

A large, stylized gear-like circular graphic in the upper left quadrant. It has a dark blue center with the text "DATA MANAGEMENT" in white, surrounded by concentric rings of lighter blue and white segments.

DATA
MANAGEMENT

A large, stylized gear-like circular graphic in the lower right quadrant. It has a dark blue center with the text "DATA ANALYSIS" in white, surrounded by concentric rings of lighter blue and white segments.

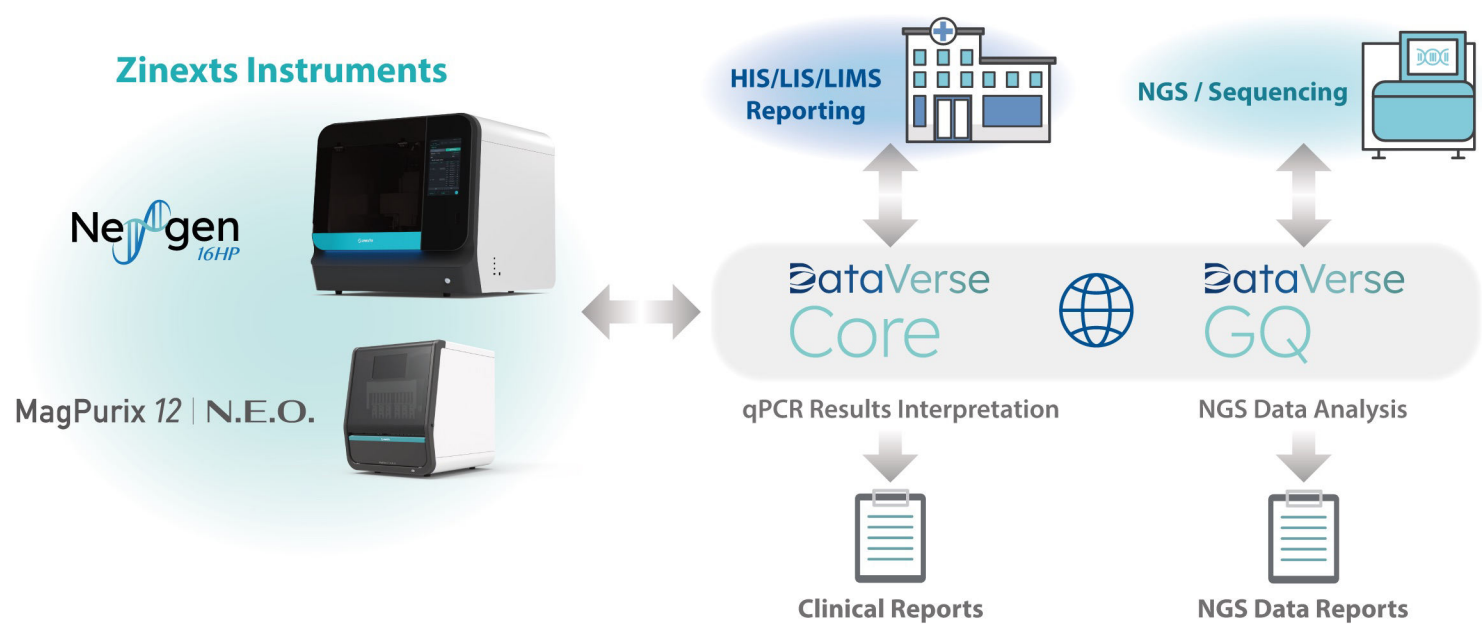
DATA
ANALYSIS

Smart Data
Integration
and Analysis

Zinexts
ataVerse

*Data Management • Sequencing Analysis • Diagnostic
Interpretation • Report Customization • Decision Support*

An end-to-end ecosystem that helps to manage data, run sequencing analysis, interpret results confidently, and deliver customizable reports securely on premises.



Why DataVerse™?



One Ecosystem

A dual-system platform developed to unify data management and advanced analytics



Offline Operation

Deployed on-premise and does not require a browser-cloud access



Data Security & Compliance

Secure login, audit logging, and optional local server integration ensures both privacy and accessibility. Follow global compliance standards, HIPAA/GDPR principles



Customized Report

Issues professional clinical reports in minutes with flexible and ready-to-use templates

Suitable for



Researchers

Effortlessly manage and analyze data with streamlined tools



Clinicians

Review and interpret results with ease to support decision-making



Healthcare Practitioners

Directly access genetic insights to enhance patient care and diagnostics

Genomic & Clinical Data Management

1. Middleware Hub

Integrates Zinexts systems into LIS/LIMS/HIS ensuring seamless data transfer and secure integration

2. Sample Data Management

Manages data from hospital systems (LIS/LIMS/HIS) and Zinexts instruments including MagPurix® N.E.O. and NeXgen™ 16HP, for effortless data exchange, eSignature, and real-time tracking

3. qPCR Assay Results Interpretation

Provides complex qPCR assay results interpretation for diagnostic decision-making support

4. Comprehensive Clinical Reporting

Consolidates hospital data and collect NGS data results from DataVerse™ GQ to generate complete clinical report with patient information

Powerful Sequencing Data Analysis

1. Multi Omics Sequencing Data Analyzer

Supports genomics (WGS/WES/panels) and other types of assay analysis

2. Sequencer Agnostic

Analyze the sequencing data from major sequencing platforms and various formats (FASTQ/VCF/BAM)

3. Trustworthy Results

Provides accurate sequencing data for reliable clinical reports with QC metrics

4. Analyze Complex Data

Detects multiple gene variations (SNVs, small indels, hotspot genotyping, CNV, and HLA-Typing)

5. Flexible Data Export

Issues NGS data reports in multiple formats (CSV/JSON/VCF/HTML/PDF) or integrates with DataVerse™ Core to issue full clinical report

6. Interpretation & Decision Support

Provides smart data interpretation with curated literature databases to support decision making

7. Tailor-Made Database

Customizable pipelines for WES/WGS/Targeted Panels on demand based on your laboratory needs

Applications

Cancer Panels

Breast Cancer Genetic Test (BRCA)

Pan-Cancer Panel

Microbiota

Microbial Identification

Probiotics Profiling

Genomic Research

Genome Sequencing

Transcriptome Sequencing

Microbiome Sequencing

Clear Data Report, Clear Clinical Support

BRCA Panel Germline Report

Theaca BRCA Panel Germline Report
Version: Zinexts-CG_BRCA_germlineR38_01.0.0

MOHW-MD- xxxxxxxxxxxx
Execute Date: 2025 10/30 16:01:27
Project ID: Zinexts_CG_BRCA251030160042

HELP

Personal Information

Name Mary Lin

Clinical ID A247515784

Patient ID P254784682

Date of Birth

Age

Sex

Specimen No.

Inspection unit

Referral Physician

Specimen Type

Collection Date

Test Date

Result: **Positive**

Variant Site

Gene/Variant	Frequency	Clinical significant
BRCA2 NC_000013.11:g.3234002del NM_000059.3:c.565delA p.Ile1889fs frameshift_variant	Allelic Frequency(AD/DP) 0.500(28,5/48) Population Frequency All: . EAS: .	ClinVar: Pathogenic
BRCA2 NC_000013.11:g.3237976del NM_000059.3:c.8970delG p.Trp2990fs frameshift_variant	Allelic Frequency(AD/DP) 0.500(9,2/11) Population Frequency All: . EAS: .	ClinVar: Pathogenic

*Gene/Variant showed the mutant gene and the variant site of this gene in chromosome(NC_), transcription(NM_) and protein(NP_).

*Variant type is the type of genetic change such as SNVs and indels.

*Allele frequency represents the frequency of the mutation in the database and the depth of sequence.

*The population frequency for an allele is the number of times that it appears divided by the total number of alleles in a given population. ALL is the frequency of this variant in whole populations; EAS is the frequency of this variant in East Asian populations.

*Clinical significance describes the criteria of ClinVar to classify genetic variants.

*Interpretation the result of Positive while Clinical significance indicated Pathogenic.

Detection purpose:

BRCA1/2 gene is a tumor suppressor gene, which is mainly responsible for repairing damaged DNA. If the BRCA1/2 gene is mutated, it may cause DNA abnormal repair function increases the risk of cancer. BRCA1 and BRCA2 are common genetic mutations in hereditary breast cancer. Statistics show that women with BRCA1 gene mutations have a lifetime chance of developing breast cancer of about 80%, and the chance of developing ovarian cancer is about 65%. If you have a BRCA2 gene mutation, the chance of developing breast cancer is about 80% for women and 6% for men. In addition, the polymerase PARP in cells is also involved in the repair of damaged DNA, and the targeted drug-PARP inhibitor can inhibit the function of PARP and block DNA repair. If the BRCA1/2 gene is mutated, coupled with PARP inhibition Drugs can strengthen the blocking of DNA repair mechanism and promote the apoptosis of cancer cells. Therefore, before using PARP inhibitors, BRCA1/2 gene testing must be performed to confirm whether there is a BRCA1/2 gene mutation.

Currently FDA approved PARP inhibitors for BRCA1/2 gene mutations include olaparib (Lynparza), talazoparib (TALZENNA), Rucaparib (RUBRACA) and niraparib (Zejula) *1 *

*1 New revision in 2022 of FDA guidelines, niraparib can be used with or without BRCA1/2 gene mutation. *

Detection targets:

BRCA1, BRCA2

Declaration

This inspection report is only for the screening results of this sample. Since the written consent of the inspection laboratory has not been obtained, this inspection report should not be partially copied, except for the full copy.

References

1. Annu Rev Pathol. 2009;4:461-87.
2. JAMA 2017; 317(23):2402-2416.
3. Am J Hum Genet 2003; 72(5):1117-1130.
4. J Clin Oncol. 2007; 25(11):1329-1333.

Details

Show

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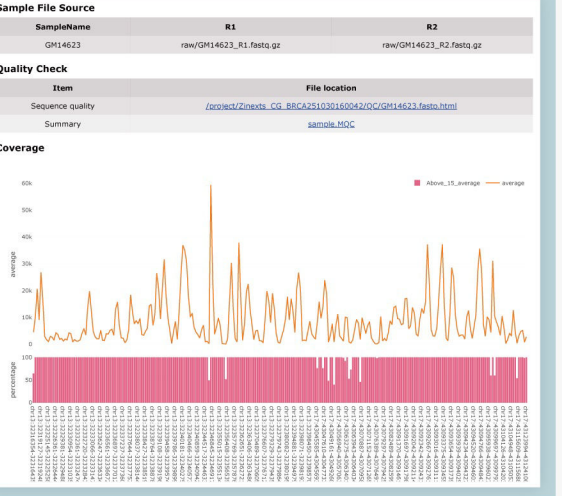
Full Customization Reports

Result: **Positive**

Variant Site	
Gene/Variant	Frequency
☒ BRCA2 NC_000013.11:g.3234002del NM_000059.3:c.565delA p.Ile1889fs frameshift_variant	Allelic Frequency(AD/DP) 0.500(28,5/48) Population Frequency All: . EAS: .
☒ BRCA2 NC_000013.11:g.3237976del NM_000059.3:c.8970delG p.Trp2990fs frameshift_variant	Allelic Frequency(AD/DP) 0.500(9,2/11) Population Frequency All: . EAS: .
☐ BRCA1 NC_000017.11:g.4304303C>A NM_007258.4:c.1171G>T p.Glu391* stop_gained	Allelic Frequency(AD/DP) 0.500(17,12/53) Population Frequency All: . EAS: .
☐ BRCA2 NC_000013.11:g.3233826T>A NM_000059.3:c.5277T>A p.Tyr1757* stop_gained	Allelic Frequency(AD/DP) 1.00(0,23/31) Population Frequency All: . EAS: .

Interpretation based on patient phenotypes association:
Pathogenic (P), Likely pathogenic (LP), Variant of Uncertain Significance (VUS), Likely benign (LB), and Benign (B)

Detailed QC Report



Check the sequencing data quality

Let's unify your patient data and diagnostics workflows



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