Genomic Alterations Identified:

- EGFR mutation p.A289T
- TERT mutation c.1-124>T
- EGFR amplification
- CDKN2A copy number LOSS

Marker Type	Marker Result	Transcript	Genomic Position	Amino Acid	Nucleotide	VAF/CNR	Class
Gene Mutations	EGFR	NM_005228.3	chr7:55221821G>A	p.A289T	c.865G>A	96.0%	Tier 1/2
	TERI	NM_198253.2	chr5:1295228G>A	p.C228T	c.I.124C>1	33.0%	Tier 1/2
Gene fusions	Negative						
Copy number alterations	EGFR			7p11.2	GAIN	24.3	
	CDKN2A			9p21.3	LOSS		

DISCUSSION

The 2016 update (4th edition) of the 2007 WHO classification of CNS tumors incorporated well established molecular parameters into the classification of gliomas that impacted the classification in several ways and provided a dynamic classification based upon both phenotype and genotype with emphasis on integrated diagnosis.(1) Glioblastomas were broadly classified into **GBM IDH-wildtype** including the special variants (Giant cell, epitheliod and gliosarcoma), **GBM-IDH mutant** and **GBM, NOS**. These were classified on the basis of IHC markers (ATRX, P53, IDH R132H) along with IDH mutational analysis. Additionally, MGMT methylation, EGFR amplification, TERT promoter mutational analysis were recommended in cases of IDH-wt GBM.

Soon after the 4th edition was published, in order to incorporate the rapid advances in molecular pathogenesis, a Consortium to inform molecular and practical approaches to CNS tumor taxonomy-not official WHO **(cIMPACT-NOW)** was established in 2016 that has been giving updates. With respect to GBM, cIMPACT-NOW update 3 recommended diagnostic criteria for **Diffuse astrocytic gliomas (Grade II/III), IDH-wt with molecular features of GBM**. (2) They reached a consensus regarding the minimal molecular criteria for identifying an IDH-wildtype diffuse astrocytic glioma that, despite appearing histologically as a WHO grade II or III neoplasm, would follow an aggressive clinical course more closely resembling that of an IDH wildtype glioblastoma: