Accession ID:	**XXXXXXX**
Sample Type:	**Blood**
Patient's Name:	**XXXXXXX**
Gender/Age	**XXXXXXX**

CliSeq HRD Homologous Recombination Deficiency

Data Uploaded On:	**XXXXXXX**	**Report Generated On:**	**XXXXXXX**

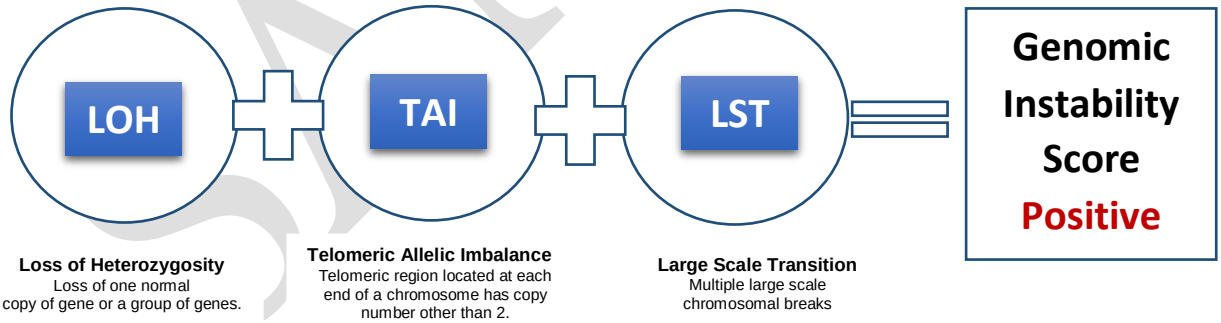
Cancer Type:-

High-grade serous ovarian cancer

SUMMARY			
HRD	**Positive**	**Genomic Instability**	**Positive**
		Mutation	**NA**

TEST RESULT			
Genomic Instability Status			**Genomic Instability Score**
LOH	**TAI**	**LST**	**55**
17	**25**	**13**	

sss



INTERPRETATION
Analysis of 3 types of genomic scars caused by Homologous Recombination Deficiency in the patient showed Positive genomic instability status. The 3 types of genomic scars are Loss of heterozygosity (LOH), Telomeric allelic imbalance (TAI), and Large scale transition (LST). If the combined score of each index exceeds score of 42, the genomic instability Status is classified as positive.

This report is automatically generated by CliSeq Interpreter

HOMOLOGOUS RECOMBINATION DEFICIENCY (HRD)

There are various DNA repairs pathways, HRR or Homologous Recombination Repair being one of them. It is a fundamental cellular process that repairs double-strand breaks (DSBs) in DNA. This repair process ensures that the genetic information is restored correctly, thus maintaining genomic stability and preventing mutations that could lead to diseases like cancer. There are certain genes that are responsible for HRR which if mutated, can lead to a dysfunction in the HRR process leading to chromosomal structural changes across the cells. The accumulation of these variants are also known as genomic instabilities. These biomarkers (LOH (Loss of heterozygosity), TOI (Telomeric imbalances), LSTs (Large scale transitions)), can be measured and used to evaluate the HRD Status and Genomic scar score (GSS).

METHODOLOGY

The Genes2Me CancerCore NGS panel enriches non-exonic, single-nucleotide polymorphism (SNP)-based on targeted next generation sequencing. This targets more than 50,000 SNPs enriched across whole genome making it capable of detecting the genomic instabilities and calculate the Genomic Scar Score biomarkers. These biomarkers (LOH (Loss of heterozygosity), TOI (Telomeric imbalances), LSTs (Large scale transitions), can be measured and used to evaluate the HRD Status and Genomic scar score (GSS). This panel helps in maximizing diagnostics insights for clinicians to guide for PARP inhibitors or platinum drugs used in the treatment of various cancers.

After raw data generation, we follow the BWA and GATK best practices framework for generation of alignment. Further, ScarHD program is used to calculate Genomic Scar Score biomarkers such as (LOH (Loss of heterozygosity), TOI (Telomeric imbalances), LSTs (Large scale transitions) and can be measured and used to evaluate the HRD Status

RECOMMENDATIONS

- Genetic counseling is advised for interpretation on the consequences of the results.
- If results obtained do not match the clinical findings, additional testing should be considered as per referring clinician's recommendation.
- Data revaluation performed upon the up gradation of databases used and results may vary in accordance.

LIMITATIONS

- Genetic testing is an important part of the diagnostic process however it may not always give a definitive answer. Accurate interpretation of test results is dependent on the availability of biological & medical information (clinical history) of the family, failing to this may leads to incorrect result interpretation and diagnosis.
- Test results are interpreted in the context of clinical findings, available scientific evidences, family history and other laboratory data.
- Genetic testing is highly accurate but rarely inaccurate results may occur for various reasons like mislabelling of samples, inaccurate clinical/medical family history ,tumour purity, rare technical errors or unusual circumstances such as bone marrow transplantation,

DISCLAIMER

- As of the inherent technological limitations of the sequencing assay, some of the regions can't be properly sequenced, so, variations in these regions may not be identified & interpreted.
- Genes2Me clarify that the generated report(s) doesn't provide any kind of diagnosis or opinion or recommendation for any disease and its cure in any manner. It is therefore recommended that the patient and/or the guardian(s) of the patient must take the consultation of the clinician or a certified physician or doctor for further course of action.
- If the provided material quality and/or quantity not up to the desired level, further procedures will be completed only after getting confirmation from referring clinician/physician only, so, in that case, test(s) result(s) may be misleading or even wrong, therefore, Genes2Me hereby disclaims all liability arising in this connection with the test(s) and report(s).
- The analysis pipeline is developed in-house and the performance characteristics of this analysis are determined by Genes2Me only.
- This test result should be used as a reference by the healthcare provider for diagnosis and development of treatment plan.
- The clinically significant mutations enlisted in this report are provided as a professional service, and are not reviewed or approved by the FDA.

REFERENCES

- Telli ML, Timms KM, Reid J, et al. Homologous Recombination Deficiency (HRD) Score Predicts Response to Platinum-Containing Neoadjuvant Chemotherapy in Patients with Triple-Negative Breast Cancer. Clin Cancer Res. 2016 Aug 1;22(15):3764-73. PMID: 26957554.
- Stewart MD, Merino Vega D, Arend RC, et. Homologous Recombination Deficiency: Concepts, Definitions, and Assays. Oncologist. 2022 Mar 11;27(3):167-174. PMID: 35274707.
- Lotan, T.L., Kaur, H.B., Salles, D.C. et al. Homologous recombination deficiency (HRD) score in germline BRCA2- versus ATM-altered prostate cancer. Mod Pathol 34, 1185–1193 (2021).
- Wen, H., Feng, Z., Ma, Y. et al. Homologous recombination deficiency in diverse cancer types and its correlation with platinum chemotherapy efficiency in ovarian cancer. BMC Cancer 22, 550 (2022).
- Andrews S, FastQC: A Quality Control Tool for High Throughput Sequence Data, 2010, (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). 4.
- Bolger AM et al., Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics (Oxford, England) (2014) Vol. 30,15: 2114-20. 5.
- Li H. et al., Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics (2010), 26(5):589-95. 6.
- Quinlan AR et al., BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics (Oxford, England) (2010) Vol. 26,6: 841-2.
- McKenna A et al., The Genome Analysis Toolkit: a MapReduce framework for analyzing next- generation DNA sequencing data. Genome research (2010) Vol. 20,9: 1297-303. 8.
- Clarke L et al. The international Genome sample resource (IGSR): A worldwide collection of genome variation incorporating the 1000 Genomes Project data. Nucleic acids research (2017) Vol. 45,D1: D854-D859. 10.
- McKusick VA, Mendelian Inheritance in Man. A Catalog of Human Genes and Genetic Disorders. Baltimore: Johns Hopkins University Press (12th edition), 1998. 14.
- Köhler S et al., The Human Phenotype Ontology in 2021. Nucleic acids research (2021) Vol. 49,D1: D1207-D1217. 15.

***This is an electronically generated report, hence doesn't require any signature.**

***For any further technical queries please contact at contact@genes2me.com**