

# ImmunolD NeXT®

## Comprehensive tissue genomic profiling for the next era of precision oncology

ImmunolD NeXT® is a comprehensive tumor tissue profiling platform that delivers multidimensional insights into key areas of cancer biology. Leveraging an augmented whole exome sequencing (WES) and whole transcriptome sequencing (WTS) approach, our specialized analytics enable a panoramic view of the tumor and immune-microenvironment.

### Highlights



#### Expertise with Challenging Sample Formats

- ~ **>90% success rate** processing FFPEs, Core needle biopsies, Fine needle aspirates, Bone marrow aspirates
- **Sample sparing** with as few as 5 FFPE slides
- **1mm<sup>3</sup>** sample volume and **25mm<sup>2</sup>/section** surface area



#### Enhanced Exome & Transcriptome Coverage

- **Proprietary ACE® augmentation** of difficult to sequence regions across 20,000 genes
- **300X Tumor /150X Normal** WES
- **200M total reads** WTS
- **Clinical-grade coverage** (>1000X) across 247 Cancer-related genes

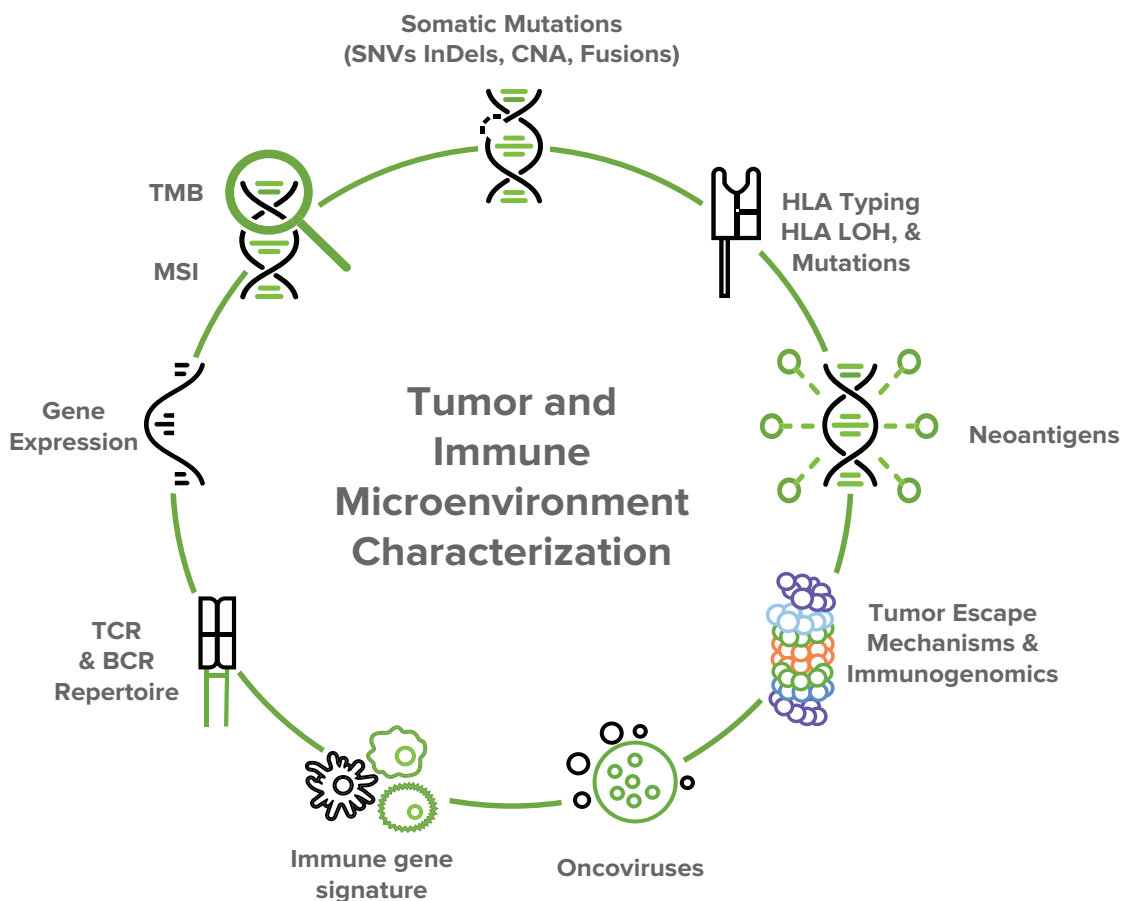


#### Proprietary Algorithms for Biomarker Analytics

- **Tumor-normal** and **tumor-only** configurations
- **HLA-LOH** Detection (DASH)<sup>1</sup>
- **HLA Typing** (HLA-Map)
- **Neoantigen Assessment** (SHERPA®)<sup>2</sup>
- **Composite Biomarkers** such as Neoantigen Presentation Score (NEOPS™)<sup>3</sup>

High accuracy with 98% sensitivity and 99% specificity

WE CAN SEE  
WHAT OTHERS MISS



**Figure 1:** Multidimensional View of Tumor and its Microenvironment – with an All-in-One Platform

### Laboratory credentials

CLIA, CAP, NY State and FDA\*

\*ImmunID NeXT Assay Master File (MF)  
filed with the FDA

### Versatile configurations and rapid TATs

Research Use (GCLP)

Personalized Cancer Therapeutics\* (GCLP-CLS)

LDT with clinical report (CLIA)

### Assay analytics

Tumor-Normal or Tumor-Only pipeline  
available for Research Use Applications.

### References:

1. Pyke et al. "A machine learning algorithm with subclonal sensitivity reveals widespread pan-cancer human leukocyte antigen loss of heterozygosity." Nature communications vol. 13,1 1925. 12 Apr. 2022
2. Pyke et al. "Precision Neoantigen Discovery Using Large-scale Immunoepitomes and Composite Modeling of MHC Peptide Presentation." Molecular & cellular proteomics : MCP vol. 20 (2021)
3. Abbott et al. "Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms." Clinical cancer research : an official journal of the American Association for Cancer Research vol. 27,15 (2021): 4265-4276

### Sales Contact

United States: [info@personalis.com](mailto:info@personalis.com)

Europe: [europe@personalis.com](mailto:europe@personalis.com)

Other Countries: [info@personalis.com](mailto:info@personalis.com)

### Personalis, Inc.

6600 Dumbarton Cir  
Fremont CA 94555

1 855-GENOME4

[www.personalis.com](http://www.personalis.com)

