conventional treatment modalities.Traditional therapies often lack specificity and can cause considerable collateral damage to healthy tissues. However, recent advancements in genomic technologies have paved the way for personalized approaches to cancer treatment, offering new hope in the form of immunotherapies tailored to individual patients. This case study explores the collaboration between GenomeScan and myNEO Therapeutics in revolutionizing cancer treatment through the development of personalized vaccines targeting neoantigens.

Background

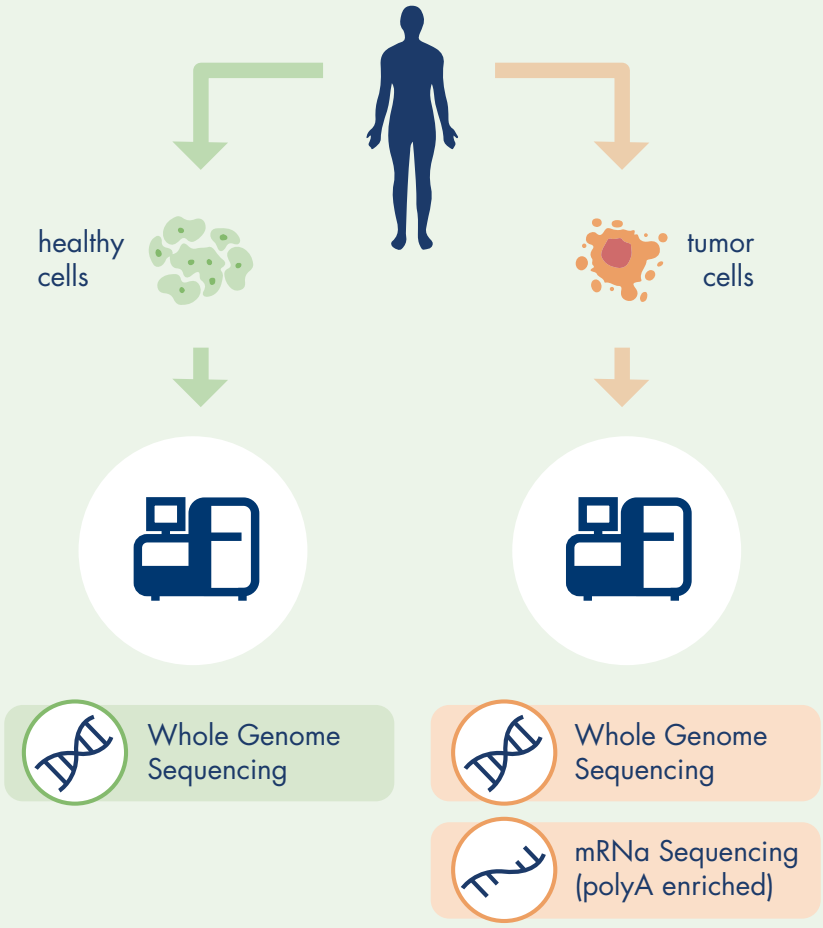
Despite decades of research and development, cancer remains a formidable adversary, claiming millions of lives annually. One of the major hurdles in cancer immunotherapy is the identification of targets capable of eliciting a potent and selective immune response against tumors. Neoantigens, derived from tumor-specific mutations, are promising targets for immunotherapy, as they are unique to cancer cells and can potentially guide a focused immune attack on malignant tissues. However, the identification of neoantigens has proven to be a challenging task, requiring advanced genomic techniques for accurate prediction and validation.

Challenge

Obtaining genomic information from a patient's tumor for neoantigen identification forms the foundation for a tailored vaccine; however, hurdles must be surmounted to optimize accuracy, efficiency, and applicability. The integration of multiple sequencing strategies, such as Whole Genome Sequencing (WGS) in combination with RNA sequencing (RNA-Seq), offers a potent approach for precise neoantigen identification by capturing both genetic mutations and transcriptional activity. Challenges arise in obtaining high-quality genetic material from tumor samples, especially with formalin-fixed, paraffin-embedded (FFPE) or fresh-frozen (FF) specimens and addressing tissue contamination necessitates precise histological examination and microdissection techniques. Additionally, bioinformatics challenges encompass accurate variant calling and neoantigen prediction, while ensuring a fast turnaround time for personalized vaccine development is essential, requiring ongoing progress in sequencing technologies and optimization of bioinformatics pipelines. Integration into clinical workflows, alongside ISO certification for quality assurance, is vital for translating sequencing data into actionable therapeutic strategies.

Solution

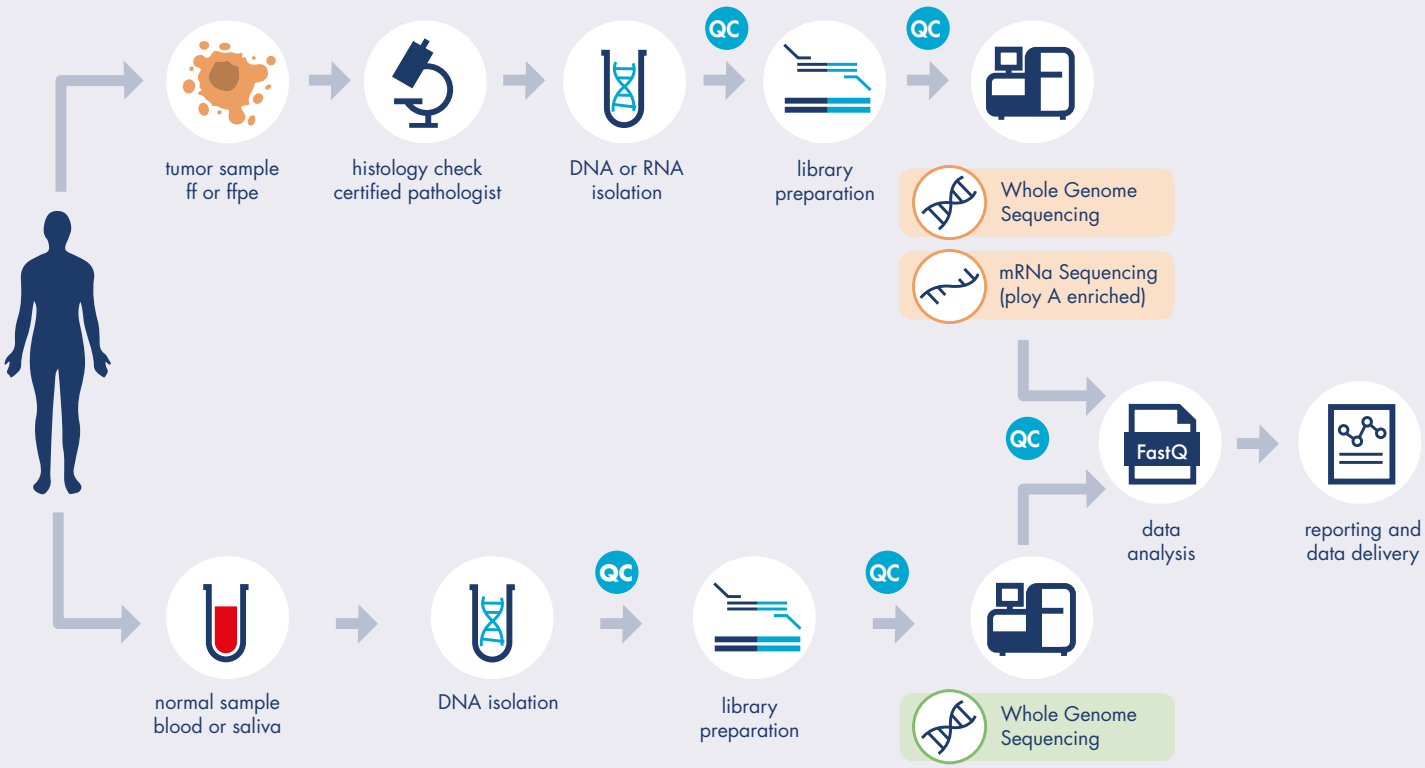
GenomeScan and myNEO Therapeutics collaborated to explore a comprehensive solution to overcome the challenges inherent in personalized vaccine development. As an ISO-certified sequencing provider (ISO 17025), GenomeScan brings to the table a wealth of expertise in overcoming obstacles associated with neoantigen prediction. Our innovative methodologies encompass tumor cell percentage assessments and precise microdissection techniques, mitigating the risks of contamination from normal tissue. Moreover, we excel in extracting high-quality DNA and RNA from challenging tumor samples, including FFPE and FF samples. Utilizing a combination of sequencing workflows such as WGS and RNA-seq for tumor and WGS for normal samples, all performed in swift turnaround time without compromising on quality, within the framework of ISO certification (ISO 17025).



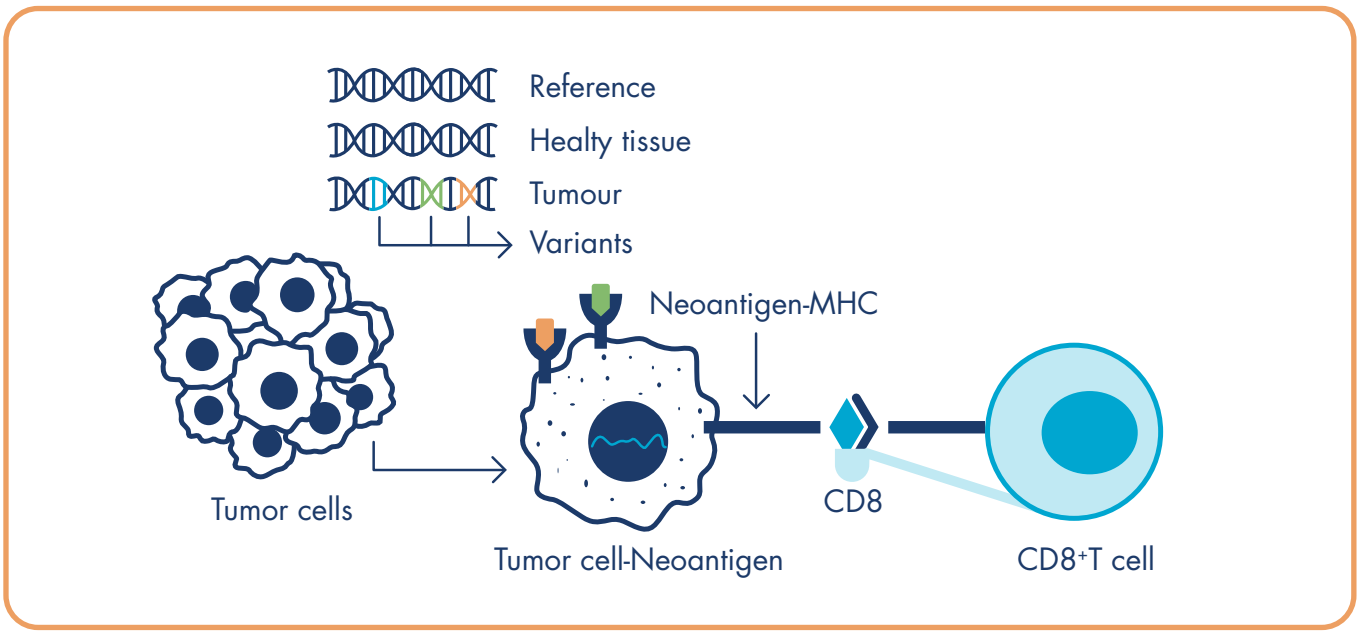
Workflow and Outcome

The workflow for comprehensive genomic analysis begins with the careful handling of tumor samples, which may be obtained in either FF or FFPE form. Before proceeding with sequencing, each tumor sample undergoes meticulous microdissection to isolate regions containing tumor cells. Histological assessment is then performed to determine the tumor cell percentage within the sample, ensuring that subsequent analyses accurately reflect the tumor's genetic makeup. Following histology, DNA and RNA are isolated from the tumor tissue, utilizing advanced extraction techniques tailored for FF or FFPE samples. For the normal samples, whether sourced from blood or saliva, the DNA isolation process is straightforward and follows established protocols. Once the DNA is extracted, it undergoes quality control checks to ensure its suitability for sequencing. Next, both tumor and normal DNA samples undergo library preparation, where the DNA is fragmented, adapters are ligated, and amplification steps are performed to generate sequencing-ready libraries. These libraries are then sequenced using state-of-the-art next-generation sequencing (NGS) platforms.

For tumor samples, WGS is employed with a sequencing depth of 300 gigabytes (Gb), ensuring comprehensive coverage of the genome. In parallel, RNA sequencing (RNA-Seq) is performed with 200 million paired-end reads, enabling the analysis of the tumor's transcriptome alongside its genomic profile. Normal samples undergo WGS sequencing with a sequencing depth of 100Gb to capture the individual's germline genomic information accurately. All generated sequencing data, both genomic and transcriptomic, are uploaded to the secure cloud infrastructure provided by myNEO Therapeutics for further analysis.



Upon data acquisition, the proprietary, best-in-class algorithms developed by myNEO Therapeutics are employed to analyze the genomic data. Tumor-specific somatic alterations unique to the tumor cells are identified and the likelihood of neoantigens to be presented via the major histocompatibility complex (MHC) and to be immunogenic, i.e. the ability to elicit a CD8 T-cell response, is predicted. This analysis allows to prioritize the best set of neoantigens for each individual patient informing the design of personalized immunotherapies.



A summary of steps applied upon data generation is as follows:

Target Selection

Various cancer events such as Single Nucleotide Variants (SNVs), Insertions and Deletions (Indels), gene fusions, Retro transposable Elements (RTE) insertions, lncRNAs, neo isoforms, as well as other events like TumorMET exon14 skipping, are considered for target selection. The overall Tumor Mutational Burden (TMB), as well as the expression of several immunotherapy-related genes, are also evaluated to correctly assess the likelihood of immunotherapy success.

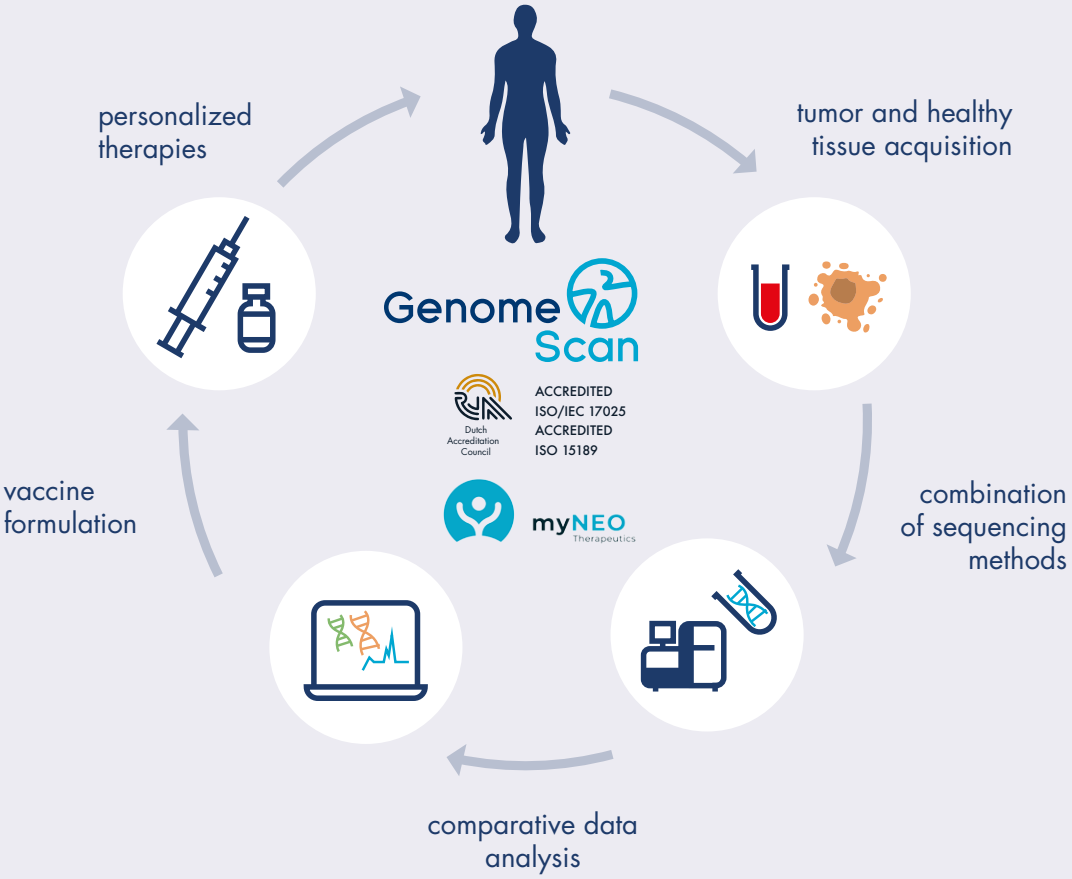
Target Prioritization

Targets are prioritized using proprietary algorithms, including neoMS for MHC-presentation prediction and neoIM for immunogenicity scoring. Functional relevance, clonality, and likelihood of immune escape are also considered during prioritization.

Vaccine Formulation and Production

Based on the identified neoantigens, personalized cancer vaccines are formulated. Utilizing innovative immunotherapy approaches, vaccines are then manufactured using the best delivery method applicable for the specific cancer indication considered.

This comprehensive approach not only underscores the transformative potential of personalized cancer vaccines but also highlights the importance of interdisciplinary collaboration in driving innovation and improving patient outcomes in oncology.



Significance

The partnership between GenomeScan and myNEO Therapeutics stands as a prime example of the significant impact that interdisciplinary collaborations can have on propelling innovation and furthering the field of precision medicine to improve patient outcomes on a global scale. Through a comprehensive approach that addresses the challenges inherent in personalized vaccine development, including sequencing complexities, bioinformatics intricacies, and integration into clinical workflows, significant strides have been made in tailoring cancer therapies to the unique genetic makeup of individual tumors.

About GenomeScan

GenomeScan is a multi-omics solution provider utilizing state-of-the-art technologies including Next Generation Sequencing (NGS). GenomeScan offers customizable solutions to pharmaceutical and biotechnology companies, healthcare providers, and academic institutions. Our service portfolio covers DNA, RNA, and epigenetics sequencing, as well as proteomics analysis with applications ranging from early discovery and preclinical drug development to clinical trials and manufacturing.

Our 15+ years of experience in the industry, in-house expertise in oncology and genetic QC, and robust bioinformatics pipelines let us stand out with the quality of our services. Additionally, short turnaround times and workflows that adhere to ISO/IEC 17025, ISO15189 and GCLP guidelines help you advance in your development programs with confidence.

Join the forefront of oncology research with GenomeScan's multi-omics solutions. For inquiries, collaborations, and a detailed consultation, contact us at **oncology@genomescan.nl**

About myNEO Therapeutics

myNEO Therapeutics is a distinguished biopharmaceutical powerhouse, dedicated to pioneer breakthrough immunotherapies to fight cancer. myNEO Therapeutics is leveraging its ImmunoEngine discovery platform to tap into novel promising tumor targets found in the dark genome – named camyotopes™ – which have the potential to unlock immunotherapy for large patient populations who currently do not respond.

In parallel, the service angle of myNEO Therapeutics, myNEO Intelligence, assists biopharma companies in transforming their decision-making process from trial & error to data-driven decisions using an AI-powered platform. Deriving insights from its expansive library of clinical and molecular data, myNEO Intelligence maps the molecular profiling of cancer patients at an individual level and then correlates the different data points to make data-driven decisions across the drug development life cycle. myNEO Intelligence can identify novel targets and biomarkers, prioritize drug candidates and indications, stratify patient populations, and predict treatment response.

For partnerships, collaborations, or more information on myNEO Therapeutics, contact: aviola.mehmeti@myneotx.com

Get in touch!

Join the forefront of oncology research with GenomeScan's multi-omics solutions.
For inquiries,collaborations, and a detailed consultation, contact us at

oncology@genomescan.nl

genomescan.nl

+31 71 5681050

oncology@genomescan.nl