

**Supplementary Table S1** Table showing the detailed analysis of genetic alterations in GBM

<i>S. No.</i>	<i>Gene Name</i>	<i>Types of Genetic Alterations (%)</i>	<i>Post Translational Modifications (PTMs)</i>	<i>Mutation Type</i>	<i>Mutation Site</i>	<i>Copy Number Alteration</i>
1	ASPM	Mutation (2%) Amplification (6.29%) Deep Deletion (0.29%)	Phosphorylation Phosphorylation Phosphorylation	Splice Nonsense Nonsense	L642= R3152* R3244*	Diploid Diploid Diploid
			Phosphorylation, Acetylation, Ubiquitination Methylation NA NA	Nonsense  Missense Missense	E2012*  R854H E918K	Diploid  Diploid Diploid
			Phosphorylation, Acetylation, Ubiquitination NA	Missense	S270P	Gain
			Phosphorylation, Acetylation, Ubiquitination Methylation	Missense Missense	A3137D T2339P	Diploid
			Phosphorylation, Acetylation, Ubiquitination Methylation	Missense	R2442Q	Diploid
			Phosphorylation	Missense	A3013V	Diploid
			Phosphorylation, Acetylation, Ubiquitination Methylation	Missense	K2586Q	Diploid
			Phosphorylation, Acetylation, Ubiquitination Methylation	Missense	A2152T	Diploid
			Phosphorylation, Acetylation, Ubiquitination Methylation	Missense	D876N	Diploid
			NA NA NA	Missense Missense Missense	L817F K2081I K884M	Diploid Diploid Diploid
2	AURKA	Mutation (0.57%) Amplification	Phosphorylation Phosphorylation, Acetylation	Missense Missense	G11R R56H	Diploid Diploid

		(1.43%)	Phosphorylation	Missense	E336D	Diploid
3	BUB1	Mutation (0.57%) Deep Deletion (0.57%)	Phosphorylation NA Phosphorylation, Ubiquitination NA Phosphorylation	Missense Splice Missense  Missense Missense	C698Y X1021_splice G533E  F818C T452M	Diploid Shallow Deletion Shallow Deletion  Shallow Deletion Shallow Deletion
4	BUB1B	Mutation (0.29%) Deep Deletion (0.57%)	NA	Splice	X950_splice	Diploid
5	CCNA2	Mutation (0.29%) Structural variant (1.43%)	Phosphorylation, Acetylation, Ubiquitination  NA	Missense  Nonsense	A25V  E269*	Gain  Gain
6	CCNB2	Amplification (0.57%)	Phosphorylation	Missense	P80S	Shallow Deletion
7	KIF2C	Amplification (0.29%)	Phosphorylation Acetylation Phosphorylation, Ubiquitination, Methylation	Missense Missense Missense	A648T E684K Q508H	Diploid Diploid Gain
8	MELK	Mutation (1.43%)	Phosphorylation	Missense	A315S	Diploid
9	NCAPG	Mutation (0.86%) Amplification (0.29%)	Phosphorylation, Ubiquitination  Phosphorylation Phosphorylation  NA Phosphorylation	Missense  Nonsense  Splice  Missense Missense	A113S  A364L X373_splice  L444V S467*	Gain  Diploid Diploid  Shallow Deletion Diploid
10	NCAPH	Mutation (0.29%) Amplification (0.29%)	NA	Missense	Q704K	Diploid

11	NUF2	Mutation (0.79%) Amplification (	Phosphorylation, Ubiquitination	Missense	S247Y	Diploid
			Ubiquitination Phosphorylation	Missense Missense	Q290H D435N	Diploid Diploid
12	PBK	Mutation (0.26%)	Phosphorylation	Missense	Q291K	Diploid
13	TOP2A	Mutation (0.79%) Deep Deletion (0.26%)	Phosphorylation, Acetylation, Sumoylation	Missense	T38A	Diploid
			Phosphorylation, Acetylation, Sumoylation	Missense	S53Y	Diploid
			Acetylation, Ubiquitination, Sumoylation	Missense	V1076F	Diploid
			Phosphorylation, Acetylation, Methylation, Sumoylation	Missense	S1483L	Diploid
			Phosphorylation, Acetylation, Sumoylation	Missense	K1492N	Diploid

**Supplementary Table S2** Table showing the detailed analysis of genetic alterations in HCC

<i>S. No.</i>	<i>Gene Name</i>	<i>Types of Genetic Alterations (%)</i>	<i>Post Translational Modifications (PTMs)</i>	<i>Mutation Type</i>	<i>Mutation Site</i>	<i>Copy Number Alteration</i>
1	ASPM	Mutation (2%) Amplification (6.29%) Deep Deletion (0.29%)	Phosphorylation Phosphorylation Phosphorylation NA NA Acetylation NA NA	Missense Missense Missense Missense Missense Missense Missense FS ins	T111A K610E F645L R792W I1051T Y2007S G2156R Q2620Tfs*17	Diploid Gain Diploid Diploid Gain Gain Shallow Deletion Gain
2	AURKA	Mutation (0.57%) Amplification (1.43%)	Phosphorylation Phosphorylation	Missense Missense	S83N R180K	Diploid Diploid
3	BUB1	Mutation (0.57%) Deep Deletion	NA NA	Missense Missense	T805I S950R	Diploid Diploid

		(0.57%)				
4	BUB1B	Mutation (0.29%) Deep Deletion (0.57%)	NA	Missense	Q460L	Diploid
5	CCNA2	Mutation (0.29%) Structural variant (1.43%)	NA	Missense	N129K	Diploid
6	CCNB2	Amplification (0.57%)	NA	No mutation		
7	KIF2C	Amplification (0.29%)	NA	No mutation		
8	MELK	Mutation (1.43%)	NA Phosphorylation NA NA	Missense Missense Missense Missense	R53L I237S/V V287I Y638Sfs*4	Diploid Diploid Diploid Diploid
9	NCAPG	Mutation (0.86%) Amplification (0.29%)	NA NA Phosphorylation, Ubiquitination	Missense Nonsense Missense	L96F S574* Y850H	Diploid Diploid Diploid
10	NCAPH	Mutation (0.29%) Amplification (0.29%)	NA	Missense	T264A	Diploid
11	NUF2	Mutation (0.86%) Amplification (9.71%)	NA NA NA	Missense Missense Missense	E13D G385D Y445C	Gain Gain Gain
12	PBK	Mutation (0.29%) Deep Deletion (5.71%)	NA	Missense	E303V	Diploid
13	TOP2A	Mutation (1.14%) Amplification (0.57%)  Deep Deletion (0.29%)	Phosphorylation NA NA  NA	Nonsense Missense Missense  Missense	R450* T689N R877W  T1315K	Diploid Gain Diploid  Diploid