GenomeScan® OncoNeoantigen

Actionable neoantigen information transforms tumor data into treatment decisions.

Cancer remains one of the most challenging and devastating diseases globally, claiming millions of lives each year despite decades of intensive research and therapeutic innovation. Traditional treatments—such as chemotherapy, radiation, and even some targeted therapies—often fall short due to their limited specificity, indiscriminately affecting both cancerous and healthy cells. This lack of precision not only leads to severe side effects but also compromises long-term treatment efficacy.

In recent years, immunotherapy has emerged as a groundbreaking advancement in oncology, fundamentally reshaping how we approach cancer treatment. By mobilizing the body's own immune system to detect and destroy malignant cells, immunotherapy offers a powerful and more selective alternative to conventional therapies.

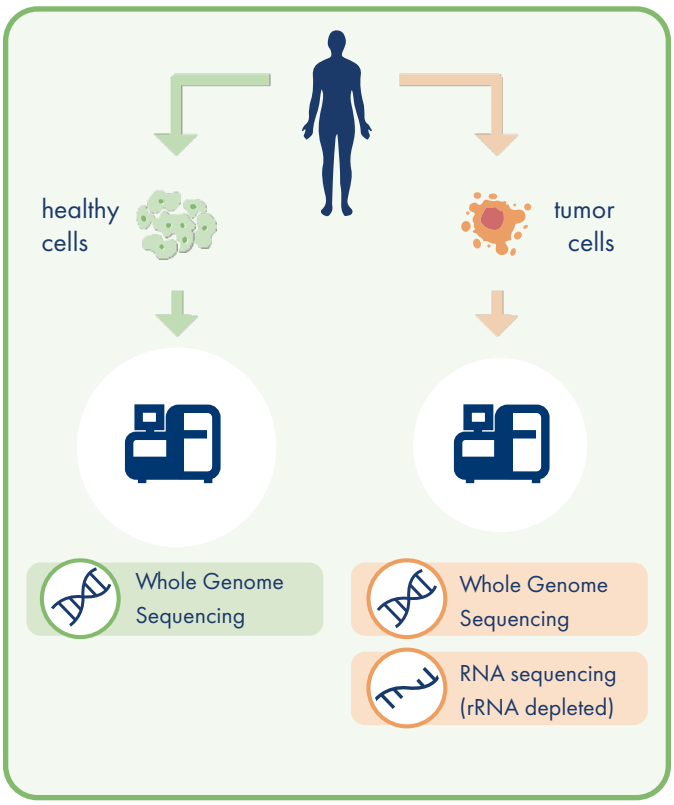
As we enter the era of precision medicine, there is an increasing demand for treatments that are not only more effective but also tailored to the unique molecular and immunological landscape of each patient's tumor. Despite the promise of immunotherapy, a significant proportion of patients still fail to respond—largely due to the absence of well-defined, tumor-specific immune targets.

This challenge highlights the urgent need for a new generation of personalized immunotherapies—ones that can identify and exploit neoantigens: mutated proteins that are unique to cancer cells and capable of eliciting a targeted immune response. Unlike self-antigens, which are shared by both healthy and malignant tissues, neoantigens are exclusively expressed by tumor cells, making them ideal candidates for immune-based interventions.

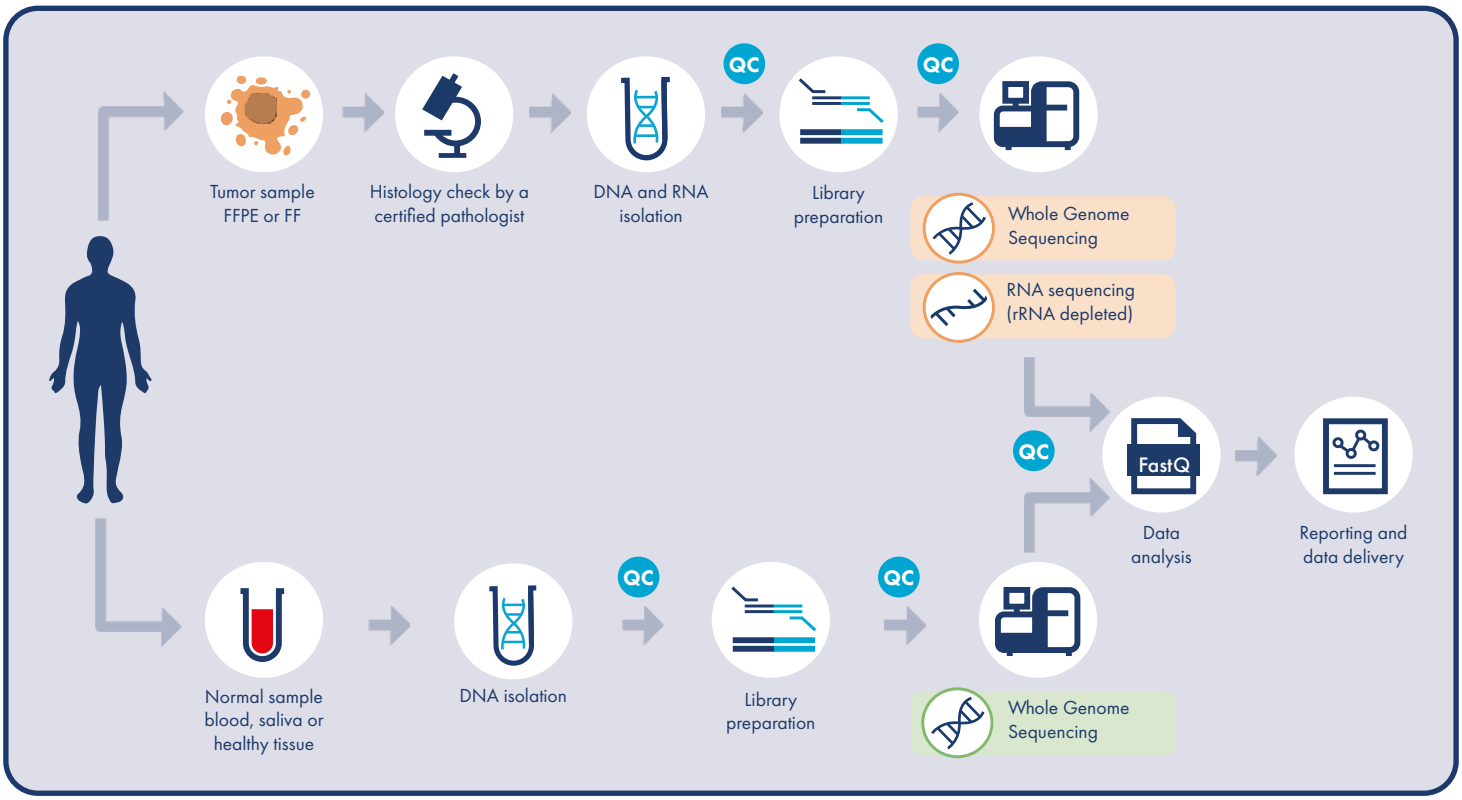
The identification and characterization of neoantigens through advanced sequencing and bioinformatics has become a foundation of personalized cancer immunotherapy. This process—often referred to as neoantigen sequencing—enables the development of custom cancer vaccines and T-cell therapies that are precisely tailored to an individual's tumor profile. However, translating a tumor biopsy into actionable neoantigen data is a complex endeavor, requiring high-quality genomic sequencing, expert pathological analysis, and sophisticated computational tools.

To meet this unmet need, we introduce GenomeScan® OncoNeoantigen — a comprehensive, ISO-accredited sequencing solution designed to identify patient-specific neoantigens with clinical-grade precision. This integrated workflow combines tumor-normal Whole Genome Sequencing (WGS) and tumor RNA sequencing (rRNA depleted), and robust data integration, enabling the discovery of actionable neoantigens for personalized cancer immunotherapy.

GenomeScan® OncoNeoantigen is designed to overcome the limitations of traditional sequencing approaches, particularly in challenging sample types such as FFPE and Fresh Frozen tissue. It delivers high-resolution, biologically validated insights that can inform the design of personalized cancer vaccines, T-cell therapies, and other immune-based interventions.



Dual sequencing strategy for tumor and matched normal samples.



Comprehensive workflow for tumor and matched normal sample processing.

Input material requirements

Sample types

- Tumor samples: FFPE or Fresh Frozen
- Matched normal samples: Blood, saliva or healthy tissue

Whole Genome Sequencing

DNA input requirements

High Molecular Weight (HMW) genomic DNA

- PCR-free workflow: ≥ 200 ng per sample
- With PCR amplification: ≥ 10 ng per sample
- Minimum volume: 25 µl per sample
- Quality: free from impurities and RNA

FFPE genomic DNA

- Minimum input: ≥ 10 ng per sample
- Recommended input: ≥100 ng per sample
- Quality: DV200 ≥ 50% (HMW DNA not expected due to fragmentation)
- Free from impurities and RNA
- Minimum volume: 25 µl per sample

Sequencing Specifications

- Platform: Illumina NovaSeq (PE150)
- Total number of reads:
  - Tumor sample: 1 billion paired-end reads per sample
  - Matched normal sample: 300 million paired-end reads per sample
- PCR-free libraries preferred
- Unique Molecular Identifiers (UMIs) for PCR-based samples
- Unique dual-indexed sequencing adaptors

RNA sequencing (rRNA depleted)

RNA Input Requirements

- Recommended input: 30 ng total RNA per sample
- Minimum input: ≥ 0.25 ng per sample
- Minimum volume: 25 µl per sample
- Minimum quality: DV200 > 25%

Sequencing Specifications

- Platform: Illumina NovaSeq (PE 150)
- Total number of reads for the tumor sample is 200 million paired-end reads per sample
- Library Preparation: Includes Unique Molecular Identifier (UMI) tags

Deliverables

- Data format: FastQ files
- Quality metrics: ≥ 80% of bases with Q30 or higher*

**Note: Due to the degraded nature of FFPE samples, quality expectations are adjusted. We aim for at least 70% of bases to have a Q-score of 30 or higher.*

Committed to your project

GenomeScan® OncoNeoantigen is backed by GenomeScan's ISO/IEC 17025 accreditation, ensuring that all laboratory processes meet the highest standards of quality, technical competence, and reproducibility. Each project begins with a pilot phase to assess sample quality and optimize workflow parameters, reducing the risk of suboptimal data and enabling informed decision-making before scaling up.

Key quality guarantees

- High mapping rates across exonic, intronic, and intergenic regions.
- Reproducibility across a wide range of input amounts.
- Expert QC at every stage, from sample intake to data delivery.

Transparent Reporting

We deliver comprehensive, consistent, and transparent project reports that describe all experimental procedures and include relevant QC metrics.

Biological Insights: From Data to Discovery

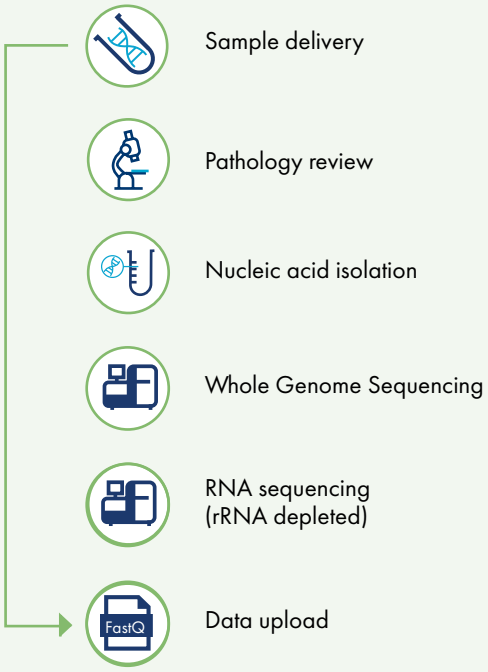
The OncoNeoantigen workflow is designed not just to generate data, but to deliver biologically meaningful insights. By integrating genomic and transcriptomic data from both tumor and normal tissue, the platform enables:

- Accurate somatic mutation calling with germline filtering.
- Expression validation of mutated genes.
- Prioritization of neoantigens based on expression, MHC-binding potential, and immunogenicity.

Key benefits

- **Truly personalized:** Captures the full mutational and transcriptional landscape of each patient's tumor.
- **Clinically adaptable:** Designed for integration into translational research and clinical development pipelines.
- **Sample versatility:** Compatible with both Fresh Frozen and FFPE tumor samples.
- **High data quality:** ISO/IEC 17025-accredited workflows ensure reproducibility and reliability.
- **Actionable insights:** Delivers data ready for downstream neoantigen prediction and immunotherapy design.

GenomeScan® OncoNeoantigen Workflow



Clinical and Research Applications

Neoantigen sequencing has broad applications across oncology:

- Personalized Cancer Vaccines: Custom-designed to stimulate an immune response against patient-specific neoantigens.
- Adoptive T-cell Therapy: T cells engineered to recognize neoantigens can be expanded and reinfused into the patient.
- Biomarker Discovery: Neoantigen load and quality can serve as biomarkers for immunotherapy response.
- Clinical Trial Stratification: Patients can be selected for trials based on their neoantigen profiles and predicted responsiveness.

About GenomeScan

GenomeScan is a trusted ISO-accredited partner for pharmaceutical companies seeking high-quality, customizable Next Generation Sequencing (NGS) solutions. With a strong foundation in clinical-grade genomics, we support drug discovery, biomarker development, and translational research through robust sequencing workflows and expert bioinformatics.

Our services are designed to accelerate therapeutic innovation by delivering precise, reproducible, and regulatory-compliant genomic data. Whether supporting early-stage research or clinical development, GenomeScan empowers pharma partners with the tools and insights needed to advance personalized medicine and targeted therapies.

genomescan.nl
+31 71 5681050
oncology@genomescan.nl

GUID024, Version 2, Authorized by QA