Accession ID:	**XXXX**
Sample Type:	Blood
Patient's Name:	**XXXXX**
Gender/Age:	Male/24 Years

CliSeq

LYMPHOMA NGS PANEL

Data Uploaded On:	XXXXXX	**Report Generated On:**	XXXXXX

CANCER TYPE:

Lymphoma

RESULTS:

List of clinically significant mutations (CSM)

Variants of potential clinical significance:

GENE	VAF	FDA Approved Drugs	
		Responsive	Resistance
TP53 (p.Arg248Gln)	80.39%		

Technical Information:

Variant	Depth	Genomic location	VAF
TP53(NM_000546.6);c.743G>A	Total: 204 Alt: 164	chr17:7674220	80.39
Gene summary: Tumor protein p53 (TP53), is a tumor suppressor and oncogene transcription factor involved in cell cycle arrest, DNA repair, and apoptosis, and is the most frequently mutated gene in cancer. TP53 somatic missense mutations are highly frequent in most cancer types. TP53 germline mutations are common in Li-Fraumeni syndrome, a cancer predisposition syndrome. TP53-NTRK1 fusion is observed in Spitz nevus and TP53-PPRAD, TP53-VAV1, TP53-EMR1, TP53-DDX39B, and TP53-SAT2 fusions are observed in osteosarcoma			

Therapeutic Summary:

Drug	Biomarker	Resistance/Responsive	Level	Clinical Indication

Fusion Details:

Alteration	Breakpoint	Location	Transcript
NPM1- ALK	NPM1 - Exon 5	Chr5:171391799	ENST00000517671.5
	ALK – Exon 20	Chr2:29223528	ENST00000389048.8

Diagnostic Implications per WHO		
Biomarker	**Diseases**	**Note**
NPM1- ALK	Lymphoma	NPM1-ALK fusion is primarily associated with certain types of leukemia, particularly acute myeloid leukemia (AML), but it can also occur in lymphomas, especially anaplastic large cell lymphoma (ALCL). In ALCL, the ALK gene is commonly rearranged, leading to an overexpression of the ALK protein, which can drive tumor growth. In cases involving the NPM1 gene, the fusion may have implications for the biology of the lymphoma and the patient's response to treatment. ALK-positive lymphomas can be aggressive, but they often respond well to targeted therapies, such as ALK inhibitors. PMID: 20207848, PMID: 37655119

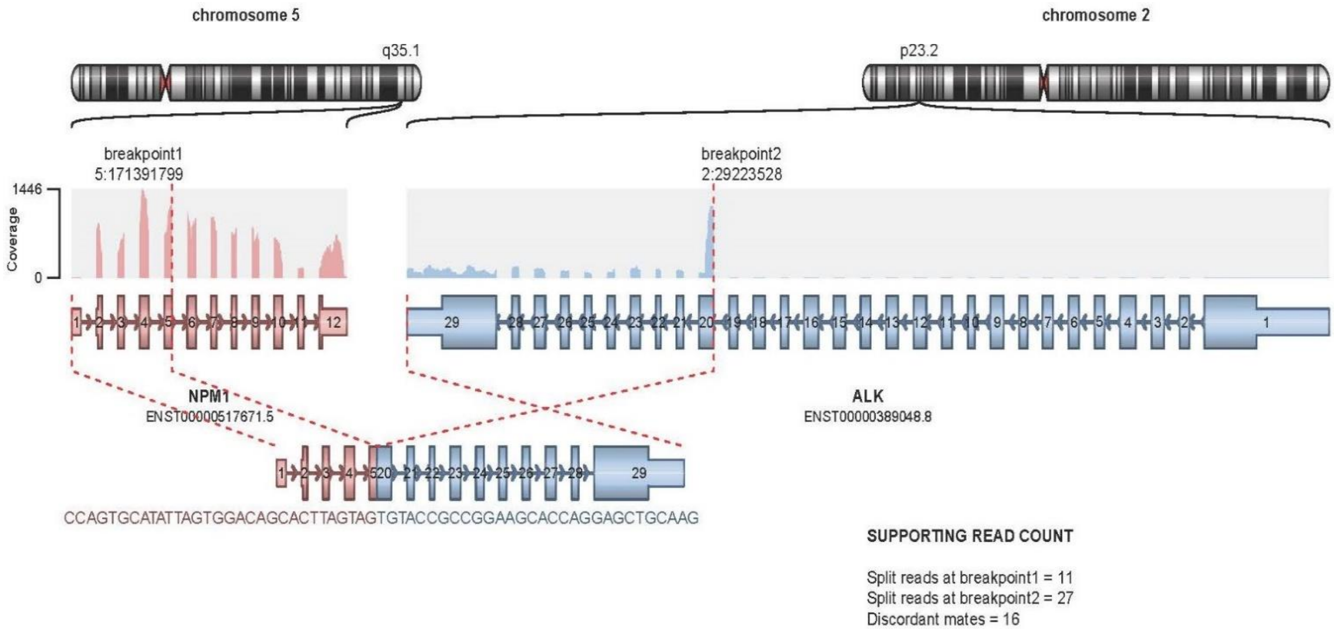

Fig :- Next-generation sequencing using a RNA targeted sequencing panel identified a NPM1::ALK fusion involving exons 1-5 in NPM1 and exons 20-29 in ALK genes respectively.

Recommendations

- Genetic counseling is advised for interpretation on the consequences of the variant(s).
- If results obtained do not match the clinical findings, additional testing should be considered as per referring clinician's recommendation.
- Genetic test results are reported based on the recommendations of Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists
- Sanger validation is recommended for the above listed variants.
- The significance/classification of the variant(s) may change based on genetic testing in the parents and other family members.
- Data revaluation performed upon the up gradation of databases used and results may vary in accordance.

AMP-ASCO-CAP CLASSIFICATION CRITERIA	Methodology
Four-tiered system to categorize somatic sequence variations based on their clinical significance **1. Tier I -** Variants of strong clinical significance. **2. Tier II -** Variants of potential clinical significance. **3. Tier III -** Variants of unknown clinical significance **4. Tier IV -** Benign or likely benign variants	The Genes2Me Lymphoma NGS panel was used for sequencing that screens for 75 clinically relevant genes (coding regions of the genome) for diseases associated with genetic mutations. It covers all major mutations like SNV, InDels & CNV adding up to a target size of 118Kb with a hybridization-based target capture technique. After raw data generation, we follow the GATK best practices framework for the identification of variants in the sample, starting with a raw data quality check using the FastQC followed by a BWA read aligner for mapping/aligning to human reference genome GRCh38. After the alignment, the GATK Mutect2 algorithm is used for variant calling. Annotation of the variants is performed using open-source available software SnpEff. Further, clinically relevant mutations are annotated using published variants in literature and a set of disease databases – ClinVar, OMIM, COSMIC, and HPO. The 1000Genome, gnomAD, and dbSNP databases are used for annotation of variants for their minor allele frequency. The dbNSFP database is used for annotation and functional prediction of all potential non-synonymous variants.

Limitations	Disclaimer
• Genetic testing is an important part of the diagnostic process however it may not always give a definitive answer. In some cases, a genetic variant may be missed due to the limitations in existing medical knowledge and testing technology. 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. The variation(s) which is/are potentially relevant – significant related to the patient's provided medical history is/are reported. • Genetic testing is highly accurate but rarely inaccurate results may occur for various reasons like mislabeling of samples, inaccurate clinical/medical family history, rare technical errors or unusual circumstances such as bone marrow transplantation, blood transfusion or the presence of change(s) in such a small percentage of cells that may not be detectable (mosaicism).	• The interpretation of variants in this report is performed to the best knowledge of the scientific & medical information available at the time of reporting. The classification of variants is based on AMP-ASCO-CAP guidelines. • As of the inherent technological limitations of the sequencing assay, some of the coding regions can't be properly sequenced, so, variations in these regions may not be identified & interpreted. It is possible that variants not identified by the assay may be associated with the provided phenotypes of the patient. • It is possible due to insufficient phenotypic information, a gene – variant may be present in data but not selected for analysis and interpretation. • The mutations have not been confirmed by Sanger sequencing. • 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.

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