Reliable Genomic DNA Extraction for Whole-Exome Cancer Risk Profiling Using the MagPurix® Automated Nucleic Acid Extraction System

MagPurix® Blood Extraction Kit enables efficient Whole-Genome Sequencing (WES) library Prep.

Executive Summary

Accurate detection of germline variants that predispose individuals to cancer relies heavily on the quality and integrity of extracted genomic DNA. In a recent pan-cancer germline analysis conducted on UAE patients, high-purity DNA extracted using the **MagPurix® Automated Extraction System (Zinexts Life Science)** enabled efficient whole-exome sequencing (WES) library preparation, high coverage sequencing performance, and confident downstream variant analysis.

The use of MagPurix® ensured consistent DNA yield and purity from whole blood, supporting reliable identification of cancer-associated germline variants across multiple cancer types. This application note highlights how MagPurix® contributes to high-confidence genomic research and precision medicine initiatives.

Study Overview

Overview	Description
Purpose	Identify population-specific germline cancer predisposition markers in the UAE population.
Sample Type	Whole blood (Blood DNA Extraction kit)
Cohort	62 cancer patients (breast, colon, leukemia, others) and 142 matched healthy controls
Extraction System	MagPurix® Automated Nucleic Acid Purification System (Zinexts, Taiwan)
Downstream Workflow	DNA quantification → Illumina TruSeq Exome library prep → NextSeq500 sequencing → Variant calling and gene/pathway analysis

Key Findings

1. High-Quality DNA Extraction Enabled Reliable WES Workflow

- Genomic DNA was extracted consistently from 400 µL blood input, following MagPurix standard protocols.
- DNA yielded suitable concentration, purity (A260/280 and A260/230), and integrity for Illumina whole-exome library preparation and sequencing.

- The resulting sequencing data achieved ~71× average exome depth with >99.9% alignment, supporting robust germline variant detection.

2. High-Confidence Variant Detection Across Multiple Cancer Types

- Over 70 pathogenic germline variants across 64 genes were identified across breast, colon, leukemia, and other cancers.
- Variants affecting DNA repair pathways (e.g., POLQ, MSH6, ATM, SLX4) were recurrent across patients.
- TEKT4 and HLA-C variants showed statistically significant association with cancer cases.

3. Pathway Enrichment Showed Clear Biological Signatures

- Enriched pathways: DNA damage response, telomere maintenance, double-strand break repair
- Depleted pathways: Mitochondrial energy metabolism and protein biosynthesis
- Findings suggest shared cancer predisposition mechanisms across patients at the germline level.

4. Importance of Reliable Extraction in Population-Genomic Studies

- The UAE population displays unique genetic background characteristics.
- The study highlights the importance of reproducible, high-purity extraction in under-studied and genetically diverse populations.

Conclusion

The MagPurix® Automated Nucleic Acid Extraction System played a central role in ensuring the high DNA integrity and reproducibility required for whole-exome sequencing and variant discovery in this population-scale cancer predisposition study. The ability of MagPurix® to deliver consistent nucleic acid quality from clinical whole blood samples directly contributed to the reliability of downstream genomic analysis and the identification of cancer-associated germline variants.

As precision oncology and hereditary risk screening expand globally, MagPurix® offers a dependable extraction solution that supports large-scale genomic research, clinical screening workflows, and personalized medicine programs.

Reference

Alnaqbi, H., Olbrich, M., Zayed, N., et al. (2025). Pan-cancer exome-wide analysis of germline mutational patterns and pathways. *Scientific Reports*. https://doi.org/10.1038/s41598-025-05296-3