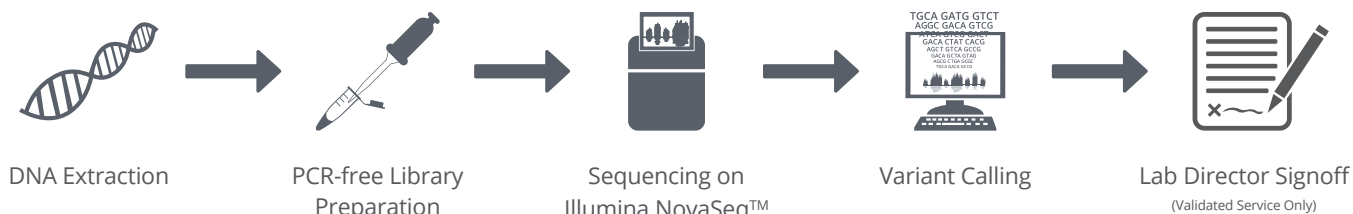


GENEWIZ clinical-grade whole genome sequencing (WGS) offers unparalleled precision and accuracy for unbiased exploration of the human genome. Our PCR-free WGS workflow empowers clinical researchers to detect disease-related genetic variants in both coding and non-coding regions. In addition, the sequencing data can be used to identify novel variants of unknown significance and reanalyzed once additional disease-related information becomes available. Our validated assay strictly adheres to requirements set forth by the Clinical Laboratory Improvement Amendments (CLIA) and the College of American Pathologists (CAP).



THE GENEWIZ DIFFERENCE

- **Superior data quality** that exceeds Illumina® benchmarks
- **PCR-free workflow** reduces bias and increases precision in challenging genomic regions
- **Dedicated Ph.D. project managers** provide consultations and ongoing support
- **Rapid turnaround** delivers results in a few weeks
- **High-throughput variant detection** facilitates patient stratification for clinical trials
- **Population-scale sequencing capacity** for large clinical trials and reference lab overflow



Clinical-grade WGS Workflow. Each stage of our modular workflow is performed in a CLIA-certified and CAP-accredited laboratory by certified staff scientists on qualified equipment. Rigorous quality control is performed throughout the process to ensure the highest quality data.

Service Levels

GENEWIZ clinical-grade WGS is available at two service levels:

- **CLIA-Validated:** This level is recommended if data is used for diagnostic purposes or is reported to patients. You will receive raw data files and a variant report signed by our accredited laboratory director.
- **CLIA Environment:** This more cost-effective option offers greater flexibility for clinical infrastructure work that does not require signoff from a laboratory director.

		CLIA-Validated	CLIA Environment
Report with Lab Director Signature		✓	✗
Applications	Germline variant detection	✓	✓
	Somatic variant detection	Coming Soon	✓
Laboratory Setting	CLIA-certified & CAP-accredited lab	✓	✓
	CLIA/CAP-certified equipment	✓	✓
	CLIA/CAP-trained personnel	✓	✓
	Secure data server with restricted access	✓	✓
Accepted Sample Types	Genomic DNA	✓	✓
	Whole blood	✓	✓
	Fresh frozen tissue	Coming Soon	✓
	Saliva	Coming Soon	✓
	FFPE	Coming Soon	✓
Data Output (Coverage)		≥90 Gb (≥30X)	45 – 270 Gb (15 – 90X)
PCR-Free Workflow		✓	✓
Variant Calling	Single nucleotide variants (SNVs)	✓	✓
	Insertions or deletions (INDELs)	✓	✓

Performance Specifications

We assessed our PCR-free WGS workflows using the well-characterized Genome in a Bottle (GIAB) reference samples, as well as DNA extracted from healthy donors. At a minimum mean aligned coverage of 22X, SNVs were detected with >99.8% sensitivity, and INDELs were detected with >95.5% sensitivity. Further, variant calling precision was consistently above 98% across several GIAB replicates.

Validated Mean Coverage		≥22x
% bases ≥10X Coverage		95%
Single nucleotide variants (SNVs)	Specificity	99.99%
	Sensitivity	99.80%
	Precision	99.70%
Insertions or deletions (INDELs)	Specificity	99.99%
	Sensitivity	95.5%
	Precision	98.9%