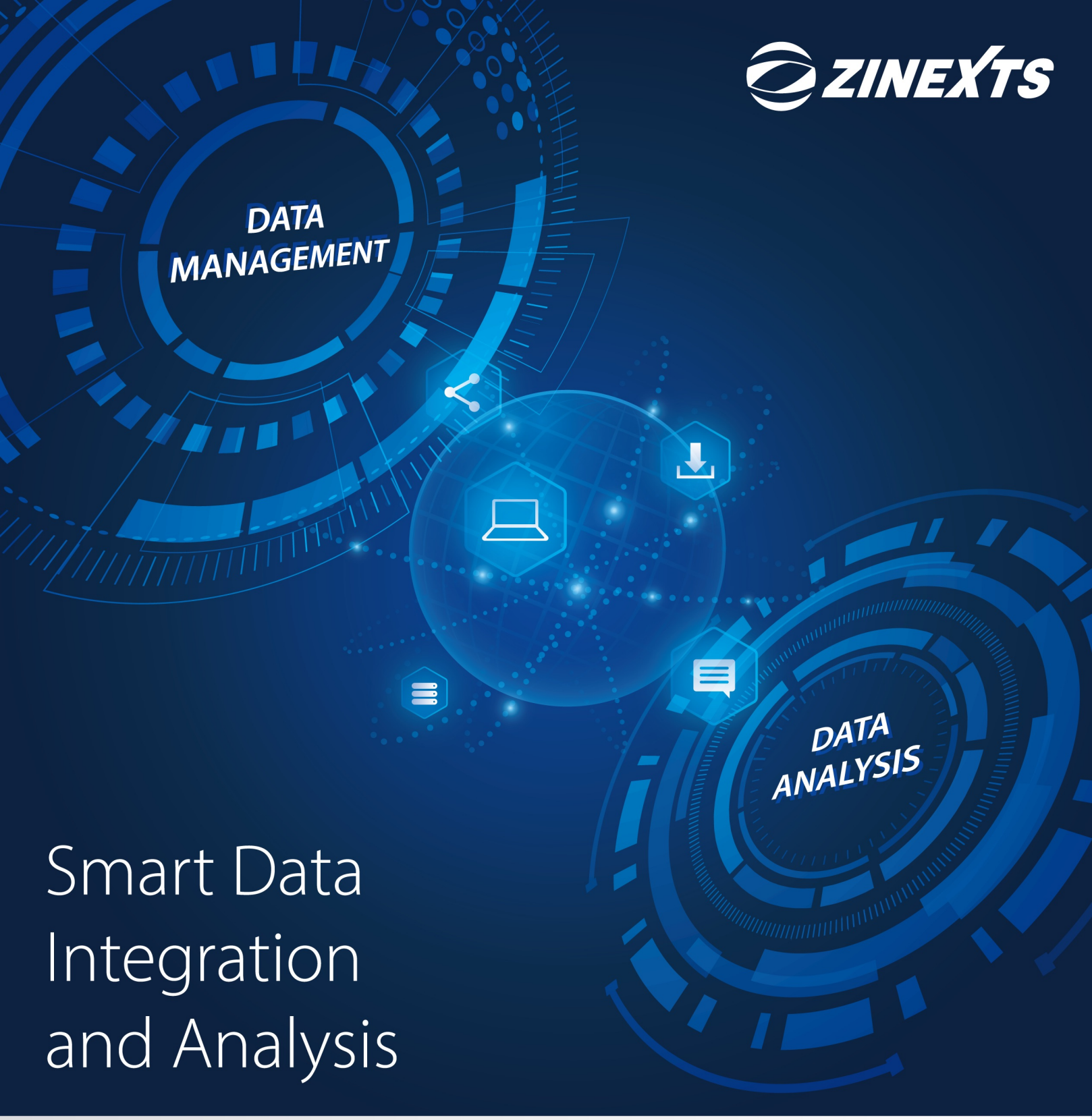
ZINEXTS

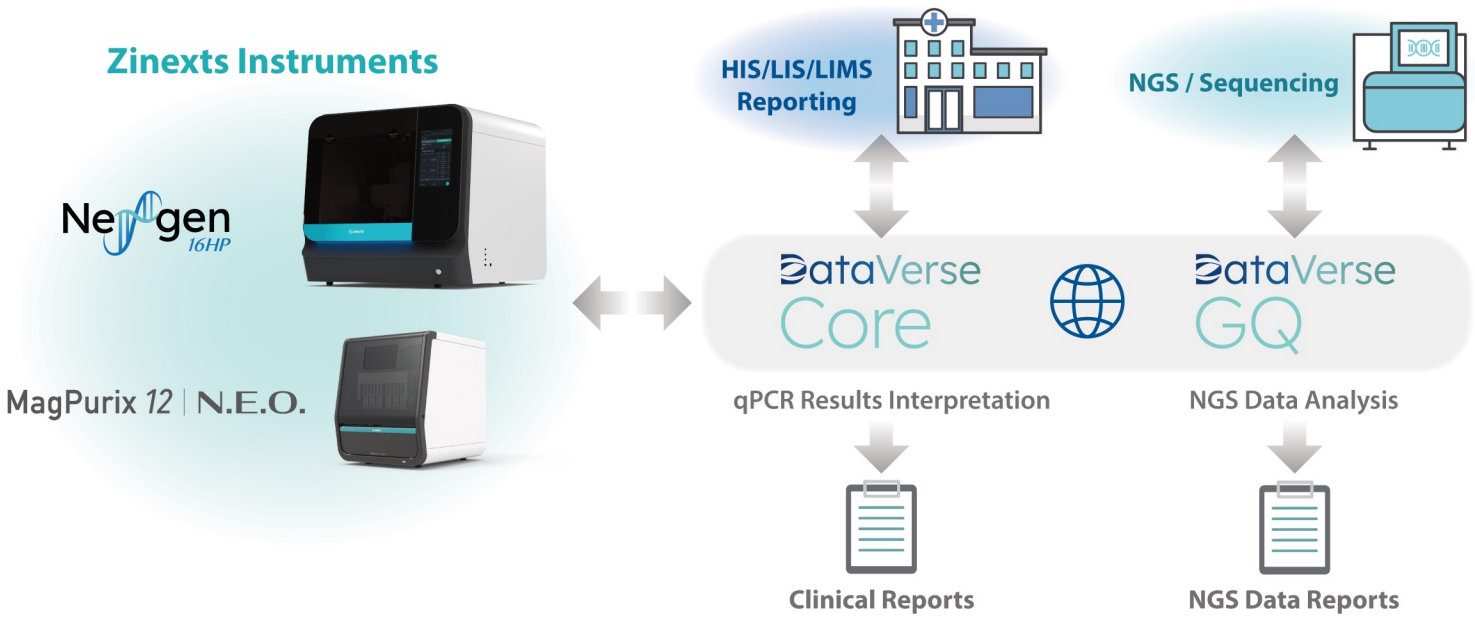


Smart Data Integration and Analysis

Zinexts DataVerse

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

Zinexts DataVerse™ Core

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

Zinexts DataVerse™ GQ

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

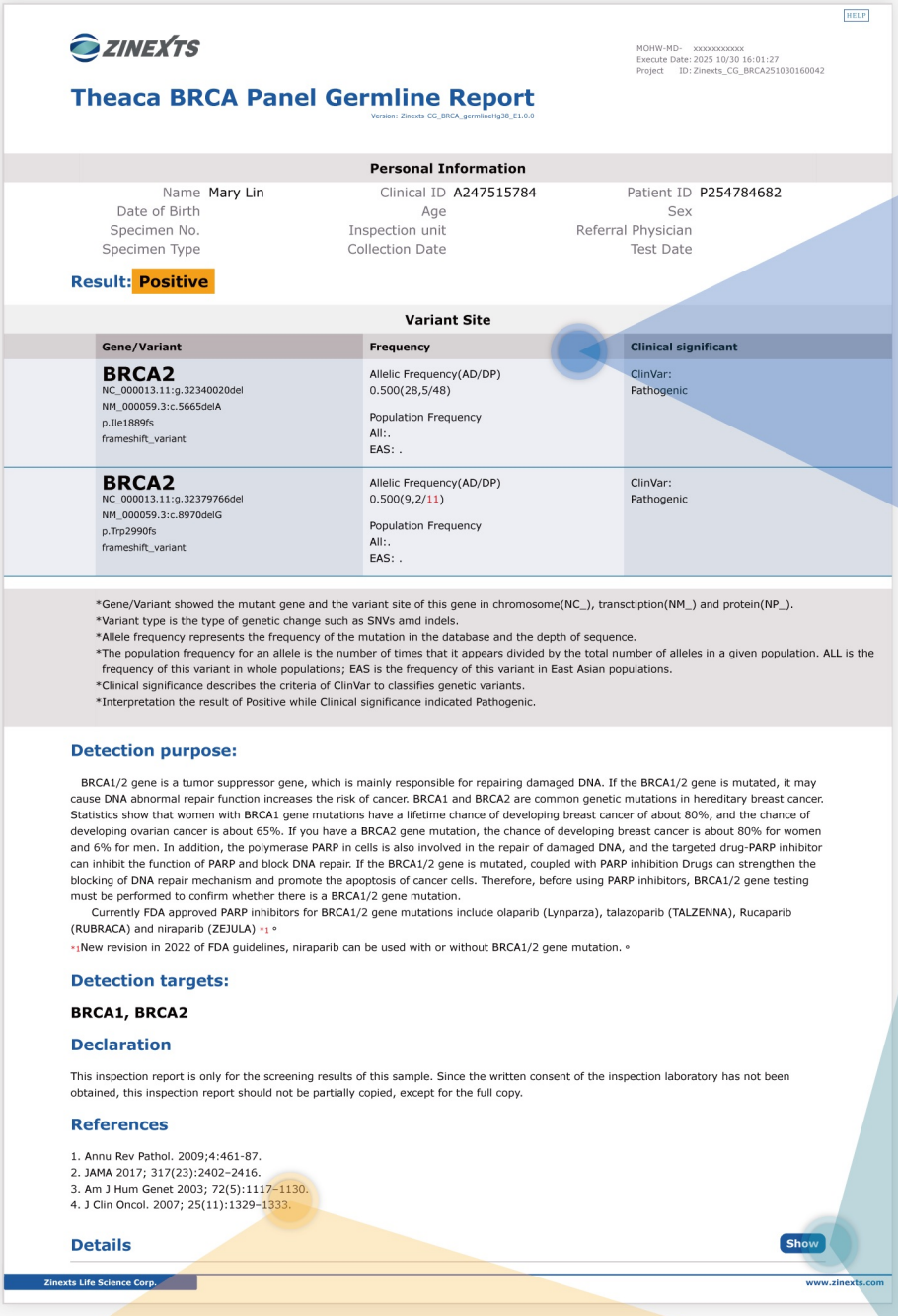
Customizable pipelines for WES/WGS/Targeted Panels on demand based on your laboratory needs

Applications

Cancer Panels	Microbiota	Genomic Research
Breast Cancer Genetic Test (BRCA)	Microbial Identification	Genome Sequencing
Pan-Cancer Panel	Probiotics Profiling	Transcriptome Sequencing
		Microbiome Sequencing

Clear Data Report, Clear Clinical Support

BRCA Panel Germline Report



ZINEXTS

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

Theaca BRCA Panel Germline Report

Version: Zinexts-CG_BRCA_germlineHg38_E1.0.0

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.32340020del NM_000059.3:c.5665delA p.Ile1889fs frameshift_variant	Allelic Frequency(AD/DP) 0.500(28,5/48) Population Frequency All:. EAS: .	ClinVar: Pathogenic
BRCA2 NC_000013.11:g.32379766del 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_), transctiption(NM_) and protein(NP_).
*Variant type is the type of genetic change such as SNVs amd 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 classifies 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 ◦

*1New 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

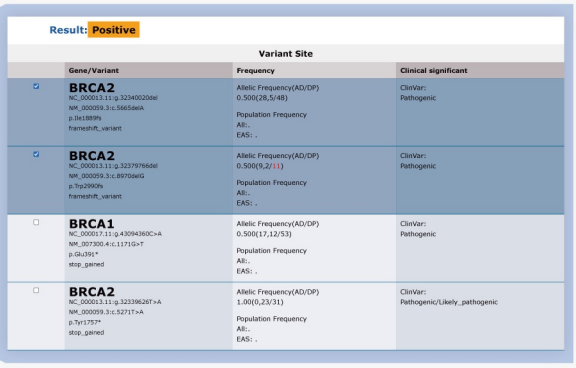
1. Annu Rev Pathol. 2009;4:461-87.
2. JAMA 2017; 317(23):2402-2416.
3. Am J Hum Genet 2003; 72(5):1117–1130.
4. J Clin Oncol. 2007; 25(11):1329–1333.

Details Show

Zinexts Life Science Corp. www.zinexts.com

Provides the scientific literature to support decision making

Full Customization Reports



Result: Positive

Variant Site

	Gene/Variant	Frequency	Clinical significant
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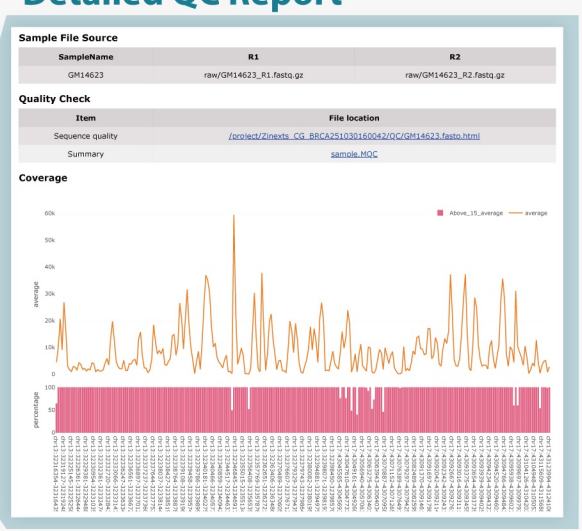
☑	**BRCA2** NC_000013.11:g.32379766del NM_000059.3:c.8970delG p.Trp2990fs frameshift_variant	Allelic Frequency(AD/DP) 0.500(9,2/11) Population Frequency All:. EAS: .	ClinVar: Pathogenic
☐	**BRCA1** NC_000017.11:g.43094360C>A NM_007300.4:c.1171G>T p.GlU391* stop_gained	Allelic Frequency(AD/DP) 0.500(17,12/53) Population Frequency All:. EAS: .	ClinVar: Pathogenic
☐	**BRCA2** NC_000013.11:g.32339626T>A NM_000059.3:c.5271T>A p.Tyr1757* stop_gained	Allelic Frequency(AD/DP) 1.00(0,23/31) Population Frequency All:. EAS: .	ClinVar: Pathogenic/Likely_pathogenic

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



Sample File Source

SampleName	R1	R2
GM14623	raw/GM14623_R1.fastq.gz	raw/GM14623_R2.fastq.gz

Quality Check

Item	File location
Sequence quality	/project/Zinexts_CG_BRCA251030160042/QC/GM14623.fastq.html
Summary	sample.MQC

Coverage

Check the sequencing data quality

Let's unify your patient data and diagnostics workflows

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ZFL-DataVerse-1125-V1