

	GBM_{cw1919}	GBM₅₂₈	GBM₃₅₆₅
Grade	WHO - IV	WHO - IV	WHO - IV
Molecular Subtype (Verhaak, 2010)	Proneural	Proneural	Mesenchymal
IDH1/2 status	WT	WT	WT
G-CIMP Status	Non G-CIMP	N/A	Non G-CIMP
Mutation Status			
RB1	Homozygous Null	Homozygous Mutation	Homozygous Null
TP53	Homozygous Null	Heterozygous Null	WT
EGFR	WT	WT	Homozygous Null
GABRA6	WT	WT	Heterozygous Null
CIC	WT	WT	Heterozygous Mutation
PIK3R1	WT	WT	WT
PIK3CA	WT	WT	WT
PTEN	WT	WT	WT
IDH1	WT	WT	WT
BRAF	WT	WT	WT
NF1	WT	WT	WT
SPTA1	WT	WT	WT
KEL	WT	WT	WT
CDH18	WT	WT	WT
SEMA3C	WT	WT	WT
PDGFRA	WT	WT	WT
ATRX	WT	WT	WT
COL1A2	WT	WT	WT
LZTR1	WT	WT	WT
ABCC9	WT	WT	WT
NLRP5	WT	WT	WT
DRD5	WT	WT	WT
TCHH	WT	WT	WT
FUBP1	WT	WT	WT
SCN9A	WT	WT	WT
IDH2	WT	WT	WT
JMJD6	WT	WT	WT
Copy Number Variants			
EGFR	Amplified	WT	WT
MYC	WT	Amplified	Amplified
MDM4	WT	WT	Amplified
PDGFRA	WT	WT	WT
TP53	Heterozygous Loss	N/A	WT
PTEN	Heterozygous Loss	N/A	Heterozygous Loss
MGMT	WT	N/A	Heterozygous Loss
CCND1	WT	N/A	Heterozygous Loss
CCND2	Heterozygous Loss	N/A	WT

RB1	WT	N/A	Heterozygous Loss
C19MC	Heterozygous Loss	N/A	Homozygous Loss
CDKN2A	WT	N/A	WT
CDK4	WT	N/A	WT

Legend	
Missense	
Nonsense	
In-frame indel	
Frameshift indel	
Splice variant	

Individual Gene Mutation Information

GBM528

Gene: RB1, Zygosity: homozygous, Consequence: SPLICE_REGION_VARIANT, CADD: 10.68, VVP: 95.0, Omicia: 0.42

Gene: TP53, Zygosity: heterozygous, Consequence: MISSENSE_VARIANT, CADD: 23.6, VVP: 95.0, Omicia: 0.947

Gene: TP53, Zygosity: heterozygous, Consequence: MISSENSE_VARIANT, CADD: 22.1, VVP: 80.0, Omicia: 0.848

GBM3565

Gene: EGFR, Zygosity: homozygous, Consequence: MISSENSE_VARIANT, CADD: 17.86, VVP: 54.0, Omicia: 0.768

Gene: RB1, Zygosity: homozygous, Consequence: FRAMESHIFT_VARIANT, CADD: 0, VVP: 96.0, Omicia: 0.8

Gene: RB1, Zygosity: homozygous, Consequence: MISSENSE_VARIANT, CADD: 18.44, VVP: 86.0, Omicia: 0.778

Gene: GABRA6, Zygosity: heterozygous, Consequence: MISSENSE_VARIANT, CADD: 6.422, VVP: 76.0, Omicia: 0.365

Gene: EGFR, Zygosity: heterozygous, Consequence: MISSENSE_VARIANT, CADD: 14.82, VVP: 25.0, Omicia: 0.599

Gene: CIC, Zygosity: heterozygous, Consequence: SPLICE_REGION_VARIANT, CADD: 7.752, VVP: 48.0, Omicia: 0.434

GBMcw1919

Gene: RB1, Zygosity: homozygous, Consequence: STOP_GAINED, CADD: 38.0, VVP: 100.0, Omicia: 0.645

Gene: TP53, Zygosity: homozygous, Consequence: INFRAME_DELETION, CADD: 0, VVP: 90.0, Omicia: 0.5