verily

Accelerating Drug Discovery with Verily's Immune Profiler

Immune Profiler is a next generation discovery tool leveraging high-resolution immune measurements and advanced analytics to accelerate and enhance biomarker and target discovery by:

- Combining cytometry, genetics, transcriptomics, epigenomics, and analytics to uncover previously inaccessible signals in the immune system.
- Overcoming signal dilution and inter-individual heterogeneity to improve sensitivity.

Applications in drug discovery

- Uncover novel disease mechanisms and pathways
- Predict and validate novel drug targets and combinations using primary human data
- Identify drug label expansion and repositioning opportunities
- Discover biomarkers that can differentiate patient outcomes (e.g. response to treatment or disease progression)

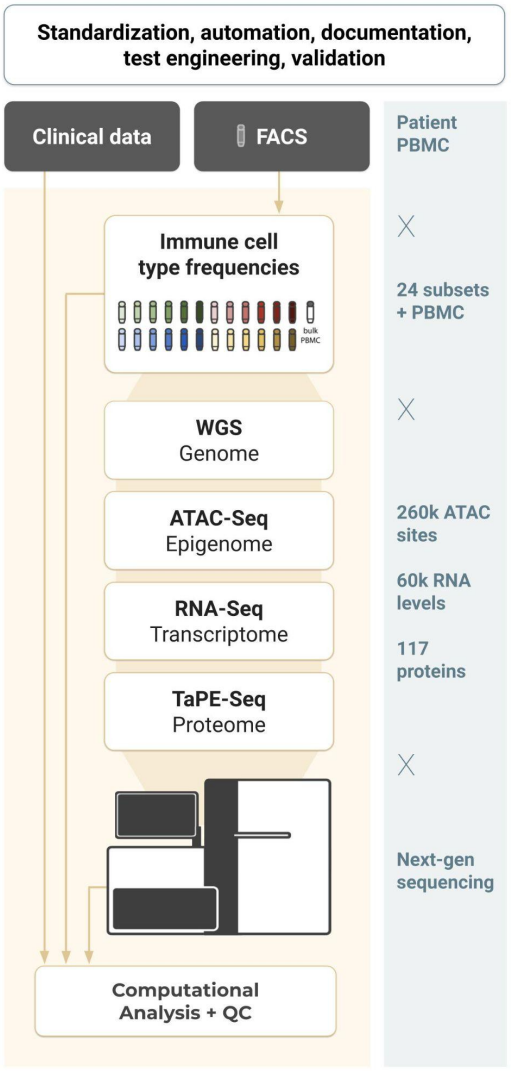

Figure 1. Immune Profiler generates high-resolution immune measurements from a single patient blood sample.

Three pillars of Immune Profiler

High Resolution Data

- Clear resolution of 24 distinct immune cell types
- Over 8 million molecular features per sample
- Holistic genotype-to-function analysis

High Production Quality

- Best-in-class production practices with full traceability and security
- Rigorous standardization
- Automated QC for rapid detection of anomalies
- Scalable infrastructure to manage petabytes of data

Novel Insights

- Direct modeling of immune function using human samples
- Computational biology team automates advanced analytics & machine learning
- Extensive multi-omic data builds confidence in hits

Insights starting from deep & broad immune phenotypes

Immune Profiler generates reproducible, high quality data, even from low input, low quality samples by:

- Isolating 24 cell subsets across immune functions (Table 1) to achieve high purity from mixed blood samples, while simultaneously enriching low frequency subsets that are difficult to study using single cell and whole blood methods
- Normalizing immune cell subsets that vary in frequency by orders of magnitude to minimize input bias and increase data quality
- Interrogating 8M+ subset-resolved molecular features per sample to obtain an extensive, coordinated view of immune function

Myeloid	
Dendritic	Conventional
	Plasmacytoid
Monocytes	Classical
	Intermediate
	Nonclassical
B cells	
Naive	Unswitched naive
	Class switched naive
	Transitional
Effector	Class switched classical memory
	IgM+ IgD- classical memory
	Atypical Memory
	Class switched plasmablast

T cells	
CD4+ αβ	Naive
	Central memory
	Effector memory
	CD45RA+ effector memory
	Regulatory
CD8+ αβ	Naive
	Central memory
	Effector memory
	CD45RA+ effector memory
γδ	Gammadelta
NK	
NK	CD56dim
	CD56bright

Table 1. Immune cell subsets captured by Immune Profiler

Core molecular workflows

30X Whole Genome Sequencing optimized to minimize bias and maximize uniformity using PCR-free library prep, coupled with our award-winning deep learning software, DeepVariant, for single nucleotide variant and insertion/deletion decisions.

Low-input ATAC-Seq optimized for high quality data from low cell inputs, enabling interrogation of rare immune cell types. The protocol also enables matched epigenomic, transcriptomic, RNA and protein measurements to be obtained from the same sorted subsets.

Low-input RNA-Seq using an optimized SMART-Seq approach that minimizes material loss during sample processing and integrates with ATAC-Seq and TaPE-Seq measurements.

Next gen Protein Measurements using Targeted Protein Estimation by sequencing (TaPE-Seq) using oligo-tethered antibodies to generate protein measurements using sequencing readouts, enabling seamless integration with ATAC-Seq and RNA-Seq workflows.

Turn data into insights with advanced analytical capabilities

Our Computational Biology team builds robust pipelines using Google engineering practices and sophisticated, scalable cloud-computing to efficiently manage petabytes of data, maximize confidence in the integrity of results, and minimize time to insights for biomarker and drug target discovery. Our approaches include:

Genetics-Driven

Identify biological mechanisms and targets with higher relevance using evolutionarily-selected genetic risk determinants, coupled with their associated functional data to build confidence in hits.

Subset-Specific

Discover novel disease monitoring and modulation approaches using subset-specific analytics to identify novel targeting modalities.

Comparative

Understand disease perturbations and therapeutic mechanisms of action with high resolution, integrated, multi-omic next-gen molecular data.

To learn more, contact us at verily.com/immune-profiler