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TATA MEMORIAL HOSPITAL
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DIAGNOSTIC SERVICES- Department of Pathology

MOLECULAR PATHOLOGY REPORT

Patient Name	Ms. SATVIKI PATIDAR	**Case No**	11E2025/003838
DMG/Category	DMG - NEURO ONCOLOGY F/ Out Patient	**Path No.**	021905/DA
Material	Paraffin Block	**Age / Gender**	7 Yrs / Female
Collection Dt	30/05/2025 00 / 13:58:52	**Mol Path No.**	2511S04650
Provisional / Final Report Dt :	15/07/2025 00:00:00/15/07/2025 00:00:0	**Req No.**	FZZMP25005896

Final Report
NGS based Targeted Panel for Solid Tumors

Test Methodology :

This assay is designed for evaluation of DNA variants and fusion transcripts using targeted gene panel SOPHiA Solid Tumor plus Solution which identifies single nucleotide variants (SNVs), indels from 55 genes, 139 RNA fusions, gene amplification events in 42 genes and MSI status. Extracted DNA and RNA are subjected to library preparation followed by paired end sequencing by synthesis technology on the Illumina Nextseq 2000 platform. Data analysis is performed using SOPHiA DDM software.

Histological Diagnosis :

left thalamopeduncular SOL: Infiltrating glial tumor (the overall features of diffusely infiltrating glioma, NOS).

Result :

No pathogenic / likely pathogenic were alteration detected in this sample.

Result Summary :

1. SNVs/DNA variants :

A. Analytical Summary :

Mean Depth of Coverage	3,236.00

B. SNVs Detected: Not Detected

C. Genes Showing Tier IV(Benign Alteration):

The assay has been standardized and validated at Molecular Pathology Laboratory, TMH. The data is analyzed using the annotation sources: dbSNP (Version 1), 1000 genomes (Version 1), ClinVar (Version 4), COSMIC (Version 3), EXAC (Version 1). The mutations are reported as per ACMG guidelines 2018 with Human Genome Variation Society (HGVS) Nomenclature.Genes with <500X coverage are not interpreted.

The results should be interpreted in the context of all available clinical and pathological information. The performance characteristics of this assay have been determined by Molecular Pathology Laboratory, TMH. This mutation panel is designed to detect targeted mutations which are in the scope of gene Panel. Mutations outside the designed amplicon regions will not be detected.

MS. MAMTA GURAV
Scientific Officer

Dr. EPARI SRIDHAR
Consultant Pathologist

"The report relates only to the sample submitted."

"The remaining sample, if any, will be retained for a period of 5 years."

"This Report has been electronically verified and authorized for release. "

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D. Genes with No Mutations:

AKT1	AKT2	AKT3	ALK	AR	ARAF	ARID1A	ARID5B	BRAF
BRCA1	BRCA2	CDKN2A	CDK4	CD274	CHEK2	CTCF	CTNNB1	DDR2
DICER1	EGFR	ERBB2	ERBB3	ERBB4	ESR1	FBXW7	FGFR1	FGFR2
FGFR3	FGFR4	FLT3	FOXL2	GNAQ	GNAS	GNA11	HIST1H3B	HRAS
H3F3A	H3F3B	IDH1	IDH2	KEAP1	KIT	KRAS	MAP2K1	MAP2K2
MET	MTOR	MYOD1	NF1	NRAS	NTRK1	NTRK2	NTRK3	PDGFRA
PIK3CA	PIK3R1	POLE	PPP2R1A	PTEN	PTPN11	RAC1	RAF1	RET
ROS1	RPL22	SF3B1	SMAD4	SMO	STK11	TERT	TP53	

2. Copy number variations (CNV) : None

3. Microsatellite Instability (MSI) Status : MSI-H not Detected

4. RNA Alertation/ Fusion :

A. Analytical Summary :

Total Passing Filter Reads	591,707.00

B. Fusion Detected : Not Detected

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