

S3 Table. Mutation results of clinical next-generation sequencing glioma panel

Pati ents	Chr	Pos	Ref	Alt	Gene	Refseq	Exon	Effect	AA	CDS	Rea d	Alt	Ref	VAF (%)	
DM G1	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co ding	p.Lys28Me t	c.83A>T	1039	97	942	9.3	
		2135				07.4									
	chr9	21971	GC	G	<i>CDKN2A</i>	NM_0011	2	Frame_shift	p.Asn71fs	c.211_215delA ACTG	668	152	516	22.8	
		142	AG			95132.1									
			TT												
	chr1	75771	G	A	<i>TP53</i>	NM_0011	8	Non_synonymous_co ding	p.Arg273C ys	c.817C>T	996	61	935	6.1	
	7	21				26112.2									
DM G14	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co ding	p.Lys28Me t	c.83A>T	1786	766	1020	42.8	
		2135				07.4								9	
	chr3	17891	C	A	<i>PIK3C</i>	NM_0062	2	Non_synonymous_co ding	p.Arg38Ser	c.112C>A	1428	826	602	57.8	
		6725			<i>A</i>	18.2									4
	chr3	17893	G	A	<i>PIK3C</i>	NM_0062	10	Non_synonymous_co ding	p.Glu545L ys	c.1633G>A	1592	115	1477	7.22	
	6091			<i>A</i>	18.2										
	chr8	38272	T	C	<i>FGFR1</i>	NM_0011	15	Non_synonymous_co ding	p.Lys687Gl u	c.2059A>G	988	823	165	83.3	
	308				74067.1										
DM G19	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co ding	p.Lys28Me t	c.83A>T	1829	743	1086	40.6	
		2135				07.4								2	
	chr1	75784	C	T	<i>TP53</i>	NM_0005	5	Non_synonymous_co	p.Val173M	c.517G>A	1021	736	285	72.0	

	7	13						46.5	ding	et					9
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2		Non_synonymous_co	p.Lys28Me	c.83A>T	3306	1026	2280	31.0
G23		2135						07.4	ding	t					3
	chr3	17895	A	G	<i>PIK3C</i>	NM_0062	21		Non_synonymous_co	p.His1047	c.3140A>G	5055	1372	3683	27.1
		2085			<i>A</i>			18.2	ding	Arg					4
	chr1	25398	C	G	<i>KRAS</i>	NM_0333	2		Non_synonymous_co	p.Gly12Ala	c.35G>C	4005	963	3042	24.0
	2	284						60.3	ding						4
	chr1	75770	G	A	<i>TP53</i>	NM_0005	8		Stop_gained	p.Arg306*	c.916C>T	2921	1139	1782	38.9
	7	22						46.5							9
	chrX	13542	G	GA	<i>ADGR</i>	NM_1538	6		Frame_shift	p.Thr343fs	c.1027dupA	4452	1003	3449	22.5
		6885			<i>G4</i>			34.3							3
	chrX	13543	C	T	<i>ADGR</i>	NM_1538	6		Non_synonymous_co	p.Ser2125P	c.6374C>T	5567	2646	2921	47.5
		2239			<i>G4</i>			34.3	ding	he					3
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2		Non_synonymous_co	p.Lys28Me	c.83A>T	1641	501	1140	30.5
G25		2135						07.4	ding	t					3
	chr1	49444	G	A	<i>KMT2</i>	NM_0034	11		Non_synonymous_co	p.Pro1002S	c.3004C>T	203	81	122	39.9
	2	367			<i>D</i>			82.3	ding	er					
	chr1	32913	T	A	<i>BRCA2</i>	NM_0000	11		Non_synonymous_co	p.Asp1618	c.4854T>A	989	556	433	56.2
	3	346						59.3	ding	Glu					2
	chr1	75784	C	T	<i>TP53</i>	NM_0011	5		Non_synonymous_co	p.Arg175H	c.524G>A	609	440	169	72.2
	7	06						26112.2	ding	is					5

DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	4619	2809	1810	60.8
G27		2135						ding	t					1
	chr1	75775	C	A	<i>TP53</i>	NM_0005	7	Non_synonymous_co	p.Cys242P	c.725G>T	1468	595	873	40.5
	7	56						ding	he					3
	chr1	75785	C	A	<i>TP53</i>	NM_0005	5	Non_synonymous_co	p.Cys135P	c.404G>T	1044	500	544	47.8
	7	26						ding	he					9
	chr1	15290	C	T	<i>NOTC</i>	NM_0004	20	Non_synonymous_co	p.Arg1076	c.3227G>A	1382	671	711	48.5
	9	983			<i>H3</i>			ding	His					5
	chrX	76855	T	TG	<i>ATRX</i>	NM_0004	24	Frame_shift	p.Met1920f	c.5757dupC	3026	1978	1048	65.3
		229							s					7
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	1396	325	1071	23.2
G28		2135						ding	t					8
	chr1	29553	A	AG	<i>NF1</i>	NM_0010	18	Frame_shift	p.Ser674fs	c.2015_2021dup	1857	748	1109	40.2
	7	461		CA						pGATGCAG				8
				GG										
				AT										
DM	chr6	26032	T	A	<i>HIST1</i>	NM_0035	1	Non_synonymous_co	p.Lys28Me	c.83A>T	636	278	358	43.7
G29		206			<i>H3B</i>			ding	t					1
	chr7	14045	A	T	<i>BRAF</i>	NM_0043	15	Non_synonymous_co	p.Val600Gl	c.1799T>A	2086	453	1633	21.7
		3136						ding	u					2
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	1458	563	895	38.6

G30		2135				07.4		ding	t					1
	chr8	38272	T	C	<i>FGFR1</i>	NM_0011	15	Non_synonymous_co	p.Lys687Gl	c.2059A>G	994	371	623	37.3
		308				74067.1		ding	u					2
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	1898	1130	768	59.5
G31		2135				07.4		ding	t					4
	chr1	75771	G	A	<i>TP53</i>	NM_0011	8	Non_synonymous_co	p.Arg273C	c.817C>T	1083	951	132	87.8
	7	21				26112.2		ding	ys					1
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	3140	1551	1589	49.3
G32		2135				07.4		ding	t					9
	chr1	49445	A	T	<i>KMT2</i>	NM_0034	10	Stop_gained	p.Leu561*	c.1682T>A	503	52	451	10.3
	2	784			<i>D</i>	82.3								4
	chr1	75775	C	T	<i>TP53</i>	NM_0005	7	Non_synonymous_co	p.Arg248G	c.743G>A	929	752	177	80.9
	7	38				46.5		ding	ln					5
	chrX	76939	G	A	<i>ATRX</i>	NM_0004	9	Stop_gained	p.Arg444*	c.1330C>T	946	725	221	76.6
		418				89.4								4
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	2780	1111	1669	39.9
G33		2135				07.4		ding	t					6
	chr1	75784	C	T	<i>TP53</i>	NM_0005	5	Non_synonymous_co	p.Arg175H	c.524G>A	1100	767	333	69.7
	7	06				46.5		ding	is					3
DM	chr1	65313	C	A	<i>JAK1</i>	NM_0022	13	Non_synonymous_co	p.Arg629M	c.1886G>T	758	39	719	5.15
G34		228				27.2		ding	et					

chr1	78434	C	A	<i>FUBP1</i>	NM_0013	3	Non_synonymous_co	p.Glu84As	c.252G>T	1293	65	1228	5.03
	728				03433.1		ding	p					
chr1	22625	G	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Gly35Val	c.104G>T	2621	84	2537	3.2
	2156				07.4		ding						
chr2	16086	C	A	<i>MYCN</i>	NM_0012	3	Non_synonymous_co	p.Leu433Il	c.1297C>A	1665	86	1579	5.17
	121				93228.1		ding	e					
chr2	29451	C	A	<i>ALK</i>	NM_0043	16	Non_synonymous_co	p.Gly927Tr	c.2779G>T	405	33	372	8.15
	786				04.4		ding	p					
chr2	29451	C	A	<i>ALK</i>	NM_0043	16	Non_synonymous_co	p.Gly926V	c.2777G>T	415	24	391	5.78
	788				04.4		ding	al					
chr2	29451	C	A	<i>ALK</i>	NM_0043	16	Non_synonymous_co	p.Gly914Tr	c.2740G>T	641	34	607	5.3
	825				04.4		ding	p					
chr2	29451	C	A	<i>ALK</i>	NM_0043	16	Non_synonymous_co	p.Trp913C	c.2739G>T	646	40	606	6.19
	826				04.4		ding	ys					
chr2	15862	C	T	<i>ACVRI</i>	NM_0011	8	Non_synonymous_co	p.Gly328G	c.983G>A	1890	647	1243	34.2
	2516				05.4		ding	lu					3
chr2	22766	C	A	<i>IRSI</i>	NM_0055	1	Non_synonymous_co	p.Gly618V	c.1853G>T	555	29	526	5.23
	1602				44.2		ding	al					
chr3	41280	C	A	<i>CTNNB</i>	NM_0010	15	Non_synonymous_co	p.Pro733Hi	c.2198C>A	849	43	806	5.06
	685			<i>I</i>	98209.1		ding	s					
chr5	17652	G	T	<i>FGFR4</i>	NM_0020	18	Non_synonymous_co	p.Gly799V	c.2396G>T	860	45	815	5.23

	4664				11.4		ding	al						
chr7	55220	G	T	<i>EGFR</i>	NM_0052	6	Non_synonymous_co	p.Gly221Tr	c.661G>T	1363	59	1304	4.33	
	271				28.3		ding	p						
chr7	12885	C	A	<i>SMO</i>	NM_0056	11	Non_synonymous_co	p.Pro641T	c.1921C>A	386	23	363	5.96	
	1596				31.4		ding	hr						
chr8	38287	C	A	<i>FGFR1</i>	NM_0011	4	Non_synonymous_co	p.Gly116V	c.347G>T	997	56	941	5.62	
	310				74067.1		ding	al						
chr8	12875	C	A	<i>MYC</i>	NM_0024	2	Non_synonymous_co	p.Pro74Thr	c.220C>A	1405	72	1333	5.12	
	0683				67.4		ding							
chr9	20397	AC	A	<i>SMARC</i>	NM_0012	4	Codon_change_plus_c	p.Gln235_	c.702_707delG	209	24	185	11.4	
	76	AG		<i>A2</i>	89396.1		odon_deletion	Gln236del	CAGCA				8	
		CA												
		G												
chr9	87570	G	T	<i>NTRK2</i>	NM_0061	19	Non_synonymous_co	p.Glu657A	c.1971G>T	579	32	547	5.53	
	231				80.4		ding	sp						
chr9	13940	G	T	<i>NOTC</i>	NM_0176	23	Non_synonymous_co	p.Arg1279	c.3835C>A	851	44	807	5.17	
	1234			<i>HI</i>	17.3		ding	Ser						
chr1	43600	C	A	<i>RET</i>	NM_0209	4	Non_synonymous_co	p.Pro273Hi	c.818C>A	317	21	296	6.62	
0	592				75.4		ding	s						
chr1	43606	G	T	<i>RET</i>	NM_0209	7	Non_synonymous_co	p.Gly453V	c.1358G>T	923	52	871	5.63	
0	749				75.4		ding	al						

chr1	43615	G	T	<i>RET</i>	NM_0209	15	Non_synonymous_co	p.Gly885Tr	c.2653G>T	559	31	528	5.55
0	574						ding	p					
chr1	43619	C	A	<i>RET</i>	NM_0209	17	Non_synonymous_co	p.Pro951Hi	c.2852C>A	676	35	641	5.18
0	169						ding	s					
chr1	49425	C	A	<i>KMT2</i>	NM_0034	39	Non_synonymous_co	p.Gly4187	c.12560G>T	874	50	824	5.72
2	928			<i>D</i>			ding	Val					
chr1	49427	C	A	<i>KMT2</i>	NM_0034	39	Non_synonymous_co	p.Gly3660	c.10979G>T	351	21	330	5.98
2	509			<i>D</i>			ding	Val					
chr1	57864	C	A	<i>GLII</i>	NM_0052	12	Non_synonymous_co	p.Pro765Hi	c.2294C>A	539	33	506	6.12
2	817						ding	s					
chr1	75784	G	T	<i>TP53</i>	NM_0011	5	Non_synonymous_co	p.Arg156S	c.466C>A	718	22	696	3.06
7	64						ding	er					
chr1	37884	C	A	<i>ERBB2</i>	NM_0044	27	Non_synonymous_co	p.Pro1209	c.3626C>A	1034	52	982	5.03
7	155						ding	His					
chr1	15290	C	A	<i>NOTC</i>	NM_0004	22	Non_synonymous_co	p.Gly1154	c.3461G>T	446	27	419	6.05
9	093			<i>H3</i>			ding+splice_site_regio	Val					
							n						
chr1	17953	C	A	<i>JAK3</i>	NM_0002	5	Non_synonymous_co	p.Gly148Tr	c.442G>T	595	30	565	5.04
9	960						ding	p					
chr1	42778	G	T	<i>CIC</i>	NM_0013	2	Non_synonymous_co	p.Arg801M	c.2402G>T	1179	68	1111	5.77
9	337						ding	et					

	chr1	42793	G	T	<i>CIC</i>	NM_0013	8	Non_synonymous_co	p.Gly1268	c.3803G>T	636	32	604	5.03
	9	184				04815.1		ding	Val					
	chr1	42797	G	T	<i>CIC</i>	NM_0013	16	Non_synonymous_co	p.Gly2107	c.6319G>T	498	30	468	6.02
	9	230				04815.1		ding	Trp					
	chrX	13543	G	T	<i>ADGR</i>	NM_1538	6	Non_synonymous_co	p.Gly2199	c.6596G>T	2044	103	1941	5.04
		2461			<i>G4</i>	34.3		ding	Val					
DM	chr1	22625	A	T	<i>H3F3A</i>	NM_0021	2	Non_synonymous_co	p.Lys28Me	c.83A>T	344	120	224	34.8
G31		2135				07.4		ding	t					8
(Pos	chr1	75771	G	A	<i>TP53</i>	NM_0005	8	Non_synonymous_co	p.Arg273C	c.817C>T	436	200	236	45.8
t)	7	21				46.5		ding	ys					7
	chr1	59247	A	G	<i>JUN</i>	NM_0022	1	Non_synonymous_co	p.Met260T	c.779T>C	1059	206	853	19.4
		964				28.3		ding	hr					5
	chr1	30133	G	A	<i>MAPK3</i>	NM_0027	2	Non_synonymous_co	p.Ser58Leu	c.173C>T	773	114	659	14.7
	6	325				46.2		ding+splice_site_regio						5

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