

Supplementary Table 1: Clinical information for 48 whole exome sequencing samples

Sample ID	Age	Gender	tumor location	Death	OS (months)	Recurrence	PFS (months)	GEP-Affy	SNP 2.5M Illumina
PGBM1	13	F	thalamic	YES	13	YES	5	NO	YES
PGBM2	5	M	left temporo-parietal	YES	6	YES	4	YES	YES
PGBM3	11	M	intraventricular (I-II)	YES	NA	YES	7	NO	YES
PGBM4	10	M	thalamic+lateral ventricular	YES	7	NA	NA	YES	YES
PGBM5	9	F	NA	YES	36	YES	18	NO	YES
PGBM6	11	M	thalamic	YES	5	NA	NA	YES	YES
PGBM8	6	F	NA	YES	12	YES	7	YES	NO
PGBM9	8	F	NA	YES	7	NO	7	YES	NO
PGBM10	11	M	NA	YES	32	YES	25	NO	NO
PGBM11	13	M	NA	YES	18	NO	18	YES	YES
PGBM12	14	M	left temporal lobe	NO	27	NO	27	NO	YES
PGBM13	14	M	occipital lobe	YES	8	NA	NA	NO	YES
PGBM14	15	M	right temporo-parietal	NO	17	NO	17	YES	YES
PGBM15	13	M	NA	YES	13	YES	9	YES	NO
PGBM16	20	F	parietal occipital	NA	NA	NA	NA	YES	NO
PGBM17	17	M	left frontal and axial	NA	NA	NA	NA	YES	NO
PGBM18	14	M	temporal lobe	NO	27	NO	27	NO	YES
PGBM19	20	M	NA	NA	NA	1	NA	NO	YES
PGBM20	11	M	NA	NA	NA	NA	NA	NO	YES
PGBM21	14	F	temporal lobe	YES	34	YES	22	NO	YES
PGBM22	NA	NA	NA	NA	NA	NA	NA	YES	NO
PGBM23	13	M	NA	NO	14	NA	NA	NO	YES
PGBM24	14	M	NA	YES	14	YES	5	YES	YES
PGBM25	12	M	temporal lobe	YES	17	YES	15	NO	YES
PGBM26	14	M	NA	YES	5	YES	5	YES	YES
PGBM27	9	F	NA	YES	10	YES	9	YES	YES
PGBM28	14	M	left temporo-parietal	NA	NA	NA	NA	NO	NO
PGBM29	15	M	NA	NA	NA	NA	NA	YES	NO
PGBM30	6	M	thalamic	NA	NA	NA	NA	YES	NO
PGBM31	7	F	NA	YES	12	YES	8	NO	YES
PGBM32	4	M	NA	YES	11	YES	10	NO	YES
PGBM33	12	M	NA	NO	8	NA	NA	NO	NO
PGBM34	12	F	NA	YES	8	NA	NA	NO	YES
PGBM35	7.3	M	parietal lobe	YES	NA	YES	7	YES	YES
PGBM36	7	M	NA	YES	25	YES	15	NO	YES
PGBM37	7	M	left cerebellar	NA	NA	NA	NA	YES	YES
PGBM38	11	M	NA	YES	NA	YES	7	NO	NO
PGBM39	12	F	parietal lobe	NO	24	NA	NA	YES	YES
PGBM40	14	F	thalamic	NO	16	NA	NA	YES	YES
PGBM41	7	F	left thalamic	YES	10	YES	9	YES	YES
PGBM42	2	F	NA	YES	8	YES	4	YES	YES
PGBM43	16	F	NA	YES	12	YES	8	YES	YES
PGBM44	6	F	NA	YES	37	YES	23	NO	NO
PGBM45	9	M	right frontal	YES	12	YES	10	YES	YES
PGBM46	14	M	NA	NO	55	NO	55	YES	NO
PGBM47	14	F	NA	YES	14	YES	12	YES	NO
PGBM48	2	M	NA	NO	117	NO	117	NO	NO
PGBM49	5.4	M	frontal lobe	NA	NA	NA	NA	YES	NO

Supplementary Table 2: Summary of sequence analysis of pediatric GBMs

† Using CCDS version 2011/04/22

Sample	Bases sequenced (after quality filtering)	Median # of reads per base in CCDS†	Median # of reads per	
			base in CCDS after duplicate removal†	CCDS bases with at least 10 reads (%)
PGBM1	13,505,091,987	94	85	92.4
PGBM2	17,119,601,726	109	70	91.3
PGBM3	17,792,909,823	111	72	91.0
PGBM4	13,363,577,977	64	52	90.5
PGBM4-blood	14,066,040,787	74	59	91.9
PGBM5	14,504,723,839	75	43	88.9
PGBM6	12,287,727,427	59	46	88.1
PGBM6-blood	13,999,868,369	67	53	88.9
PGBM8	12,897,621,735	109	88	93.5
PGBM9	12,045,904,509	104	85	93.1
PGBM10	11,619,534,201	100	82	93.1
PGBM11	16,935,710,296	112	104	93.9
PGBM12	18,612,864,498	95	56	91.1
PGBM13	10,904,833,155	51	41	87.3
PGBM13-blood	13,552,900,813	73	58	91.9
PGBM14	15,701,377,658	86	53	91.0
PGBM14-blood	10,213,821,624	50	30	83.4
PGBM15	10,582,247,277	86	67	92.1
PGBM16	11,521,709,389	106	80	92.3
PGBM17	12,870,074,056	68	57	91.9
PGBM18	16,596,170,697	113	104	94.3
PGBM19	12,687,545,184	65	53	91.3
PGBM20	13,400,490,858	69	56	91.5
PGBM21	16,068,676,400	102	95	93.8
PGBM22	11,061,729,809	93	74	92.8
PGBM23	14,088,721,409	68	44	89.1
PGBM24	10,190,203,445	49	41	87.9
PGBM25	12,094,215,054	62	52	90.5
PGBM26	19,718,043,045	123	81	91.7
PGBM27	17,672,965,295	98	62	90.5
PGBM28	13,235,175,617	88	65	92.0
PGBM29	4,376,261,391	38	22	83.9
PGBM30	11,331,964,823	100	78	92.5
PGBM31	9,457,007,712	48	29	85.4
PGBM32	15,996,029,641	101	94	94.1
PGBM33	10,601,377,271	89	72	92.7
PGBM34	9,753,010,363	46	27	83.7
PGBM35	16,828,099,833	115	68	91.3
PGBM36	12,731,008,997	68	38	88.2
PGBM37	20,336,444,728	134	78	92.9
PGBM38	9,929,368,120	51	29	85.5
PGBM39	13,628,886,633	65	52	89.7
PGBM40-blood	13,251,854,585	71	59	91.4
PGBM40	11,824,281,050	58	46	87.2
PGBM41-blood	14,095,936,522	68	53	88.5
PGBM41	17,799,081,592	120	78	91.3
PGBM42	12,032,711,376	64	54	89.9
PGBM43	14,904,682,891	88	80	92.4
PGBM44	14,651,870,734	102	94	93.6
PGBM45	17,328,188,664	90	60	91.7
PGBM46	10,137,136,155	82	69	92.7
PGBM47	10,003,457,301	80	66	92.3
PGBM48	12,519,238,552	111	91	93.4
PGBM49	11,864,031,610	103	81	92.5

Supplementary Table 3: Candidate somatic mutations in the 6 tumor samples with matched germline DNA

Tumor variants were considered to be somatic when matched normal had more than ≥ 10 reads and 0 variant reads

Sample	# Somatic mutations		
	Normal has ≥ 0 reads	Normal has ≥ 5 reads	Normal has ≥ 10 reads**
PGBM6	20	17	13
PGBM13	32	32	31
PGBM4	14	12	12
PGBM39	19	19	16
PGBM14	29	18	14
PGBM40	10	6	3

**Variants shown in table below

Sample	Gene	Transcript accession	Nucleotide variant	Amino acid change	Mutation type
PGBM6	AHNAK	NM_001620.1	c.10565C>T	p.(Pro3522Leu)	nonsynonymous SNV
PGBM39	AHRR	NM_020731.4	c.496G>A	p.(Asp166Asn)	nonsynonymous SNV
PGBM14	ATRX	NM_000489.3	c.5269G>T	p.(Glu1757*)	stopgain SNV
PGBM4	ATRX	NM_000489.3	c.3168delG	p.(Lys1057Argfs*61)	frameshift deletion
PGBM13	ATRX	NM_000489.3	c.5215C>T	p.(Arg1739*)	stopgain SNV
PGBM6	ATRX	NM_000489.3	c.5399T>C	p.(Met1800Thr)	nonsynonymous SNV
PGBM13	BMPER	NM_133468.3	c.1476G>T	p.(Lys492Asn)	nonsynonymous SNV
PGBM39	BRAF	NM_004333.4	c.1799T>A	p.(Val600Glu)	nonsynonymous SNV
PGBM13	C13orf40	NM_001146197.1	c.3703G>C	p.(Glu1235Gln)	nonsynonymous SNV
PGBM13	C20orf195	NM_024059.2	c.16G>T	p.(Ala6Ser)	nonsynonymous SNV
PGBM13	C8orf73	NM_001100878.1	c.1933G>A	p.(Asp645Asn)	nonsynonymous SNV
PGBM13	CD5L	NM_005894.2	c.568C>T	p.(Arg190Cys)	nonsynonymous SNV
PGBM13	CHMP7	NM_152272.3	c.1012G>T	p.(Asp338Tyr)	nonsynonymous SNV
PGBM13	CMYA5	NM_153610.3	c.2674C>T	p.(Arg892*)	stopgain SNV
PGBM39	COL19A1	NM_001858.4	c.1969A>T	p.(Thr657Ser)	nonsynonymous SNV
PGBM13	CR2	NM_001006658.2	c.1559G>A	p.(Arg520His)	nonsynonymous SNV
PGBM14	CSMD3	NM_198123.1	c.1352C>A	p.(Ala451Asp)	nonsynonymous SNV
PGBM39	DSPP	NM_014208.3	c.3447A>C	p.(Glu1149Asp)	nonsynonymous SNV
PGBM6	DUSP6	NM_001946.2	c.848G>A	p.(Arg283Gln)	nonsynonymous SNV
PGBM40	EIF4E1B	NM_001099408.1	c.140G>A	p.(Gly47Glu)	nonsynonymous SNV
PGBM14	FBXW7	NM_033632.2	c.566_567del	p.(Lys189Serfs*66)	frameshift deletion
PGBM4	FCGBP	NM_003890.2	c.14369G>A	p.(Gly4790Asp)	nonsynonymous SNV
PGBM6	FGFR1	NM_023110.2	c.1966A>G	p.(Lys656Glu)	nonsynonymous SNV
PGBM39	GNAS	NM_001077490.1	c.644C>T	p.(Ser215Phe)	nonsynonymous SNV
PGBM39	GPR172A	NM_024531.3	c.1052G>A	p.(Gly351Asp)	nonsynonymous SNV
PGBM4	GRIPAP1	NM_020137.3	c.2414A>G	p.(Lys805Arg)	nonsynonymous SNV
PGBM4	GYS2	NM_021957.3	c.1889C>T	p.(Thr630Met)	nonsynonymous SNV
PGBM4	H3F3A	NM_002107.4	c.83A>T	p.(Lys28Met)	nonsynonymous SNV
PGBM6	H3F3A	NM_002107.4	c.83A>T	p.(Lys28Met)	nonsynonymous SNV
PGBM13	H3F3A	NM_002107.4	c.103G>A	p.(Gly35Arg)	nonsynonymous SNV
PGBM14	H3F3A	NM_002107.4	c.103G>A	p.(Gly35Arg)	nonsynonymous SNV
PGBM13	HMX3	NM_001105574.1	c.622G>T	p.(Gly208Cys)	nonsynonymous SNV
PGBM13	HOOK1	NM_015888.4	c.206A>G	p.(Asp69Gly)	nonsynonymous SNV
PGBM14	KCNS2	NM_020697.2	c.395_397del	p.(Glu133del)	nonframeshift deletion
PGBM13	KIAA1217	NM_019590.3	c.3988G>A	p.(Val1330Met)	nonsynonymous SNV
PGBM4	KIAA1826	NM_032424.1	c.904C>T	p.(Arg302*)	stopgain SNV
PGBM39	KRT27	NM_181537.3	c.167G>A	p.(Gly56Glu)	nonsynonymous SNV
PGBM40	LOXL4	NM_032211.6	c.247G>T	p.(Ala83Ser)	nonsynonymous SNV
PGBM6	LPHN2	NM_012302.2	c.3287C>A	p.(Pro1096Gln)	nonsynonymous SNV
PGBM39	LRP1	NM_002332.2	c.2218C>T	p.(Pro740Ser)	nonsynonymous SNV
PGBM13	LSP1	NM_002339.2	c.970G>A	p.(Gly324Arg)	nonsynonymous SNV
PGBM39	LUM	NM_002345.3	c.547C>T	p.(Leu183Phe)	nonsynonymous SNV
PGBM4	LYPD5	NM_001031749.2	c.695G>A	p.(Arg232Gln)	nonsynonymous SNV
PGBM14	MARK1	NM_018650.3	c.1259G>A	p.(Arg420Gln)	nonsynonymous SNV
PGBM14	MFGE8	NM_005928.2	c.118_120del	p.(Glu40del)	nonframeshift deletion
PGBM40	MTF1	NM_005955.2	c.1532C>A	p.(Ala511Glu)	nonsynonymous SNV
PGBM13	MTUS2	NM_001033602.2	c.1472C>T	p.(Thr491Met)	nonsynonymous SNV
PGBM13	MYO5C	NM_018728.3	c.4626C>A	p.(Asp1542Glu)	nonsynonymous SNV
PGBM39	NCAM2	NM_004540.3	c.2230A>G	p.(Ser744Gly)	nonsynonymous SNV
PGBM4	NDST2	NM_003635.3	c.329G>A	p.(Arg110His)	nonsynonymous SNV

PGBM6	<i>NF1</i>	NM_001042492.2	c.3735_3744del	p.(Phe1247Glyfs*16)	frameshift deletion
PGBM6	<i>NF1</i>	NM_001042492.2	c.6746_6748del	p.(Val2251del)	nonframeshift deletion
PGBM13	<i>NLRP2</i>	NM_017852.3	c.1379C>T	p.(Ala460Val)	nonsynonymous SNV
PGBM6	<i>OR1E1</i>	NM_003553.2	c.437C>T	p.(Ala146Val)	nonsynonymous SNV
PGBM13	<i>OR4C6</i>	NM_001004704.1	c.662G>T	p.(Cys221Phe)	nonsynonymous SNV
PGBM6	<i>OR51A7</i>	NM_001004749.1	c.136C>T	p.(Leu46Phe)	nonsynonymous SNV
PGBM4	<i>PCDHB14</i>	NM_018934.2	c.1966G>A	p.(Ala656Thr)	nonsynonymous SNV
PGBM14	<i>PHF3</i>	NM_015153.2	c.310_312del	p.(Glu106del)	nonframeshift deletion
PGBM4	<i>PIK3C2A</i>	NM_002645.2	c.458C>T	p.(Ala153Val)	nonsynonymous SNV
PGBM13	<i>PRIC285</i>	NM_001037335.2	c.4842C>A	p.(Asp1614Glu)	nonsynonymous SNV
PGBM6	<i>PTEN</i>	NM_000314.4	c.634-2A>C	splicing	splicing
PGBM13	<i>PTGDR</i>	NM_000953.2	c.146G>T	p.(Cys49Phe)	nonsynonymous SNV
PGBM39	<i>RAB23</i>	NM_016277.3	c.551C>T	p.(Thr184Met)	nonsynonymous SNV
PGBM13	<i>RANBP2</i>	NM_006267.4	c.7106G>A	p.(Arg2369His)	nonsynonymous SNV
PGBM13	<i>RERE</i>	NM_001042681.1	c.8C>T	p.(Ala3Val)	nonsynonymous SNV
PGBM13	<i>RGMA</i>	NM_020211.2	c.1248G>T	p.(Arg416Ser)	nonsynonymous SNV
PGBM13	<i>RHOBTB1</i>	NM_014836.4	c.1502C>T	p.(Pro501Leu)	nonsynonymous SNV
PGBM13	<i>RYR2</i>	NM_001035.2	c.13130C>T	p.(Ser4377Leu)	nonsynonymous SNV
PGBM39	<i>SDHA</i>	NM_004168.2	c.772G>C	p.(Gly258Arg)	nonsynonymous SNV
PGBM14	<i>SESN3</i>	NM_144665.2	c.649_650del	p.(Asp217Serfs*19)	frameshift deletion
PGBM13	<i>SFXN4</i>	NM_213649.1	c.971C>A	p.(Ser324Tyr)	nonsynonymous SNV
PGBM14	<i>TKT</i>	NM_001135055.2	c.1644C>T	p.(Trp548Cys)	nonsynonymous SNV
PGBM6	<i>TMC2</i>	NM_080751.2	c.2173C>A	p.(Pro725Thr)	nonsynonymous SNV
PGBM13	<i>TMEM132D</i>	NM_133448.2	c.89G>T	p.(Gly30Val)	nonsynonymous SNV
PGBM6	<i>TNP2</i>	NM_005425.4	c.62C>T	p.(Pro21Leu)	nonsynonymous SNV
PGBM14	<i>TP53</i>	NM_000546.4	c.817C>T	p.(Arg273Cys)	nonsynonymous SNV
PGBM14	<i>TP53</i>	NM_000546.4	c.743G>A	p.(Arg248Gln)	nonsynonymous SNV
PGBM4	<i>TP53</i>	NM_000546.4	c.785delG	p.(Gly262Valfs*83)	frameshift deletion
PGBM13	<i>TP53</i>	NM_000546.4	c.767delC	p.(Thr256Asnfs*89)	frameshift deletion
PGBM39	<i>TRIM28</i>	NM_005762.2	c.499G>A	p.(Val167Met)	nonsynonymous SNV
PGBM13	<i>TTN</i>	NM_133378.4	c.24060C>A	p.(Phe8020Leu)	nonsynonymous SNV
PGBM4	<i>UBE2I</i>	NM_194261.2	c.28G>A	p.(Ala10Thr)	nonsynonymous SNV
PGBM13	<i>UBE3A</i>	NM_000462.3	c.1619T>G	p.(Leu540Arg)	nonsynonymous SNV
PGBM14	<i>URB2</i>	NM_014777.2	c.156G>T	p.(Leu52Phe)	nonsynonymous SNV
PGBM39	<i>USP26</i>	NM_031907.1	c.2138T>A	p.(Ile713Asn)	nonsynonymous SNV
PGBM13	<i>ZCCHC4</i>	NM_024936.2	c.100G>T	p.(Ala34Ser)	nonsynonymous SNV
PGBM14	<i>ZCCHC5</i>	NM_152694.2	c.1085A>T	p.(Gln362Leu)	nonsynonymous SNV
PGBM39	<i>ZNF622</i>	NM_033414.2	c.525G>T	p.(Glu175Asp)	nonsynonymous SNV
PGBM39	<i>ZNF622</i>	NM_033414.2	c.327G>C	p.(Met109Ile)	nonsynonymous SNV

Supplementary Table 4: Summary of somatic mutations in pediatric glioblastoma and 5 cancer types from Parsons et al.

	Pediatric GBM	Adult GBM	Medulloblastoma	Pancreas	Colorectal	Breast
Number of samples analyzed	6	21	22	24	11	11
Number of mutated genes	80	685	218	1007	769	1026
Number of nonsilent mutations	87	748	183	1163	849	1112
Missense	71 (81.6%)	622 (83.2%)	130 (71.0%)	974 (83.7%)	722 (85%)	909 (81.7%)
Nonsense	4 (4.6%)	43 (5.7%)	18 (9.8%)	60 (5.2%)	48 (5.7%)	64 (5.8%)
Insertion	0	3 (0.4%)	5 (2.7%)	4 (0.3%)	4 (0.5%)	5 (0.4%)
Deletion	10 (11.5%)	46 (6.1%)	14 (7.7%)	43 (3.7%)	27 (3.2%)	78 (7.0%)
Duplication	0	7 (0.9%)	7 (3.8%)	31 (2.7%)	18 (2.1%)	3 (0.3%)
Splice site or UTR	2 (2.3%)	27 (3.6%)	9 (4.9%)	51 (4.4%)	30 (3.5%)	53 (4.8%)
Average number of nonsilent mutations per sample	15	36	8	48	77	101
Observed/expected number of nonsense alterations		1	2.48	1.18	1.25	1.37
Total number of substitutions	77	937	199	1486	893	1157
Substitutions at C:G base pairs						
C:G to T:A**	40 (50.6%)	601 (64.1%)	109 (54.8%)	798 (53.8%)	534 (59.8%)	422 (36.5%)
C:G to G:C**	3 (3.8%)	67 (7.2%)	12 (6.0%)	142 (9.6%)	61 (6.8%)	325 (28.1%)
C:G to A:T**	21 (26.6%)	114 (12.1%)	41 (20.6%)	246 (16.6%)	130 (14.6%)	175 (15.1%)
Substitutions at T:A base pairs						
T:A to C:G**	5 (6.3%)	87 (9.3%)	19 (9.5%)	142 (9.6%)	69 (7.7%)	102 (8.8%)
T:A to G:C**	3 (3.8%)	24 (2.6%)	14 (7.0%)	79 (5.3%)	59 (6.6%)	57 (4.9%)
T:A to A:T**	7 (8.9%)	44 (4.7%)	4 (2.0%)	77 (5.2%)	40 (4.5%)	76 (6.6%)
Substitutions at specific dinucleotides						
5'-CpG-3'***	no data	404 (43.1%)	85 (42.7%)	563 (37.9%)	427 (47.8%)	195 (16.9%)
5'-TpC-3'***	no data	102 (10.9%)	14 (7.0%)	218 (14.7%)	99 (11.1%)	395 (34.1%)

Supplementary Table 5: Mutations in selected genes H3F3A, ATRX, DAXX, IDH1, PDGFRA, EGFR, TP53

Sample	Gene	Transcript accession	Nucleotide variant	Amino acid change	Mutation type
PGBM1	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM2	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM3	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM5	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM6	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM4	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM8	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM9	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM10	<i>H3F3A</i>	NM_002107.4	c.83A>T	p.(Lys27Met)	Missense
PGBM11	<i>H3F3A</i>	NM_002107.4	c.103G>A	p.(Gly34Arg)	Missense
PGBM14	<i>H3F3A</i>	NM_002107.4	c.103G>A	p.(Gly34Arg)	Missense
PGBM12	<i>H3F3A</i>	NM_002107.4	c.103G>A	p.(Gly34Arg)	Missense
PGBM13	<i>H3F3A</i>	NM_002107.4	c.103G>A	p.(Gly34Arg)	Missense
PGBM15	<i>H3F3A</i>	NM_002107.4	c.103G>A	p.(Gly34Arg)	Missense
PGBM16	<i>H3F3A</i>	NM_002107.4	c.104G>T	p.(Gly34Val)	Missense
PGBM1	<i>ATRX</i>	NM_000489.3	c.3364delT	p.(Cys1122Valfs*8)	Frameshift indel
PGBM4	<i>ATRX</i>	NM_000489.3	c.3168delG	p.(Lys1057Argfs*61)	Frameshift indel
PGBM6	<i>ATRX</i>	NM_000489.3	c.5399T>C	p.(Met1800Thr)	Missense
PGBM11	<i>ATRX</i>	NM_000489.3	c.4179_4182del	p.(Ser1394Asnfs*95)	Frameshift indel
PGBM12	<i>ATRX</i>	NM_000489.3	c.5178_5179insA	p.(Glu1727Argfs*7)	Frameshift indel
PGBM13	<i>ATRX</i>	NM_000489.3	c.5215C>T	p.(Arg1739*)	Nonsense
PGBM14	<i>ATRX</i>	NM_000489.3	c.5269G>T	p.(Glu1757*)	Nonsense
PGBM15	<i>ATRX</i>	NM_000489.3	c.6761A>G	p.(His2254Arg)	Missense
PGBM16	<i>ATRX</i>	NM_000489.3	c.6331C>T	p.(Arg2111*)	Nonsense
PGBM17	<i>ATRX</i>	NM_000489.3	c.4766G>T	p.(Gly1589Val)	Missense
PGBM18	<i>ATRX</i>	NM_000489.3	c.4276C>T	p.(Arg1426*)	Nonsense
PGBM19	<i>ATRX</i>	NM_000489.3	c.4745_4746insA	p.(Lys1584Glufs*17)	Frameshift indel
PGBM20	<i>ATRX</i>	NM_000489.3	c.7327A>G	p.(Asn2443Asp)	Missense
PGBM22	<i>ATRX</i>	NM_000489.3	c.4745_4746insA	p.(Lys1584Glufs*17)	Frameshift indel
PGBM22	<i>ATRX</i>	NM_000489.3	c.3904delA	p.(Arg1302Glufs*44)	Frameshift indel
PGBM22	<i>ATRX</i>	NM_000489.3	c.6406G>A	p.(Asp2136Asn)	Missense
PGBM19	<i>DAXX</i>	NM_001350.4	c.1885_1886insC	p.(Cys629Serfs*29)	Frameshift indel
PGBM21	<i>DAXX</i>	NM_001350.4	c.712C>T	p.(Arg238*)	Nonsense
PGBM17	<i>IDH1</i>	NM_005896.2	c.395G>A	p.(Arg132His)	Missense
PGBM18	<i>IDH1</i>	NM_005896.2	c.395G>A	p.(Arg132His)	Missense
PGBM23	<i>IDH1</i>	NM_005896.2	c.395G>A	p.(Arg132His)	Missense
PGBM29	<i>IDH1</i>	NM_005896.2	c.395G>A	p.(Arg132His)	Missense
PGBM2	<i>PDGFRA</i>	NM_006206.4	c.[1154A>T;1155G>A]	p.(Lys385Ile)	Missense
PGBM16	<i>PDGFRA</i>	NM_006206.4	c.1154A>T	p.(Lys385Met)	Missense
PGBM34	<i>PDGFRA</i>	NM_006206.4	c.2525_2527del	p.(Asp842_Ile843delinsVal)	Nonframeshift indel
PGBM12	<i>PDGFRA</i>	NM_006206.4	c.2545T>G	p.(Tyr849Asp)	Missense
PGBM22	<i>EGFR</i>	NM_005228.3	c.2165C>T	p.(Ala722Val)	Missense
PGBM27	<i>EGFR</i>	NM_005228.3	c.2950G>A	p.(Asp984Asn)	Missense
PGBM1	<i>TP53</i>	NM_000546.4	c.916C>T	p.(Arg306*)	Nonsense
PGBM1	<i>TP53</i>	NM_000546.4	c.455_459del	p.(Pro152Argfs*27)	Frameshift indel
PGBM2	<i>TP53</i>	NM_000546.4	c.637C>T	p.(Arg213*)	Nonsense
PGBM3	<i>TP53</i>	NM_000546.4	c.393_395del	p.(Asn131del)	Nonframeshift indel
PGBM4	<i>TP53</i>	NM_000546.4	c.785delG	p.(Gly262Valfs*83)	Frameshift indel
PGBM8	<i>TP53</i>	NM_000546.4	c.817C>T	p.(Arg273Cys)	Missense
PGBM9	<i>TP53</i>	NM_000546.4	c.818G>C	p.(Arg273Pro)	Missense
PGBM11	<i>TP53</i>	NM_000546.4	c.488A>G	p.(Tyr163Cys)	Missense
PGBM12	<i>TP53</i>	NM_000546.4	c.1024C>T	p.(Arg342*)	Nonsense
PGBM12	<i>TP53</i>	NM_000546.4	c.524G>A	p.(Arg175His)	Missense
PGBM13	<i>TP53</i>	NM_000546.4	c.767delC	p.(Thr256Asnfs*89)	Frameshift indel
PGBM14	<i>TP53</i>	NM_000546.4	c.817C>T	p.(Arg273Cys)	Missense
PGBM14	<i>TP53</i>	NM_000546.4	c.743G>A	p.(Arg248Gln)	Missense
PGBM15	<i>TP53</i>	NM_000546.4	c.548_549insGCCCCCA	p.(Asp184_Asp393delinsProPro)	Nonframeshift indel
PGBM16	<i>TP53</i>	NM_000546.4	c.1024C>T	p.(Arg342*)	Nonsense
PGBM17	<i>TP53</i>	NM_000546.4	c.659A>G	p.(Tyr220Cys)	Missense

PGBM18	<i>TP53</i>	NM_000546.4	c.586C>T	p.(Arg196*)	Nonsense
PGBM18	<i>TP53</i>	NM_000546.4	c.817C>T	p.(Arg273Cys)	Missense
PGBM19	<i>TP53</i>	NM_000546.4	c.800G>A	p.(Arg267Gln)	Missense
PGBM19	<i>TP53</i>	NM_000546.4	c.689C>T	p.(Thr230Ile)	Missense
PGBM20	<i>TP53</i>	NM_000546.4	c.742C>T	p.(Arg248Trp)	Missense
PGBM21	<i>TP53</i>	NM_000546.4	c.799C>T	p.(Arg267Trp)	Missense
PGBM21	<i>TP53</i>	NM_000546.4	c.455C>T	p.(Pro152Leu)	Missense
PGBM22	<i>TP53</i>	NM_000546.4	c.1009C>T	p.(Arg337Cys)	Missense
PGBM22	<i>TP53</i>	NM_000546.4	c.524G>A	p.(Arg175His)	Missense
PGBM23	<i>TP53</i>	NM_000546.4	c.761T>G	p.(Ile254Ser)	Missense
PGBM24	<i>TP53</i>	NM_000546.4	c.586C>T	p.(Arg196*)	Nonsense
PGBM25	<i>TP53</i>	NM_000546.4	c.1024C>T	p.(Arg342*)	Nonsense
PGBM26	<i>TP53</i>	NM_000546.4	c.524G>A	p.(Arg175His)	Missense
PGBM27	<i>TP53</i>	NM_000546.4	c.751A>C	p.(Ile251Leu)	Missense
PGBM28	<i>TP53</i>	NM_000546.4	c.818G>A	p.(Arg273His)	Missense
PGBM29	<i>TP53</i>	NM_000546.4	c.29T>G	p.(Val10Gly)	Missense
PGBM30	<i>TP53</i>	NM_000546.4	c.733G>A	p.(Gly245Ser)	Missense
PGBM5	<i>NF1</i>	NM_000267.3	c.6787_6790del	p.(Tyr2264Thrfs*5)	Frameshift indel
PGBM6	<i>NF1</i>	NM_000267.3	c.3735_3744del	p.(Phe1247Glyfs*16)	Frameshift indel
PGBM6	<i>NF1</i>	NM_000267.3	c.6683_6685del	p.(Val2230del)	Nonframeshift indel
PGBM10	<i>NF1</i>	NM_000267.3	c.2970delA	p.(Met991*)	Nonsense
PGBM18	<i>NF1</i>	NM_000267.3	c.1866T>A	p.(Cys622*)	Nonsense
PGBM18	<i>NF1</i>	NM_000267.3	c.4466delT	p.(Leu1489Hisfs*64)	Frameshift indel
PGBM19	<i>NF1</i>	NM_000267.3	c.1318C>T	p.(Arg440*)	Nonsense
PGBM21	<i>NF1</i>	NM_000267.3	c.5839C>T	p.(Arg1947*)	Nonsense
PGBM22	<i>NF1</i>	NM_000267.3	c.7846C>T	p.(Arg2616*)	Nonsense
PGBM22	<i>NF1</i>	NM_000267.3	c.2659G>A	p.(Ala887Thr)	Missense
PGBM22	<i>NF1</i>	NM_000267.3	c.1381C>T	p.(Arg461*)	Nonsense
PGBM25	<i>NF1</i>	NM_000267.3	c.4575delG	p.(Gly1526Valfs*27)	Frameshift indel
PGBM26	<i>NF1</i>	NM_000267.3	c.6787_6790del	p.(Tyr2264Thrfs*5)	Frameshift indel
PGBM28	<i>NF1</i>	NM_000267.3	c.2026_2027insC	p.(Ile679Aspfs*21)	Frameshift indel
PGBM32	<i>NF1</i>	NM_000267.3	c.4879A>T	p.(Thr1627Ser)	Missense
PGBM33	<i>NF1</i>	NM_000267.3	c.1641+1G>T		Splicing

Supplementary Table 6: Comparison of genes mutated in pediatric GBM and in each of the 4 described adult GBM molecular subgroups

		Pediatric GBM		adult GBM Gene-expression based molecular subtypes												
Pathway	Gene	No. of tumors	% of tumors	Proneural			Neural			Classical			Mesenchymal			
				No. of tumors	% of tumors	p-value*	No. of tumors	% of tumors	p-value*	No. of tumors	% of tumors	p-value*	No. of tumors	% of tumors	p-value*	
Chromatin Remodelling	H3F3A	33/91	36	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	ATRX	59/191	31	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	DAXX	2/70	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	IDH1	8/84	10	11/37	30	0.0124	1/19	5	1	0/22	0	0.2006	0/38	0	0.0564	
Cell Signalling	EGFR	2/49	4	6/37	16	0.0703	5/19	26	0.0155	7/22	32	0.0029	2/38	5	1	
	PDGFRA	4/49	8	4/37	11	0.7208	0/19	0	0.5702	0/22	0	0.3033	0/38	0	0.1283	
	NF1	13/49	26	2/37	5	0.011	3/19	16	0.5261	1/22	5	0.0499	14/38	37	0.3542	
	PIK3CA	3/49	6	3/37	8	1	1/19	5	1	1/22	5	1	1/38	3	0.6286	
	PIK3R1	5/49	10	7/37	19	0.3477	2/19	11	1	1/22	5	0.6583	0/38	0	0.0652	
	PTEN	3/49	6	6/37	16	0.1646	4/19	21	0.0892	5/22	23	0.0971	12/38	32	0.0032	
Cell Cycle	TP53	27/49	55	20/37	54	1	4/19	21	0.0149	0/22	0	<0.0001	12/38	32	0.0325	
	CDKN2A	3/49	6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	RB1	5/49	10	1/37	3	0.2302	1/19	5	1	0/22	0	0.3151	5/38	13	0.742	

*Fisher's two tailed test to compare between pediatric GBM and different subtypes of adult GBM (Proneural, Neural, Classical, Mesenchymal).

N/A: not available

Supplementary Table 7: Top 100 differentially expressed genes by standard deviation, used for unsupervised hierarchical clustering, ordered as presented in Figure 3b

	G34 Mutant				K27 Mutant					SD	Mean(G34)-Mean(K27)
	PGBM14	PGBM15	PGBM16	PGBM11	PGBM2	PGBM4	PGBM6	PGBM8	PGBM9		
FOXG1	11.79	11.92	11.32	11.89	4.11	0.00	4.17	3.17	1.72	4.96	9.09
SP8	5.47	9.88	7.95	9.13	0.00	0.68	0.00	2.07	0.00	4.20	7.56
DLX6-AS1	2.72	10.83	10.20	9.38	0.00	2.70	2.29	0.00	0.00	4.58	7.28
DLX2	4.03	10.96	9.26	9.25	1.26	3.69	1.20	0.38	0.00	4.28	7.07
DLX1	5.07	11.45	10.02	9.88	2.74	4.87	0.68	2.51	0.93	4.12	6.76
DLX6	3.74	10.05	9.02	7.35	1.32	1.58	2.23	0.85	0.00	3.80	6.35
C14orf23	7.70	6.80	5.78	7.34	0.77	0.00	2.26	0.49	2.20	3.16	5.76
DLX5	3.87	9.48	7.36	6.77	0.26	0.58	3.55	1.20	0.93	3.39	5.57
FZD7	8.71	8.54	10.49	9.06	2.98	1.81	3.77	6.37	4.04	3.14	5.41
PCK1	5.40	6.79	7.78	3.58	0.00	0.00	1.26	0.00	2.91	3.03	5.05
NPY	7.01	6.22	11.08	11.00	3.20	3.64	4.57	3.87	3.94	3.08	4.99
MOXD1	5.62	6.93	10.28	10.20	6.64	3.36	1.26	4.53	4.49	2.98	4.20
TRD@	8.31	4.15	6.92	10.72	1.38	4.89	1.89	5.04	3.83	2.99	4.12
NEUROD1	3.32	8.05	3.05	9.67	0.00	3.49	1.26	3.41	4.91	3.05	3.41
CES1	10.48	2.46	4.04	5.86	2.83	0.00	4.14	4.65	0.00	3.19	3.39
LOC441179	1.38	8.96	5.35	8.56	3.04	0.26	3.79	2.32	4.41	2.99	3.30
KIRREL3	0.85	5.77	7.36	8.79	0.68	3.68	1.26	2.56	4.69	2.93	3.12
LOC100292909	4.04	7.45	9.93	5.33	0.00	4.17	1.38	6.41	6.58	3.05	2.98
TFPI2	0.38	5.25	9.53	6.41	0.00	0.00	0.85	8.74	2.87	3.81	2.90
LOC100192378	1.14	8.73	7.59	6.04	7.39	0.00	5.00	2.83	0.00	3.40	2.83
HLA-DQA1	4.52	3.95	6.79	5.76	0.14	0.14	4.96	9.56	0.00	3.33	2.30
HES5	2.89	9.44	8.08	6.58	1.07	8.77	2.00	5.55	5.86	3.02	2.09
PLN	0.58	10.65	4.64	7.78	4.03	0.00	3.83	6.28	5.30	3.32	2.03
HLA-DQB1	0.93	3.98	5.51	5.79	0.58	0.26	0.93	8.58	0.26	3.07	1.93
LOC100271840	3.83	6.14	2.94	8.37	1.96	1.14	0.68	5.57	8.06	2.88	1.84
AQP9	9.75	1.54	0.58	3.96	1.58	2.07	3.02	6.13	1.68	2.91	1.06
CXCL14	9.76	5.11	4.93	5.49	1.77	1.20	12.02	7.85	6.34	3.48	0.49
OGDHL	5.28	0.49	0.49	8.73	0.77	6.28	6.78	1.32	2.85	3.15	0.14
SLC14A1	1.20	0.68	6.00	2.26	7.90	0.49	0.00	5.75	0.14	3.01	-0.32
CNGA3	0.00	1.43	6.83	5.15	8.57	0.00	1.14	3.35	6.10	3.17	-0.48
DDIT4L	11.53	5.58	2.89	3.14	8.93	3.38	8.05	7.96	4.80	3.02	-0.84
COL6A2	4.22	4.24	4.43	0.00	0.26	0.58	8.39	6.61	5.35	2.95	-1.02
CHI3L1	13.30	4.92	7.45	9.87	8.21	8.10	13.68	12.75	7.74	3.05	-1.21
MET	8.83	5.51	4.41	6.11	3.61	12.84	4.77	11.84	4.14	3.45	-1.22
ASCL1	1.20	11.78	10.24	9.84	11.13	9.68	7.69	8.75	10.35	3.15	-1.25
C8orf34	0.85	5.86	4.73	3.63	10.63	1.63	4.11	7.12	3.52	2.95	-1.64

SLC6A15	1.38	7.21	2.79	0.49	6.18	7.81	0.00	2.63	6.80	3.08	-1.72
CRABP1	0.85	4.82	0.49	1.20	0.00	4.46	1.07	4.93	8.57	2.89	-1.97
C1orf192	1.77	0.68	5.78	0.00	9.55	0.85	1.00	7.12	1.81	3.41	-2.01
IL8	6.79	5.48	5.28	4.15	2.63	3.29	10.42	11.62	9.20	3.21	-2.01
AKR1C1	12.64	3.91	4.78	4.50	9.00	9.68	5.31	9.40	9.05	3.03	-2.03
SLC39A12	0.93	2.96	3.83	4.12	8.75	0.38	6.07	7.77	2.20	2.91	-2.07
FSTL5	0.68	3.93	0.38	4.90	10.54	5.79	0.00	4.83	2.29	3.35	-2.22
LTF	10.01	0.00	5.68	5.88	10.11	0.00	8.63	11.40	8.30	4.22	-2.30
NEFL	4.12	5.89	0.58	1.72	3.91	10.69	1.63	7.85	2.89	3.27	-2.31
C2orf40	2.70	6.16	3.97	5.22	10.44	4.54	0.58	9.94	9.27	3.41	-2.44
CDH13	1.00	0.00	6.84	1.93	6.38	0.00	6.89	6.15	5.92	3.07	-2.63
C7orf57	2.74	0.00	3.00	0.00	9.32	1.43	0.00	6.90	2.98	3.25	-2.69
CCL20	6.00	0.77	1.49	0.00	1.81	0.77	7.35	8.71	5.38	3.28	-2.74
KCNA5	2.61	0.00	0.14	1.26	7.63	0.00	5.40	0.38	5.45	2.91	-2.77
GRIA2	7.99	1.72	9.15	10.53	10.14	11.82	10.06	9.04	9.80	2.90	-2.82
SERPINA3	11.80	1.00	9.61	9.56	12.19	7.09	13.37	11.61	9.99	3.71	-2.86
CDH19	0.00	1.96	5.28	7.79	9.32	5.22	7.31	5.76	5.66	2.87	-2.90
SLC44A5	0.00	9.04	5.74	8.13	8.92	8.93	7.99	7.96	9.93	3.01	-3.02
BCHE	1.63	9.34	9.31	9.49	10.45	10.93	10.57	10.45	10.73	2.91	-3.18
LOC157503	0.00	4.22	0.00	6.86	8.43	7.50	3.52	4.99	5.51	3.01	-3.22
SCN7A	0.00	3.07	2.87	7.23	8.69	2.41	8.44	6.54	6.71	3.07	-3.27
OTX2	0.00	5.19	2.49	0.00	8.92	0.00	8.56	6.81	1.68	3.70	-3.27
DPP10	3.10	10.40	2.74	2.23	8.04	8.03	7.10	7.95	8.36	2.95	-3.28
AKR1C2	12.37	1.20	2.29	2.04	8.07	9.35	3.64	9.28	8.41	4.03	-3.28
PAK7	0.00	6.65	3.05	2.26	7.67	8.49	3.12	5.31	6.94	2.86	-3.31
CALB1	7.79	0.00	1.14	2.61	3.32	7.24	6.17	7.92	6.57	3.02	-3.36
RALGAPA2	0.00	0.38	3.57	3.90	7.38	8.85	0.00	5.57	5.08	3.24	-3.41
STMN2	4.09	10.37	2.38	8.83	7.94	11.89	9.93	9.05	10.51	3.13	-3.45
DCC	0.00	7.97	1.89	5.32	6.13	9.29	7.47	6.39	7.94	3.04	-3.65
GRIN2A	2.89	0.77	2.41	0.68	9.86	1.54	4.00	5.29	6.17	2.99	-3.69
CTNNA2	1.26	9.33	6.22	4.86	11.04	8.95	8.03	8.75	8.92	2.94	-3.72
KLRC4	4.25	0.58	0.00	2.91	1.00	6.99	8.50	5.69	7.25	3.17	-3.95
PCDH7	2.00	7.03	2.32	10.51	10.94	8.51	8.87	9.09	9.70	3.32	-3.96
ALDH3A3	0.14	5.89	0.00	1.07	6.85	2.20	6.51	6.33	6.78	3.04	-3.96
RALYL	0.93	5.21	3.90	2.32	8.76	8.21	2.77	7.45	8.43	2.99	-4.04
TTC9B	0.68	2.85	0.68	0.85	1.07	7.62	6.68	4.89	6.42	2.89	-4.07
TMEFF2	0.85	8.22	3.58	5.65	8.61	9.90	7.58	7.85	9.37	2.96	-4.08
INSM1	0.38	0.68	0.00	0.00	0.00	8.04	1.26	5.33	7.61	3.41	-4.18
UGT8	0.49	4.48	5.46	8.07	8.90	9.54	7.29	8.46	10.00	3.03	-4.21
RIT2	0.58	6.96	4.67	6.08	9.99	10.69	7.24	7.15	9.00	3.04	-4.24
OGN	0.00	3.10	0.00	0.14	12.07	0.14	3.56	6.22	3.29	3.99	-4.25
H19	3.32	2.00	4.80	4.38	7.12	6.50	11.57	5.65	8.60	2.89	-4.26
NEGR1	0.00	8.91	1.81	7.28	10.16	9.38	7.69	8.15	8.46	3.52	-4.27
SHISA6	4.07	2.85	4.24	0.26	9.25	4.38	8.80	5.71	7.55	2.91	-4.28
KLRC3	4.94	0.14	2.70	4.41	4.55	8.46	7.81	7.09	8.83	2.89	-4.30
FAM19A5	0.00	2.54	7.12	4.71	8.87	8.64	8.25	6.31	9.57	3.23	-4.74
SLC7A2	5.08	0.14	1.93	0.38	7.67	5.77	5.45	7.69	6.82	2.98	-4.80
SUSD5	6.98	3.51	0.14	4.36	9.03	8.53	9.60	8.14	7.99	3.15	-4.91
ODZ2	2.58	6.04	1.20	4.12	8.22	7.21	10.37	7.23	9.07	3.05	-4.93
DLK1	6.85	5.16	0.00	2.43	6.68	3.92	11.63	9.52	11.05	3.93	-4.95
MYT1	1.63	4.14	0.93	0.26	4.15	9.02	6.90	5.78	7.93	3.14	-5.02
KCND2	2.72	5.26	2.20	6.52	9.36	9.93	8.35	8.46	9.99	2.99	-5.04
KCNJ9	0.77	3.70	0.93	0.00	8.38	7.11	7.67	2.83	6.00	3.23	-5.05
LHFPL3	6.18	4.49	3.49	7.94	11.34	10.58	10.26	9.37	11.40	2.99	-5.07
FAM5C	5.73	2.35	0.26	5.26	8.02	9.32	8.23	8.06	9.05	3.16	-5.14
DBC1	1.63	2.10	1.96	3.29	9.49	7.00	10.00	6.35	6.28	3.23	-5.57
OPCML	0.49	4.28	4.80	5.00	9.81	9.14	8.76	8.25	10.58	3.32	-5.67
CA10	3.51	2.20	2.14	2.04	6.50	8.97	8.03	8.05	9.60	3.18	-5.76
GPR17	1.07	2.93	0.00	0.00	6.49	5.31	5.19	8.68	8.63	3.43	-5.86
CADM2	1.43	4.88	0.26	5.59	9.30	9.03	9.14	8.26	9.30	3.54	-5.97
NXPH1	0.14	4.79	3.55	3.88	8.34	10.20	8.91	8.69	9.68	3.48	-6.08
SFRP2	3.49	2.51	2.38	0.49	10.24	7.76	7.35	7.95	8.62	3.44	-6.17
OLIG1	4.75	2.93	5.34	4.13	8.65	12.51	11.25	10.75	12.15	3.78	-6.77
MEGF11	0.00	0.85	1.43	2.49	8.21	7.80	8.33	7.09	10.24	3.91	-7.14

Supplementary Table 8: Numbers of CNAs of each type identified in each tumour sample

ID	GAINS				DELETIONS				LOH				Total Losses	Total CNAs	CNA Grouping Group 1/2	H3F3A Mut Y/N	ATRX Mut Y/N	DAXX Mut Y/N
	Whole Chr.	Broad	Focal	Total Gains	Whole Chr.	Broad	Focal	Total Dels	Whole Chr.	Broad	Focal	Total LOH						
PGBM1	0	2	2	4	0	0	0	0	1	3	2	6	6	10	2	Y	Y	N
PGBM2	3	1	2	6	0	0	0	0	4	10	2	16	16	22	2	Y	N	N
PGBM3	2	10	7	19	0	0	0	0	3	22	5	30	30	49	2	Y	N	N
PGBM4	0	15	9	24	0	0	0	0	4	17	3	24	24	48	2	Y	Y	N
PGBM5	0	4	0	4	0	0	0	0	2	19	4	25	25	29	2	Y	N	N
PGBM6	0	3	1	4	0	0	0	0	0	5	6	11	11	15	2	Y	Y	N
PGBM11	0	7	11	18	0	0	2	2	0	16	2	18	20	38	2	Y	Y	N
PGBM12	1	2	0	3	0	0	3	3	1	22	8	31	34	37	2	Y	Y	N
PGBM13	1	2	1	4	0	0	0	0	1	4	1	6	6	10	2	Y	Y	N
PGBM14	0	3	1	4	0	0	0	0	11	10	1	22	22	26	2	Y	Y	N
PGBM18	0	2	1	3	0	0	0	0	1	3	2	6	6	9	1	N	Y	N
PGBM19	1	0	0	1	0	0	0	0	17	3	0	20	20	21	2	N	Y	Y
PGBM20	1	5	4	10	0	0	0	0	1	23	17	41	41	51	2	N	Y	N
PGBM21	0	4	3	7	0	0	0	0	13	7	1	21	21	28	2	N	N	Y
PGBM23	0	1	0	1	0	0	0	0	0	3	0	3	3	4	1	N	N	N
PGBM24	0	10	1	11	0	0	2	2	8	15	3	26	28	39	2	N	N	N
PGBM25	0	6	11	17	0	1	4	5	11	14	3	28	33	50	2	N	N	N
PGBM26	2	4	11	17	0	0	0	0	8	5	3	16	16	33	2	N	N	N
PGBM27	3	5	14	22	0	1	0	1	9	14	5	28	29	51	2	N	N	N
PGBM31	0	7	5	12	0	0	0	0	1	3	0	4	4	16	2	N	N	N
PGBM32	0	2	2	4	0	0	0	0	0	2	3	5	5	9	1	N	N	N
PGBM34	3	11	8	22	0	1	1	2	4	18	2	24	26	48	2	N	N	N
PGBM35	0	1	1	2	0	0	0	0	3	1	0	4	4	6	1	N	N	N
PGBM36	0	0	2	2	0	0	0	0	0	1	2	3	3	5	1	N	N	N
PGBM37	0	1	0	1	0	0	0	0	0	5	2	7	7	8	1	N	N	N
PGBM39	3	1	0	4	0	0	3	3	3	2	12	17	20	24	2	N	N	N
PGBM40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	N	N	N
PGBM41	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	N	N	N
PGBM42	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	N	N	N
PGBM43	0	5	16	21	0	0	4	4	5	18	9	32	36	57	2	N	N	N
PGBM45	0	1	6	7	0	0	0	0	0	1	6	7	7	14	2	N	N	N
Totals	20	115	119	254	0	3	19	22	111	267	105	483	505	759				
Mean	0.65	3.71	3.84	8.19	0.00	0.10	0.61	0.71	3.58	8.61	3.39	15.58	16.29	24.48				

Supplementary Table 9: CNA regions identified in each tumour sample

Sample	GAINS			DELETIONS			LOH		
	Whole Chr	Broad	Focal	Whole Chr	Broad	Focal	Whole Chr	Broad	Focal
PGBM1		11q13.1-11q25	11q22.3				16	10q21.3-10q26.3	11q14.1
		17p13.2-17p13.3	18q23					15q	15q26.3
								Xp21.2-Xp22.33	
PGBM2	4	10q25.3-10q26.3	5p14.3-5p12				3	5q	5p15.31
	8		13q34				7	5p15.2-5p14.3	5p15.33
	19						9	10p	
							18	10q	
								12q24.31-12q24.33	
								13q14.11-13q34	
								14q	
								17p13.1-17p13.3	
								21q	
								22q	
PGBM3	7	1q	1q31.2-1q31.3				4	1p	5q31.3
	X	9p	5q21.1				8	2p14-2q37.3	5q33.1-5q34
		14q11.2-14q24.2	6p24.3				10	3p	14q24.3
		14q24.3-14q31.3	6p12.1-6p11.2					5q11.2-5q21.3	17q11.2
		16p	17q21.31					5q22.2-5q23.2	11q14.1
		18p	17q11.2					5q23.2-5q31.1	
		20p12.3-20p13	11p14.1-11p13					5q31.1-5q32	
		21q						5q35.1-5q35.3	
		12q15-12p13.33						7q31.31-7q32.1	
		11p12-11p11.2						8q11.1-8q12.1	
								8q13.2-8q21.13	
								9q	
								11p14.1-11p15.5	
								11p11.2	
								12q15-12q24.33	
							12p13.31-12p12.3		
							12q12-12q13.13		
							13q		
							14q31.3-14q32.33		
							17q21.33-17p13.3		
							17q21.33-17q25.3		
							22q		
PGBM4		1p13.3-1q44	4q12				9	3q11.2-3q25.33	7p22.1-7p22.3
		2p15-2p25.3	4q31.21				11	4q12-4q25	7q31.2-7q31.31
		3q25.33-3q29	4q31.23				16	4q32.3-4q35.2	8p11.22-8p11.21
		3q26.32-3q29	4q34.1				20	5q21.1-5q35.3	
		4q25-4q26	7q31.2					6q13-6q27	
		4q26-4q28.2	8q24.21					7p21.3-7p21.1	
		4q31.3-4q32.1	10q26.13					7p21.1-7p11.2	
		4q32.1-4q32.3	10q26.2					7q35.1-7q36.3	
		10q23.31-10q23.33	20p13					8p12-8p23.3	
		12q12-12q13.13						8q	
		12q23.3-12q24.31						10q21.2-10q22.3	
		14q11.2						12p	
		14q21.1-14q21.2						12q	
		14q21.2-14q21.3						13q	
		16q11.2-16q23.1						14q	
							17p		
							22q		
PGBM5		15q11.2-15q14					1	2p	13q31.1
		15q25.1-15q26.3					6	2q11.2-2q12.3	13q31.3
		17q21.32-17q25.3						2q31.1-2q34	13q32.1-13q32.2
		19p13.11-19p12						2q34-2q37.3	17q11.2
								3p21.31-3p26.3	
								5q	
							9p21.2-9p24.3		
							10p14-10p15.3		
							10p12.1-10q26.3		
							11p		

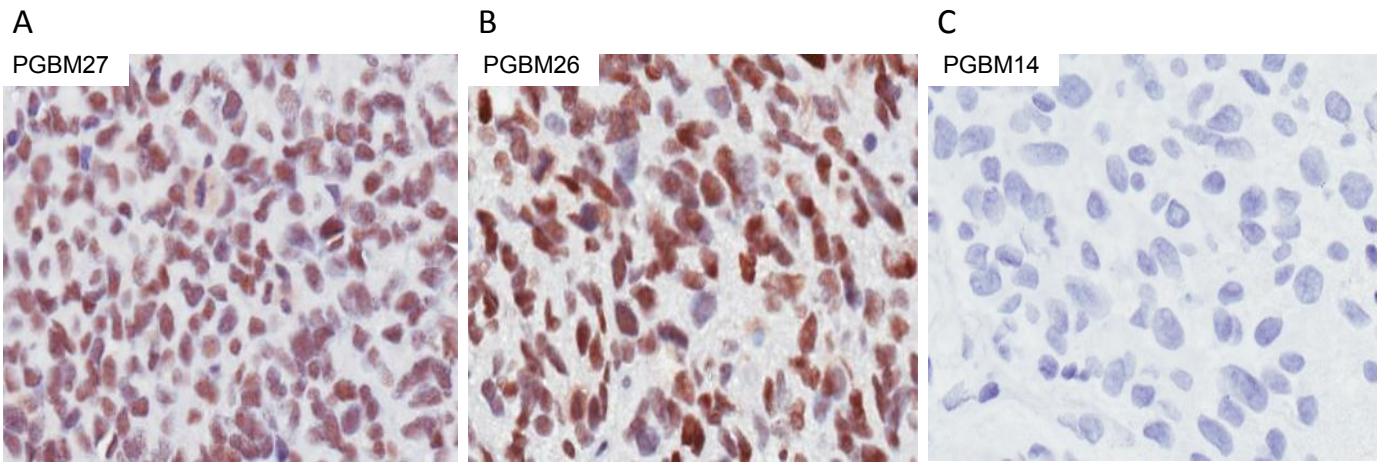
							12q13.11-12q24.33	
							14q23.3-14q32.33	
							15q15.1-15q22.2	
							16q	
							17p	
							17q11.2-17q21.32	
							19q	
							21q11.2-21q21.1	
							21q21.2-21q21.3	
PGBM6		1q	10q22.3				1p31.1-1p11.2	4q26-4q27
		9p23-9p21.1					9p23-9p24.3	10q23.1
		9q31.1-9q34.3					9p21.1-9q31.1	10q23.1
							10q23.31-10q25.1	10q23.1
							19q	10q22.3
								10q22.3
PGBM11		2p24.2-2p25.3	5q31.3		10q23.31		1q31.1-1q44	2q22.2-2q22.1
		2q24.2-2q37.3	7p21.3		Xp11.3		1q24.2-1q21.1	5q13.1
		5p15.2-5p15.33	7p22.2				9p22.1-9p24.3	
		5q13.2-5q31.3	7p22.3				9p21.3-9p21.2	
		7p21.1-7p21.3	7p22.3				10q23.31-10q26.3	
		10p12.31-10p15.3	9p21.3				10q21.1-10q23.1	
		17q24.2-17q25.3	10q22.3				11p	
			10p11.22-10p11.21				12q	
			16q21-16q22.1				13q	
			20p13				16p11.2-16q24.3	
			Xp11.22-Xp11.21				17p11.2-17p13.3	
							18q11.2-18q12.2	
							18q12.2-18q23	
							20p	
							20q	
							21q	
PGBM12	7	3q26.31-3q29			4q31.23	8	1q23.2-1q43	5q34
		22q13.2-22q13.33			10q22.1		2p	11q14.1
					17p13.3		3q12.1-3q26.1	11q22.1
							3q26.1-3q26.31	11q22.1
							4q	11q22.1-11q24.3
							8p21.1-8p12	15q26.3
							8p11.22-8p11.21	16q24.3
							9p24.1-9p24.3	18q23
							9p24.1-9p13.1	
							9q31.1-9q21.11	
							9q31.1-9q33.2	
							9q33.2-9q34.3	
							10p	
							10q11.21-10q25.1	
							10q25.1-10q26.3	
							14q	
							14q31.3-14q32.31	
							15q	
							16p	
							18q21.2-18q23	
							19p13.11-19p13.3	
							19q13.32-19q13.43	
PGBM13	20	1q	5q13.2-5q13.3			17	3p12.1-3q26.1	6q12
		12p12.3-12p13.33					4p15.31-4p16.3	
							4p15.31-4q35.2	
							11q24.3-11q25	
PGBM14		4p15.33-4q13.1	4q32.1-4q32.3			2	3q	18q23
		4q26-4q35.2				6	4q13.1-4q26	
		17q12-17q25.3				7	9p	
						8	9q	
						10	13q	
						11	14q	
						12	15q	
						16	19q13.42-19q13.43	
						18	21q	

						19	22q	
						20		
PGBM18		1q	13q13.3			10	3q27.2-3q29	8p23.2-8p23.3
		9q					9p	12q24.33
							22q12.1-22q13.33	
PGBM19	X					1	13q	
						2	14q	
						3	15q	
						4		
						5		
						6		
						8		
						9		
						10		
						11		
						12		
						16		
						17		
						19		
						20		
						21		
						22		
PGBM20	19	10p12.2-10p15.3	2p24.3-2p24.2			9	1p	5q23.2
		15q25.1-15q26.3	2q14.2				3q11.2-3q28	6p24.3
		16p13.12-16p13.3	2q14.3				5q31.1-5q34	6p22.3
		18p11.31-18p11.21	15q23				5q35.2-5q35.3	6p21.2-6p21.1
		20p13-20q11.23					6p22.3-6p21.32	6p21.1
							6q12-6q13	6p12.1-6p11.2
							6q13-6q14.1	6q15
							6q23.3-6q24.2	6q22.31
							8p23.1-8p23.3	6q24.3-6q25.1
							10q25.3-10q26.3	6q25.3
							11p12-11q25	6q25.3
							11p13-11p12	6q26
							11p14.1-11p15.5	6q27
							12p12.1-12p13.33	6q27
							14q11.2-14q23.3	11p14.111p13
							14q23.3-14q31.3	18q12.3
							16p13.12-16q24.3	18q21.1
							17p	
							17q	
							18q11.2-18q12.1	
							18q11.1-18q12.3	
							18q12.3	
							22q	
PGBM21		2q11.2-2q21.2	20p12.1-20p11.23			1	6p21.1-6p25.3	Xp22.32
		6p21.1-6q27	22q11.23			2	13q	
		17q24.2-17q24.3	Xp22.33			3	14q	
		20q12-20q13.33				4	15q	
						5	20p13-20q12	
						8	21q	
						9	22q	
						10		
						11		
						16		
						17		
						18		
						19		
PGBM23		7q					13q	
							17p13.1-17p13.3	
							19q	
PGBM24		2p24.1-2p25.3	12p13.2-12p13.1		9p21.3	3	3q28-3q29	11p14.3
		2q24.1-2q33.2			15q14	4	9p	11p14.2-11p14.1
		2q33.2-2q35				5	9q34.13-9q34.3	11p11.2

		4q26-4q31.22				6	10p15.3-10q26.12	
		7p14.1-7p11.2				8	11p15.2-11p15.5	
		7q11.23-7q36.3				12	11p15.2-11p15.1	
		10q26.12-10q26.3				17	11p14.1-11p13	
		13q21.31-13q34				18	11p13-11p12	
		15q23-15q26.3					13q12.11-13q21.31	
		16p13.3					14q12-14q32.33	
							15q11.2-15q23	
							16p11.2-16p13.3	
							16q12.1-16q24.3	
							19q13.2-19q13.43	
							22q	
PGBM25		4q26-4q28.1	2q33.2-2q33.3	9p21.3-9p21.2	2q22.1-2q22.2	1	4q32.3-4q35.2	4p14-4p13
		7p	3q13.32		3q13.2	2	5q15-5q35.3	4q28.2
		8p	3q26.33-3q27.1		9p23	3	6p-6q13	17p13.3
		8q24.13-8q24.22	4q12		Xp21.2	9	6p12.1-6p11.2	
		10q26.3	8q11.21-8q11.23			10	6q13-6q25.3	
		15q25.1	8q24.22			11	6q25.3-6q27	
			9p24.3-9p24.2			16	8q12.1-8q23.3	
			10q21.1			17	8q24.22-8q24.3	
			10q25.1			18	12q	
			10q25.3			19	13q	
			10q26.2-10q26.3			20	14q	
							15q14-15q26.3	
							21q	
							22q	
PGBM26	16	9q33.3-9q34.3	5p13.2			2	1q42.13-1q44	19p13.2
	20	12q24.31-12p13.33	7q21.2			3	13q	19p13.2
		14q	10p12.2			4	15q	19p12-19p11
		21q	13q14.3			5	19p13.3	
			13q21.1			6	22q	
			13q31.1			8		
			13q33.1			10		
			13q33.2			17		
			13q34					
			19p13.12					
			19p13.11-19p13.12					
PGBM27	2	5q12.1-5p15.33	2p25.1	10p15.1-10p15.3		3	1q42.2-1q43	5q22.3
	7	9q31.3-9q21.33	2p24.3-2p24.2			4	2p24.1-2p24.2	5q12.2-5q12.3
	16	9q21.33-9q21.13	2p24.1			6	2p21-2p22.3	17q21.32
		12p	5q23.1			8	5q	18q23
		21q	5q22.2			11	5q14.2-5q22.2	18q23
			7p11.2			17	5p13.3-5p13.2	
			7q21.13			18	7q34-7q11.21	
			7q21.2			19	9q33.3-9q32	
			7q33			X	9q21.13-9p24.3	
			7q33				10q25.1-10q26.2	
			10p15.1				11q13.2-11q23.1	
			11q12.1-11q11				11p15.4-11p15.5	
			15q26.3				15q	
			19q13.43				22q	
PGBM31		3q28-3q29	5p15.33			17	3p24.3-3p26.3	
		8q21.13-8q24.12	9p13.3				3p14.2-3q26.31	
		9p21.3-9p24.3	9q21.33				8p	
		9p21.2-9p13.3	18q22.2-18q22.3					
		9q	19p13.3					
		20q13.2-20q13.33						
		22q11.23-22q11.21						
PGBM32		1q	6q14.1				1p	6q12
		6p12.3-6p25.3	22q11.23-22q12.1				6q14.1-6q27	6q13
								6q13
PGBM34	3	1q32.1-1q21.2	1p36.22-1p36.21	9p21.3-9p21.1	6q12	10	1p	19p13.3
	4	1p36.21-1p33	1p32.2-1p32.1			11	2q14.3-2p23.1	19p13.2
	7	8q21.13-8q24.3	1p31.1			12	2q34-2q37.3	

		9q21.11-9q31.3	1p13.3			17	3p25.3-3p26.3	
		19p13.2-19p12	19p13.3				4q28.1-4q23.1	
		20p13-20q11.21	22q11.21-22q11.22				5q23.1-5q35.3	
		20q11.22-20q13.12	22q11.21				6p	
		21q	22q11.21				6q	
		22q13.2-22q13.31					8p12-8p23.3	
		Xp21.3-Xq27.3					9p	
		Xp21.3-Xp22.33					13q	
							14q	
							15q11.2-15q22.2	
							15q22.2-15q26.3	
							19p12-19q12	
							20q13.12-20q13.2	
							22q	
							Xq27.3-Xq28	
PGBM35		17q21.32-17q25.3	10q11.22			9	22q	
						16		
						18		
PGBM36			14q32.33				22q	7p22.1
			18q23					7q22.1
PGBM37		1q					2q14.1-2q31.3	9q34.3
							6q12-6q27	20p12.1
							8q24.22-8q24.3	
							9p21.1-9p24.3	
							16q22.1-16q24.3	
PGBM39	3	21q			9p21.3	10	12p13.31-12p13.33	5p15.32-5p15.33
	7				9p21.3	12	12p12.3-12p11.23	5p15.2
	19				9p21.3	18		5p15.1
								5p14.3
								9p23
								9p23
								9p22.3
								9p22.3-9p22.2
								9p21.2
								9p21.2-9p13.2
								12p13.31
								12p12.3
PGBM40	ZERO ALTERATIONS							
PGBM41								8p11.22
PGBM42							22q11.23-22q13.33 (CN)	
PGBM43		5p14.3-5p13.3	4q12		4q34.3	1	2p	4p12
		6q15-6p25.3	4q12		7p14.1	4	3q13.33-3q29	5p15.32-5p15.31
		9p13.3-9q34.3	4q12		11q22.3-11q23.1	7	5q11.2-5q21.3	5q31.3-5q32
		9p24.1-9p24.3	5p15.33		20q13.31	11	9p22.1-9p21.2	6q24.3
		10p12.1-10p13	5p15.33-5p15.32			18	10q	9p23-9p22.3
			5p15.2				12q21.2-12q23.1	10p11.23
			5p15.1				13q	12q24.31-12q24.32
			5p12				14q	16q23.2-16q23.3
			7q31.2-7q31.31				15q	19p13.3
			9p13.3				16q	
			9p21.1				17p	
			10q23.33-10q24.1				17q11.2-17q23.2	
			10p11.21-10p11.1				19q	
			10p11.22				20p	
			13q13.3				20q	
			19p13.3				22q	
							Xp	
							Xq11.2-Xq21.31	
PGBM45		1q	2p24.3				1p32.2-1p34.1	2p23.3-2p24.1
			2p25.1					3p12.3-3p12.1

		2p25.1						6p25.2-6p25.3
		2p25.3						9p23
		7p11.2						10p15.1-10p14
		9p24.3						12q21.1-12q21.2

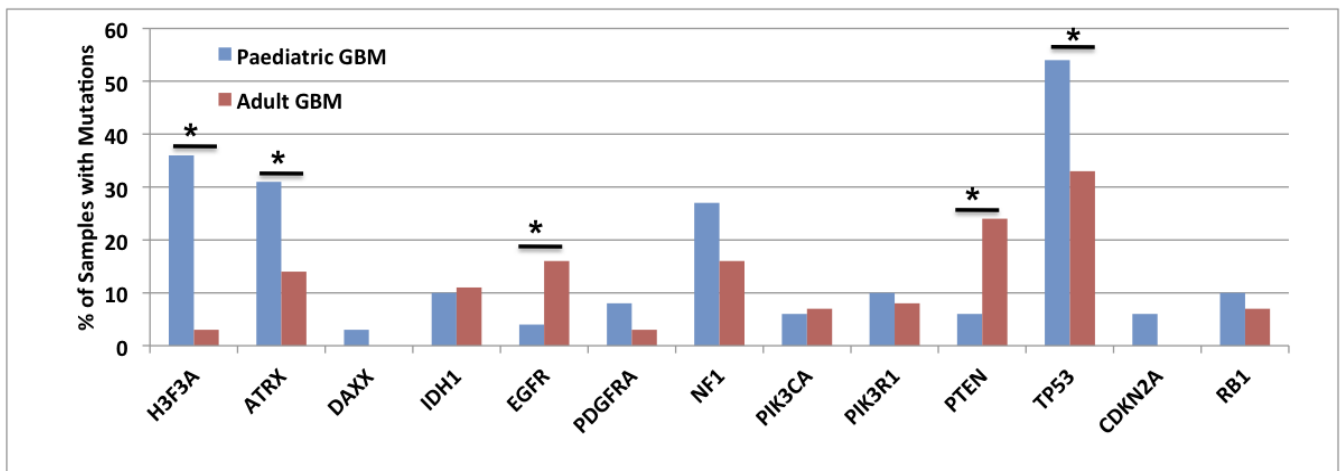


Supplementary Figure 1: Immunohistochemical staining for ATRX showing concordance between sequencing data and protein expression in samples. A). & B). ATRX is expressed in these two samples (PGBM27 & PGBM26) with wild type *ATRX* following whole exome sequencing. C). ATRX is not expressed in PGBM14 where mutations in *ATRX* were identified following whole exome sequencing.

Pathway	Gene	Paediatric GBM		Adult GBM		p-value [†]
		No. of tumors	% of tumors	No. of tumors	% of tumors	
Chromatin Remodelling	H3F3A	32/90	36	11/318	3	<0.0001
	ATRX	59/190	31	23/161	14	0.0002
	DAXX	2/69	3	0/217*	0*	0.0576
	IDH1	8/83	10	24/221	11	0.8367
Cell Signalling	EGFR	2/48	4	35/221	16	0.0362
	PDGFRA	4/48	8	4/116	3	0.234
	NF1	13/48	27	36/221	16	0.0979
	PIK3CA	3/48	6	16/221	7	1
	PIK3R1	5/48	10	18/221	8	0.575
	PTEN	3/48	6	54/221	24	0.0034
Cell Cycle	TP53	26/48	54	73/221	33	0.008
	CDKN2A	3/48	6	0/22	0	0.5467
	RB1	5/48	10	15/221	7	0.3694

[†]Fisher's two-tailed comparison test for paediatric and adult GBM.

*105 of 217 samples were sequenced without DAXX mutation reported, 112 of 217 samples don't have DAXX mutation



Supplementary Figure 2a: *ATRX* & *DAXX* mutation data for paediatric GBM were from WES, Sanger sequencing and *ATRX* IHC analysis described in this study, and Heaphy *et al*²⁰. Other paediatric GBM results were from our study. *H3F3A* mutation data for adult GBM were obtained using Sanger sequencing. Adult GBM *ATRX* results were calculated from our study and Heaphy *et al*²⁰. Datasets described by Verhaak *et al*¹⁸, Parsons *et al*¹¹, and Heaphy *et al*²⁰ were used for all the other results of adult GBM.

		Adult GBM Gene-expression based molecular subtypes													
		Paediatric GBM		Proneural			Neural			Classical			Mesenchymal		
Pathway	Gene	No. of tumors	% of tumors	No. of tumors	% of tumors	p-value*	No. of tumors	% of tumors	p-value*	No. of tumors	% of tumors	p-value*	No. of tumors	% of tumors	p-value*
Chromatin Remodelling	H3F3A	32/90	36	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	ATRX	59/190	31	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	DAXX	2/69	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	IDH1	8/83	10	11/37	30	0.0125	1/19	5	1	0/22	0	0.1993	0/38	0	0.05554
Cell Signalling	EGFR	2/48	4	6/37	16	0.0734	5/19	26	0.0166	7/22	32	0.0032	2/38	5	1
	PDGFRA	4/48	8	4/37	11	0.7235	0/19	0	0.5713	0/22	0	0.3008	0/38	0	0.1264
	NF1	13/48	27	2/37	5	0.0102	3/19	16	0.5259	1/22	5	0.0499	14/38	37	0.3585
	PIK3CA	3/48	6	3/37	8	1	1/19	5	1	1/22	5	1	1/38	3	0.6266
	PIK3R1	5/48	10	7/37	19	0.3498	2/19	11	1	1/22	5	0.6572	0/38	0	0.0636
	PTEN	3/48	6	6/37	16	0.1687	4/19	21	0.0937	5/22	23	0.098	12/38	32	0.0033
Cell Cycle	TP53	26/48	54	20/37	54	1	4/19	21	0.0162	0/22	0	<0.0001	12/38	32	0.0494
	CDKN2A	3/48	6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	RB1	5/48	10	1/37	3	0.2261	1/19	5	0.6666	0/22	0	0.1727	5/38	13	0.7442

*Fisher's two tailed test to compare between pediatric GBM and different subtypes of adult GBM (Proneural, Neural, Classical, Mesenchymal).

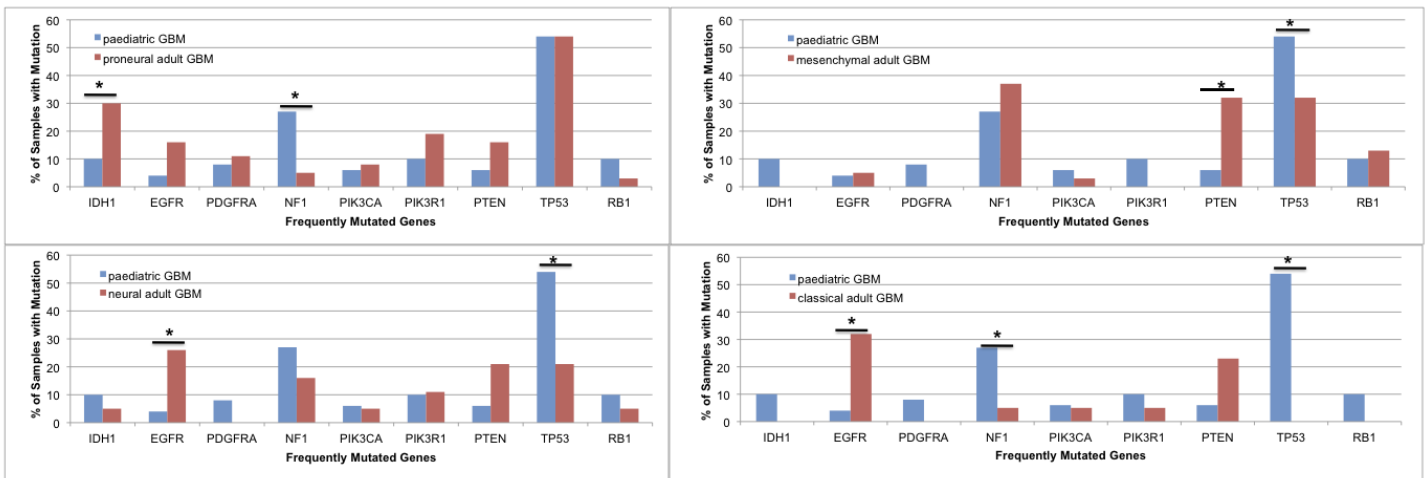
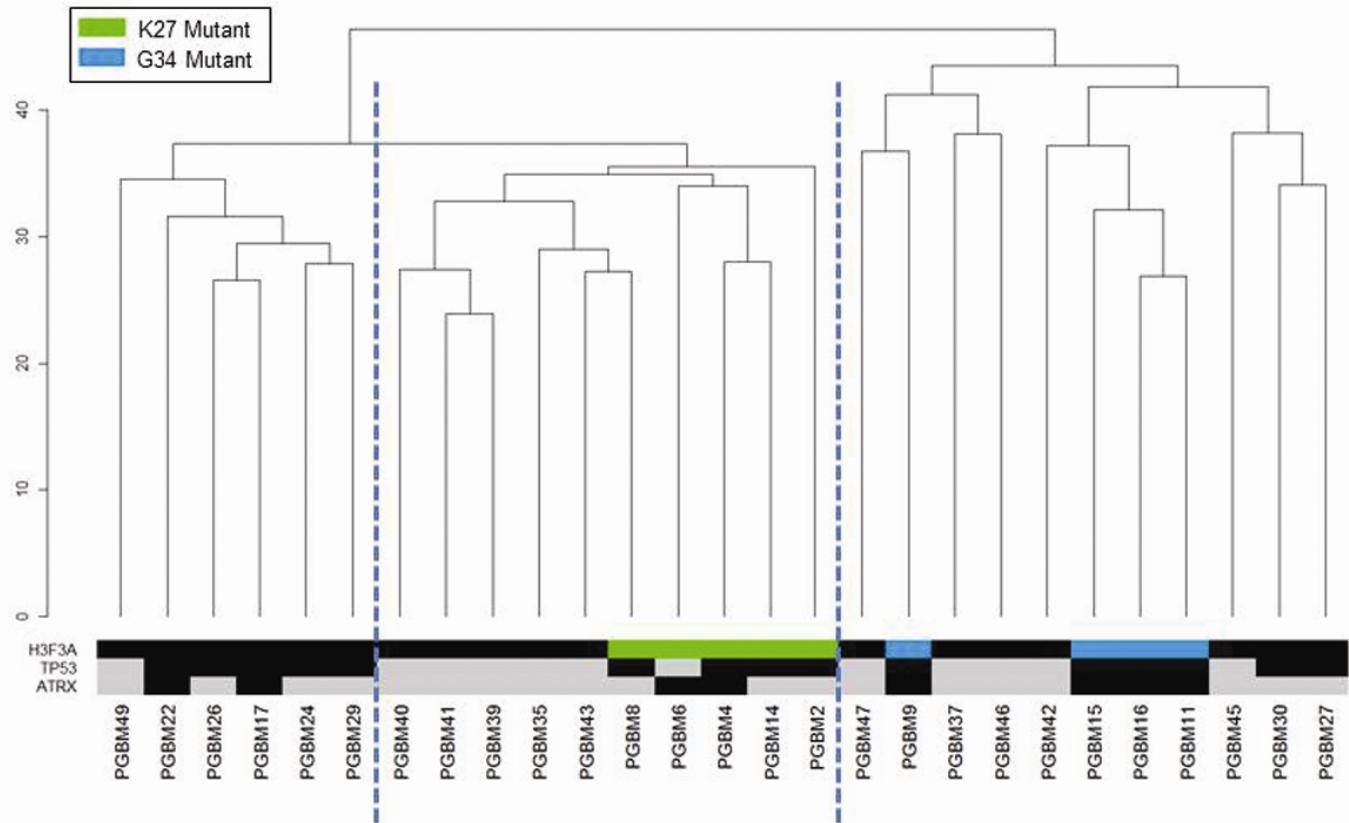
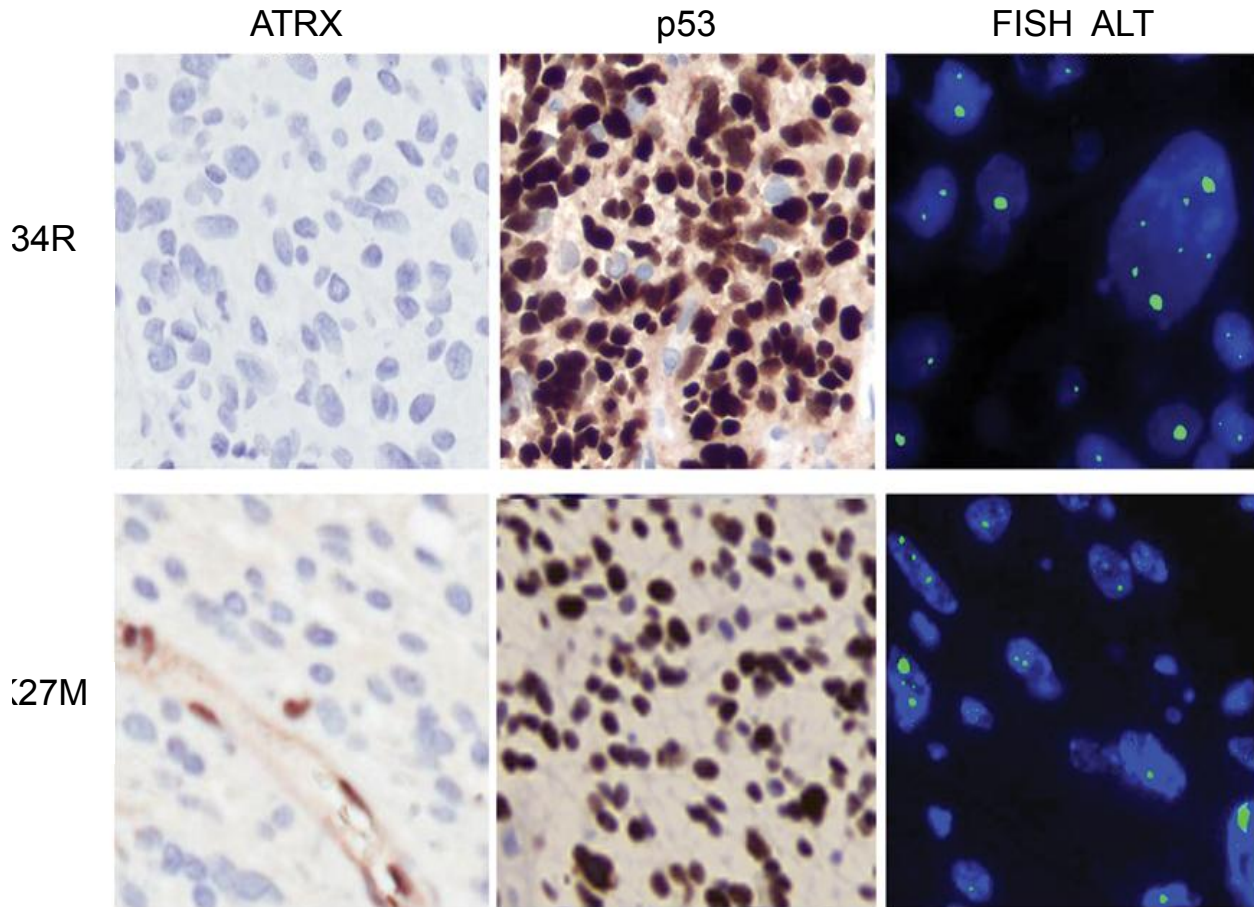


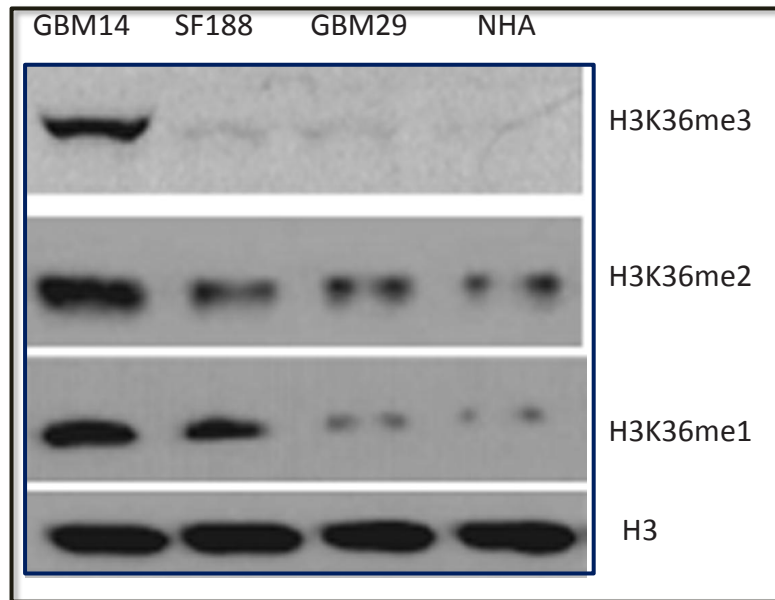
Figure 2b: Comparison of frequently mutated genes indicates that paediatric GBM is distinct from the previously identified molecular subgroups in adult GBM¹⁸. Dark blue indicates mutations in *H3F3A*, *ATRX* and *DAXX* we identified and specific to paediatric GBM; *IDH1* (light blue) mutations are representative of proneural subgroup of adult GBM and not paediatric GBM. Mutations in *PDGFRA* and *TP53* in children had similar rates to adult proneural GBM while *NF1* and *RB1* mutations were more similar to the mesenchymal subgroup (green). Bar graphs showed limited overlap between paediatric and adult GBM. Fisher's t-test used to compare subgroups. *p-value<0.05. NA=not available.



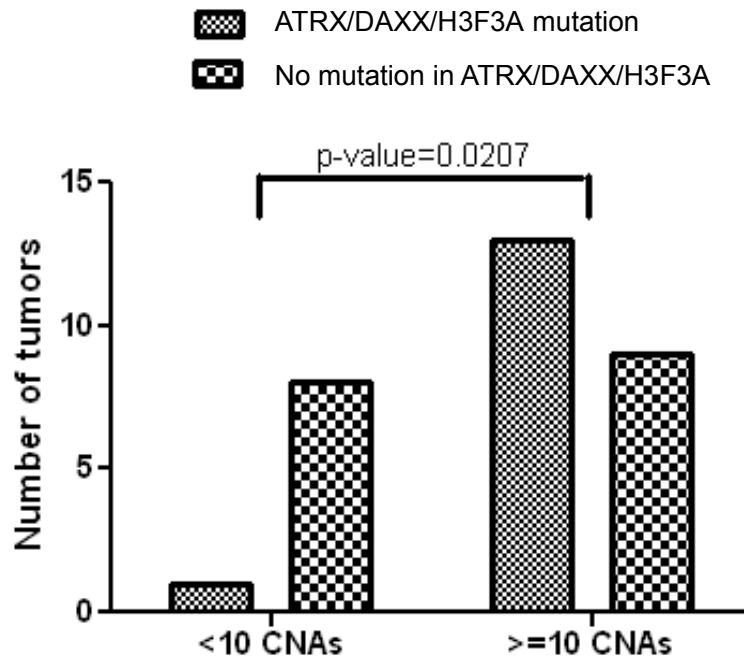
Supplementary Figure 3: Unsupervised clustering of the 100 genes most differentially regulated in 27 paediatric glioblastoma also analyzed by whole exome sequencing show samples with K27M H3.3 and G34V H3.3 mutations to cluster separately from each other and from samples wild type for H3.3.



Supplementary Figure 4: Immunohistochemical staining for ATRX (left panel), P53 (middle panel) of consecutive slides from representative patients with G34V (upper panel) or K27H3.3 (lower panel) show homogeneous loss of ATRX and abnormal P53 across the vast majority of tumour cells. Alternative lengthening of telomeres was present in a large proportion of tumor cells as shown here by fluorescence in situ hybridization (right panel).



Supplementary Figure 5: H3.3 Lysine 36 is methylated in a G34V mutant (GBM 14). Cell lysates from GBM14, (which harbours G34V mutation), GBM29 (wild type for H3.3), a primary paediatric GBM cell line SF188 and normal human astrocytes (all wild type for H3.3) were analyzed with antibodies recognizing the three methylated forms of K36. Even though we cannot differentiate H3.3K36me3 from global H3K36me3 levels, results indicate increased methylation of K36 me1, me2 and me3 in the one sample tested carrying the G34V mutation.



Supplementary Figure 6: Single nucleotide polymorphism (SNP) array profiling reveals differences in copy number aberrations (CNAs) in *ATRX*, *H3F3A* and *TP53* -mutated paediatric glioblastoma. Focal losses or gains comprising genes relevant in paediatric GBM overlapped with previous reports^{3,4,12}. Samples were split into a group with relatively stable genomes (<10 CNAs, bland genome in¹²) and a group with more unstable genomes (>=10 CNAs). Samples with a mutation in at least one of *ATRX*, *H3F3A* and *TP53* were significantly associated with an unstable genome ($p=0.0207$, Fisher's exact test).

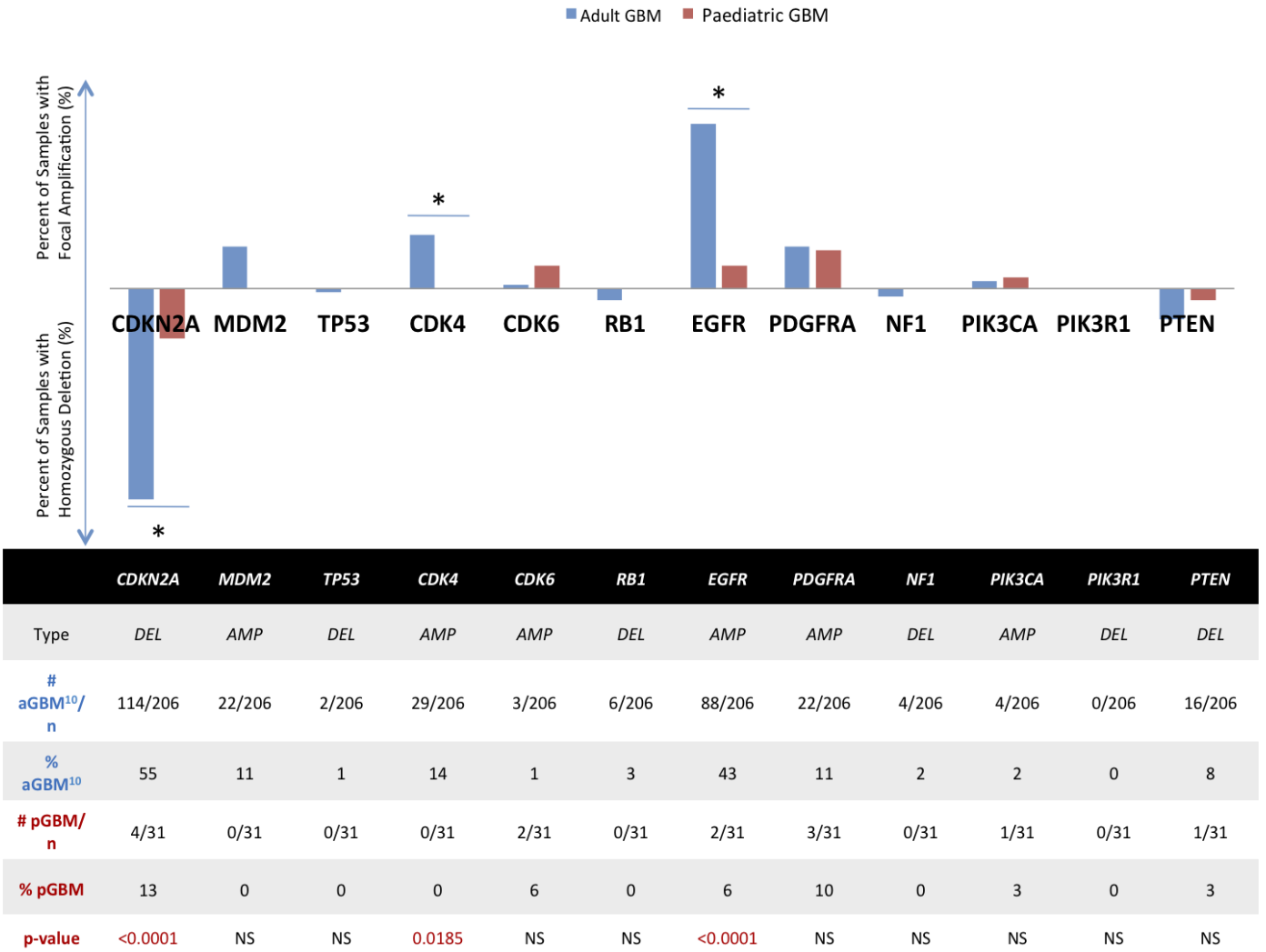


Figure7: Comparison of copy number alterations at important gene loci between paediatric and adult GBM.