

# PredicineWES+™

## Liquid Biopsy Boosted by Whole Exome Sequencing

### Genome-wide Molecular Insights

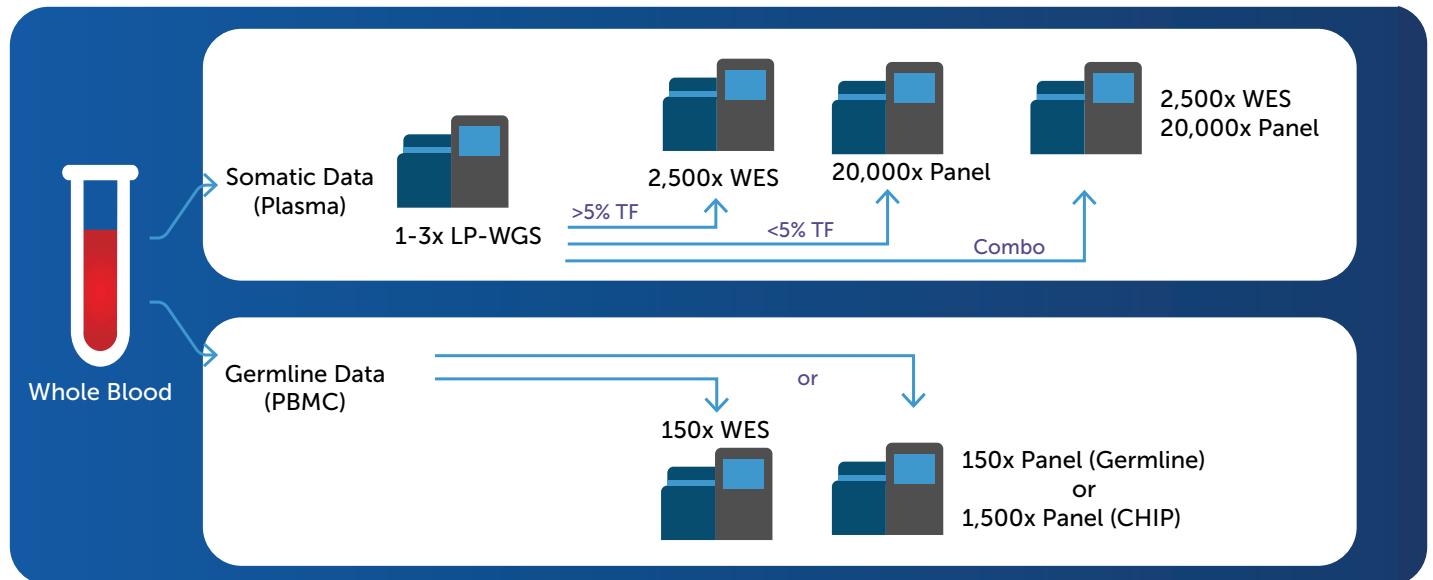
Genomic profiling of cell-free DNA (liquid biopsy) using whole exome sequencing (WES+) provides insights into genome-wide variation and a high resolution of structural variations, rearrangements, and exon duplicates.

### Liquid Biospy Sequencing

PredicineWES+™ liquid biopsy sequencing solution offers rapid turnaround time for clinical applications. From a single sample, we provide low-pass whole genome sequencing (LP-WGS) data combined with broader coverage using WES and in-depth profiling using PredicineATLAS™ focused pan cancer panels, based on tumor fraction of the sample.

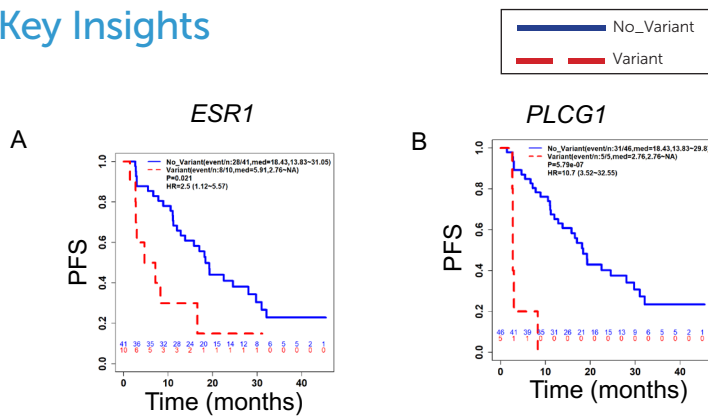
Screening with LP-WGS allows for informed decision making due to the additional breadth and depth of coverage provided by whole exome and focused pan-cancer panel sequencing.

### Workflow Flexibility



Plasma (ATLAS Boosted Regions)					Urine (ATLAS Boosted Regions)			
Variant Type	Reportable Range	Allele Frequency/ Copy Number	Sensitivity	Positive Predictive Value (PPV)	Reportable Range	Allele Frequency/ Copy Number	Sensitivity	Positive Predictive Value (PPV)
Single Nucleotide Variations	≥0.05%	0.375% AF	100%	100%	≥0.1%	0.3% AF	98.2%	100%
		0.25% AF	99.1%	100%		0.1% AF	36.4%	100%
		0.1% AF	45.5%	100%		0.3% AF	98.3%	100%
Indels	≥0.05%	0.375% AF	100%	100%	≥0.1%	0.3% AF	98.3%	100%
		0.25% AF	100%	100%		0.1% AF	50.0%	100%
		0.1% AF	66.7%	100%		0.3% AF	100%	100%
DNA Re-arrangement	≥0.05%	0.375% AF	100%	100%	≥0.1%	0.3% AF	100%	100%
		0.25% AF	100%	100%		0.1% AF	33.3%	100%
		0.1% AF	66.7%	100%		0.3% AF	100%	100%
Copy Number Gain	≥2.18	2.21-2.28 copies	100%	100%	≥2.2	2.25-2.34 copies	100%	100%
Plasma (WES Region)					Urine (WES Region)			
Variant Type	Reportable Range	Allele Frequency	Sensitivity	Positive Predictive Value (PPV)	Reportable Range	Allele Frequency	Sensitivity	Positive Predictive Value (PPV)
Single Nucleotide Variations	≥0.05%	2.5% AF	95.2%	100%	≥0.01%	2.5% AF	95.2%	100%
Sequencing	Illumina NGS							
TAT	10 days							
Specimen Type and Requirement	Liquid biopsy	CLIA	RUO		Tissue biopsy	CLIA	RUO	
		20 mL blood 20-40 mL urine	2-5 mL plasma 4-10 mL blood 20-40 mL urine			≥ 1mm <sup>3</sup> tissue (5-10 FFPE slides)	≥ 1mm <sup>3</sup> tissue (5-10 FFPE slides)	

## Key Insights



### Baseline alterations associated with shorter progression-free survival (PFS)

Baseline alterations in 91 genes were significantly associated with worse PFS, including alterations previously implicated in CDK4/6i and ET resistance such as AR, ATM, AURKA, BRCA2, CCND1, DDR2, ESR1, FAT1, FGFR4, FOXP1, MYC, RB1, and RUNX1T1 (A). In addition, baseline alterations in 61 genes outside of the PredicineATLAS™ panel were detected, such as PLCG1 (phospholipase C, gamma 1) (B)

## Conclusions

- Previously reported and novel baseline alterations were significantly associated with shorter progression-free survival.
- PredicineWES+™ extends the gold standard for deriving TMB to plasma, detects additional prognostic biomarkers at baseline and reveals novel alterations at progression that may underly resistance.
- For more detail, please see link to poster below.

2021. Blood tumor mutational burden and blood copy number burden by genome-wide circulating tumor DNA assessment predict outcome and resistance in hormone-receptor positive, HER2 negative metastatic breast cancer patients treated with CDK4/6 inhibitor. SABCs. December 7-10, 2021.