Predicine L-P WGS

Ultra Low-Pass WGS cfDNA Assay for CNV Analysis

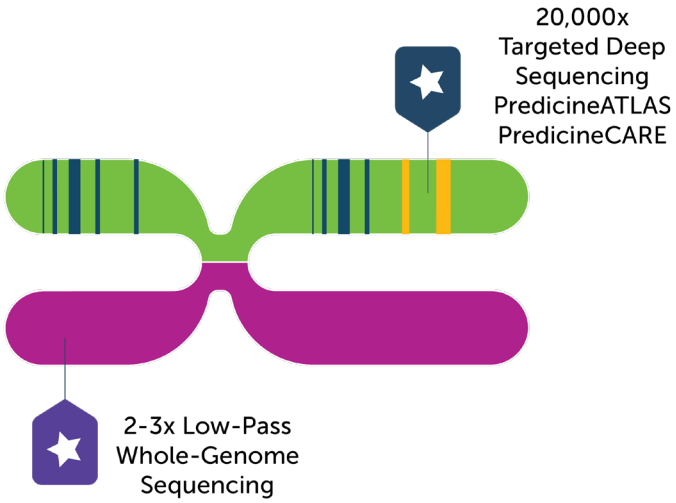
Ultra low-pass whole genome sequecning for comprehensive coverage of chromosomal abnormalities in cancer

3x

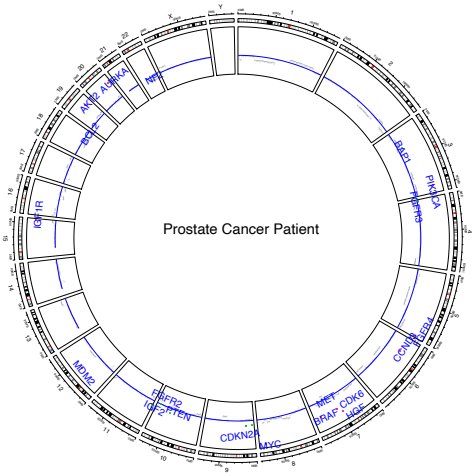
Broad genome coverage

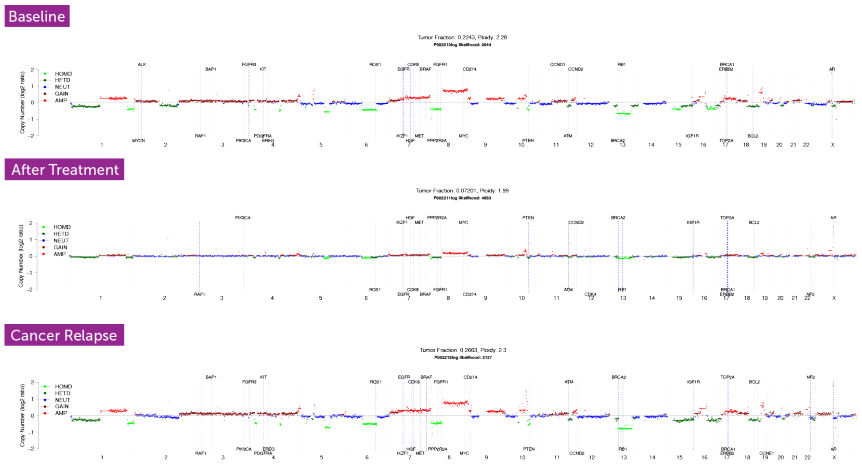
2 data sets

Ultra L-P WGS data combined with targeted deep sequencing panel from a single sample



Longitudinal monitoring of prostate cancer using cfDNA





Methods and Reporting

- Analyzes gene fusions, chromosomal rearrangements, and copy number variants
- Measures tumor fraction to predict patient outcome
- Test results are provided in an interpretive report with clinically relevant genomic findings listed

PERFORMANCE SPECIFICATIONS

	Reportable Range	Allele Frequency/Copy Number	Sensitivity	Positive Predictive Value (PPV)
Single Nucleotide Variations	≥0.05%	≥0.5% AF	100%	100%
		0.25% - 0.5% AF	98.6%	99.2%
		<0.25% AF	78.3%	97.9%
Indels	≥0.05%	≥0.5% AF	100%	100%
		0.25% - 0.5% AF	98.6%	100%
		<0.25% AF	80%	100%
Re-arrangement	≥0.05%	≥0.5% AF	100%	100%
		0.375 - 0.5% AF	96.7%	100%
		0.25% - 0.375% AF	90%	100%
		<0.25% AF	33.3%	100%
Copy Number Gain	≥2.18	≥2.375 copies	100%	100%
		2.23 - 2.375 copies	100%	100%
		<2.23 copies	45%	81.8%
Copy Number Loss	≤1.85	≤1.75 copies	100%	100%
		1.75 - 1.80 copies	93.6%	91.7%
		≤1.85 copies	66%	88.6%
Regions Analyzed				
Sequencing and Bioinformatics	Illumina NGS			
Assay Sensitivity	0.25% report down to 0.05%			
Turnaround Time	10 days			
Target Sequence Coverage	3x for biofluid, 3x for tissue			
Specimen Type and Requirement		**RUO**	**CLIA**	
	Liquid biopsy	2ml plasma 1 tube of whole blood 40ml urine	8ml plasma 2 tubes of whole blood	
	Tissue biopsy	10 FFPE slides	10 FFPE slides	

Workflow

PROJECT CONSULTATION | SAMPLE COLLECTION | SAMPLE TRANSPORT | SAMPLE PROCESSING | BIOINFORMATICS ANALYSIS | PROJECT REPORT | DATA INTERPRETATION

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