PredicineWES+™

Liquid Biopsy Boosted Whole Exome Sequencing

Genome-wide Molecular Insights

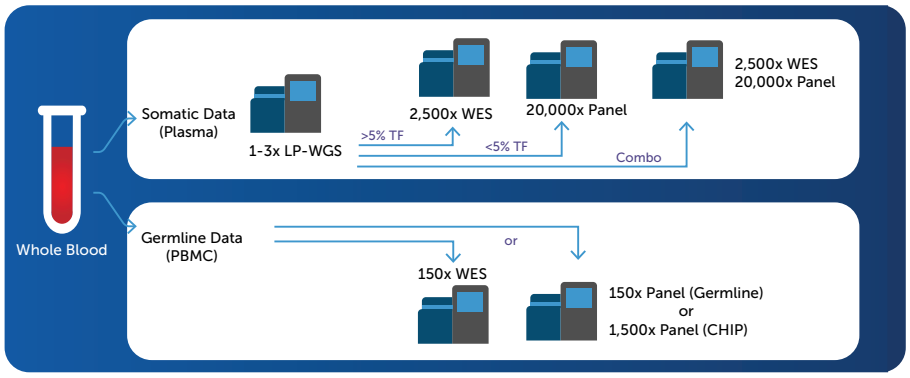
Genomic profiling of cell-free DNA (liquid biopsy) using whole exome sequencing (WES+) provides insights into genome-wide variation and a high resolution of structural variations, rearrangements, and exon duplicates.

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 from 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



Input Requirements

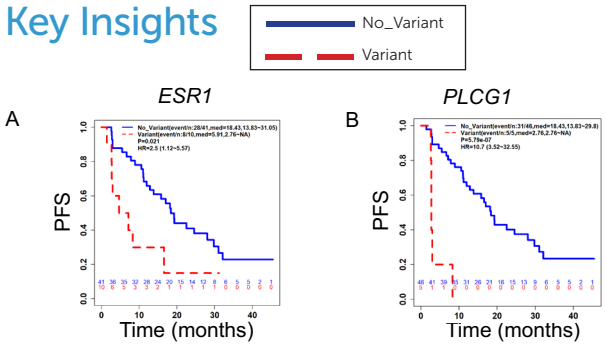
- 5-10ml blood, 4-6ml plasma, or 5-30ng cfDNA
- 40ml urine

Deliverables

- Tumor fraction & ploidy analysis
- SNV, CNV, Indel and rearrangement
- TMB, MSI & HRD*

*RUO use only

Key Insights



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.

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)

2021. Blood tumor mutational burden and clood 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. Decmber 7-10, 2021.

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