

SUPPLEMENTARY TABLE S1. SUMMARY OF MOST SIGNIFICANT ($P < 0.0001$) AND MOST FREQUENT (MORE THAN 10%) LOCI/CHROMOSOMAL REGIONS THAT SHOW GAIN, LOSS, OR LOH EVENTS IN OUR GLIOMA SPECIMEN POPULATION

Region	Region length (bp)	Cytoband	Event	Frequency %	Genes	Gene symbols (most relevant)
chr1:115,840,349-115,876,362	36013	p13.2	CNA Gain	10	1	NGF
chr1:149,922,848-149,988,544	65696	q21.2	LOH	50	2	CEZANNE, OTUD7B
chr1:155,317,904-155,629,055	311151	q22	LOH	52	9	MSTO1, POU5F1, POU5F1P4, RAG1AP1
chr1:155,667,155-155,859,034	191879	q22	LOH	52	9	DAP3, GON4L, MSTO1, MSTO2P, SYT11
chr1:193,213,301-193,217,695	4394	q31.2	CNA Loss	83	1	CDC73
chr1:196,739,898-196,749,828	9930	q31.3	CNA Gain	55	2	CFHR1, CFHR3
chr1:204,489,678-204,513,016	23338	q32.1	CNA Gain	10	2	MDM4, MDMX
chr1:52,443,723-52,721,809	278086	p32.3	LOH	58	5	BTF3L4, KTI12, RAB3B, TXNDC12, ZFYVE9
chr1:65,408,346-65,411,168	2822	p31.3	CNA Loss	47	1	JAK1
chr2:102,600,599-102,690,086	89487	q11.2	LOH	10	2	IL1R1, IL1R2
chr2:135,776,317-135,793,615	17298	q21.3	LOH	57	1	YSK4
chr2:136,069,060-136,554,290	485230	q21.3	LOH	70	7	LCT, R3HDM1, UBXD2, UBXN4, ZRANB3
chr2:191,839,231-191,875,802	36571	q32.2	LOH	10	1	STAT1
chr2:212,523,834-212,545,268	21434	q34	CNA Gain	10	1	ERBB4
chr2:39,165,218-39,371,315	206097	p22.1	LOH	63	4	ARHGEF33, LOC100271715, LOC375196, SOS1
chr2:72,541,761-72,683,915	142154	p13.2	LOH	58	1	EXOC6B
chr2:72,709,625-73,013,622	303997	p13.2	LOH	58	1	EXOC6B
chr2:73,507,166-73,530,188	23022	p13.1	LOH	52	2	AK125051, EGR4
chr2:89,133,378-89,546,704	413326	p11.2	CNA Gain	100	1	AK128525
chr2:89,595,025-90,039,208	444183	p11.2	LOH	55	4	IGKV, IGVK-A2, O1/O11 and JK2, X63945
chr2:97,830,490-97,830,617	127	q11.2	CNA Gain	55	3	ANKRD36, ANKRD36B, UNQ2430
chr2:97,877,087-97,892,459	15372	q11.2	CNA Gain	60	1	ANKRD36
chr3:128,881,127-128,957,157	76030	q21.3	LOH	62	1	CNBP
chr3:129,071,880-129,239,936	168056	q21.3	LOH	63	9	IFT122, MBD4, RPL32P3, SNORA7B, WDR10
chr3:129,277,407-129,297,056	19649	q22.1	LOH	58	1	PLXND1
chr3:162,547,269-162,579,189	31920	q26.1	CNA Gain	63	1	BC073807
chr3:178,887,940-178,890,195	2255	q26.32	CNA Loss	45	1	PIK3CA
chr3:41,279,127-41,279,409	282	p22.1	CNA Gain	33	1	CTNNB1
chr3:50,652,110-50,849,185	197075	p21.2	LOH	73	2	DOCK3, MAPKAPK3
chr3:51,672,135-51,751,052	78917	p21.2	LOH	57	4	GRM2, KIAA0809, RAD54L2, TEX264

(continued)

SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>Region</i>	<i>Region length (bp)</i>	<i>Cytoband</i>	<i>Event</i>	<i>Frequency %</i>	<i>Genes</i>	<i>Gene symbols (most relevant)</i>
chr3:51,813,991-51,874,005	60014	p21.2	LOH	58	3	IQCF1, IQCF3, IQCF4
chr3:96,923,610-97,002,877	79267	q11.2	LOH	73	1	EPHA6
chr4:123,772,260-123,787,008	14748	q27	LOH	35	1	FGF2
chr4:151,527,605-151,711,993	184388	q31.3	LOH	58	1	LRBA
chr4:33,671,209-33,927,782	256573	p15.1	LOH	70	2	AK093205, BC036345
chr4:54,953,877-55,013,933	60056	q12	CNA Gain	15	2	GSX2, PDGFRA
chr4:55,104,887-55,111,661	6774	q12	CNA Gain	23	1	PDGFRA
chr4:55,547,604-55,550,739	3135	q12	CNA Gain	43	1	KIT
chr4:8,723,398-9,224,570	501172	p16.1	LOH	53	2	HMX1, LOC650293
chr4:81,208,868-81,211,146	2278	q21.21	LOH	45	1	FGF5
chr4:81,254,228-81,396,086	141858	q21.21	LOH	63	1	C4orf22
chr5:1,288,678-1,299,683	11005	p15.33	CNA Gain	10	2	TERT, hTERT
chr5:109,760,655-109,965,808	205153	q22.1	LOH	67	1	TMEM232
chr5:130,694,713-131,312,095	617382	q31.1	LOH	55	5	ACSL6, CDC42SE2, FNIP1, KIAA0837, RAPGEF6
chr5:131,322,267-131,325,504	3237	q31.1	LOH	50	2	ACSL6, KIAA0837
chr5:45,355,167-45,400,441	45274	p12	LOH	50	1	HCN1
chr5:82,264,465-82,674,039	409574	q14.2	LOH	12	3	SCARNA18, TMEM167A, XRCC4
chr6:128,395,712-128,603,328	207616	q22.33	CNA Loss/ LOH	47	1	PTPRK
chr6:137,773,942-137,915,296	141354	q23.3	CNA Loss	10	1	OLIG3
chr6:64,857,929-64,963,774	105845	q12	LOH	53	1	EYS
chr7:116,278,598-116,346,115	67517	q31.2	CNA Gain	40	1	MET
chr7:120,001,452-120,112,158	110706	q31.31	LOH	50	1	KCND2
chr7:131,738,693-131,812,436	73743	q32.3	CNA Gain	53	1	PLXNA4
chr7:140,488,112-140,501,245	13133	q34	CNA Gain	37	1	BRAF
chr7:141,088,912-141,093,395	4483	q34	CNA Gain	52	1	LOC100131199
chr7:143,437,619-143,499,302	61683	q35	CNA Gain	50	4	CTAGE6, CTAGE6P, FAM115C, LOC154761
chr7:143,502,088-143,523,707	21619	q35	CNA Gain	50	2	FAM115C, LOC154761
chr7:155,283,922-155,307,419	23497	q36.3	CNA Gain	50	1	CNPY1
chr7:155,534,017-155,556,313	22296	q36.3	CNA Gain	53	1	RBM33
chr7:157,655,357-157,710,847	55490	q36.3	CNA Gain	50	2	BC034557, PTPRN2
chr7:18,228,131-18,252,377	24246	p21.1	LOH	15	1	HDAC9

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SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>Region</i>	<i>Region length (bp)</i>	<i>Cytoband</i>	<i>Event</i>	<i>Frequency %</i>	<i>Genes</i>	<i>Gene symbols (most relevant)</i>
chr7:55,164,378-55,177,039	12661	p11.2	CNA Gain	55	1	EGFR
chr7:69,294,773-69,298,934	4161	q11.22	LOH	60	1	AUTS2
chr7:80,231,843-80,287,180	55337	q21.11	CNA Gain	38	1	CD36
chr7:99,348,344-99,449,452	101108	q22.1	LOH	62	2	CYP3A4, CYP3A43
chr8:100,594,007-100,650,009	56002	q22.2	LOH	67	1	VPS13B
chr8:127,653,938-129,117,940	1464002	q24.21	CNA Gain	12	15	MYC, POU5F1B, POU5F1P1, PVT1, TMEM75
chr8:3,564,838-3,564,979	141	p23.2	CNA Gain	50	1	CSMD1
chr8:35,534,363-35,632,919	98556	p12	LOH	55	1	UNC5D
chr8:39,233,131-39,386,080	152949	p11.22	CNA Loss	62	3	ADAM3A, ADAM5P, tMDC
chr8:42,162,499-42,300,732	138233	p11.21	LOH	25	6	DKK4, IKBKB, IKK-beta, POLB, SLC20A2, VDAC3
chr8:43,028,010-43,253,538	225528	p11.21	LOH	52	2	HGSNAT, POTEA
chr8:67,593,564-67,961,024	367460	q13.1	LOH	55	11	COPS5, LRRC67, PTTG3, SGK3, SNHG6, TCF24
chr8:99,945,650-100,021,792	76142	q22.2	LOH	67	2	OSR2, STK3
chr9:10,080,757-10,082,949	2192	p23	CNA Loss	28	1	PTPRD
chr9:101,907,066-101,915,474	8408	q22.33	CNA Gain	13	1	TGFBF1
chr9:133,696,872-133,706,252	9380	q34.12	CNA Gain	12	1	ABL1
chr9:135,807,481-135,811,210	3729	q34.13	CNA Gain	87	1	TSC1
chr9:21,966,077-22,045,357	79280	p21.3	CNA Loss	42	6	CDKN2A, CDKN2B, CDKN2B-AS1, CDKN2BAS
chr9:5,106,345-5,107,687	1342	p24.1	CNA Loss	32	1	JAK2
chr9:77,124,093-77,189,552	65459	q21.13	CNA Gain	17	1	RORB
chr9:9,905,304-9,937,813	32509	p23	CNA Loss	28	1	PTPRD
chr9:98,227,882-98,235,731	7849	q22.32	CNA Gain	17	1	PTCH1
chr10:22,285,508-22,290,708	5200	p12.31	LOH	57	1	DNAJC1
chr10:22,604,059-22,743,403	139344	p12.2	LOH	62	6	BMI1, COMMD3, COMMD3-BMI1, SPAG6
chr10:47,058,830-47,058,947	117	q11.22	CNA Loss	77	1	ANXA8
chr10:70,252,806-70,278,403	25597	q21.3	CNA Loss	55	1	SLC25A16
chr10:70,364,109-70,379,237	15128	q21.3	CNA Loss	55	1	TET1
chr10:70,538,635-70,568,271	29636	q21.3	CNA Loss	53	1	CCAR1
chr10:74,179,130-74,647,848	468718	q22.1	LOH	68	4	CBARA1, CCDC109A
chr10:74,679,123-74,707,846	28723	q22.1	LOH	63	4	FKSG71, LZP, OIT3, PLA2G12B
chr10:74,806,110-74,832,518	26408	q22.1	LOH	80	1	P4HA1
chr10:74,836,345-74,977,469	141124	q22.1	LOH	80	8	ECD, FAM149B1, HSGT1, NUDT13, P4HA1

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SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>Region</i>	<i>Region length (bp)</i>	<i>Cytoband</i>	<i>Event</i>	<i>Frequency %</i>	<i>Genes</i>	<i>Gene symbols (most relevant)</i>
chr10:75,393,095-75,403,007	9912	q22.2	LOH	60	1	MYOZ1
chr10:76,216,794-76,312,960	96166	q22.2	LOH	53	1	ADK
chr10:89,643,156-89,657,506	14350	q23.31	CNA Loss	23	1	PTEN
chr11:66,834,065-67,156,086	322021	q13.2	LOH	55	12	ADRBK1, ANKRD13D, POLD4, RHOD, SSH3
chr11:85,074,287-85,298,573	224286	q14.1	LOH	50	1	DLG2
chr12:112,008,084-112,122,577	114493	q24.12	LOH	73	2	ATXN2, BRAP
chr12:25,370,571-25,378,581	8010	p12.1	CNA Gain	12	1	KRAS
chr12:44,552,264-44,730,534	178270	q12	LOH	53	2	DKFZp434K2435, TMEM117
chr12:69,215,181-69,223,109	7928	q15	CNA Gain	12	1	MDM2
chr12:79,754,574-79,767,935	13361	q21.2	LOH	50	1	SYT1
chr12:80,063,279-80,084,228	20949	q21.2	LOH	65	1	PAWR
chr12:88,818,490-88,943,151	124661	q21.32	LOH	63	1	KITLG
chr13:20,146,459-20,215,321	68862	q12.11	LOH	52	1	MPHOSPH8
chr13:32,895,437-32,895,818	381	q13.1	CNA Loss	17	1	BRCA2
chr13:48,968,806-48,977,636	8830	q14.2	CNA Loss	25	2	P2RY5, RB1
chr14:106,224,107-106,317,560	93453	q32.33	CNA Gain	98	8	FLJ00382, FLJ00385, IGHD, IGHE, SNC73
chr14:45,348,246-45,726,930	378684	q21.2	LOH	52	13	FAM179B, FANCM, FKBP3, KLHL28, PRPF39
chr14:67,224,058-67,485,693	261635	q23.3	LOH	80	1	GPHN
chr15:28,532,377-28,915,625	383248	q13.1	LOH	73	18	GOLGA8F, GOLGA8G, HERC2, HERC2P9
chr15:28,962,607-29,013,140	50533	q13.1	LOH	58	1	WHAMML2
chr15:42,907,543-42,920,911	13368	q15.2	LOH	58	2	DKFZp686O248, STARD9
chr15:42,983,043-43,013,759	30716	q15.2	LOH	60	2	KIAA1300, STARD9
chr15:44,228,978-44,372,804	143826	q15.3	LOH	50	1	FRMD5
chr15:48,386,383-48,501,733	115350	q21.1	LOH	52	7	CTXN2, JSX, MYEF2, SLC12A1, SLC24A5
chr15:72,150,286-72,483,254	332968	q23	LOH	55	3	GRAMD2, MYO9A, SENP8
chr15:72,599,338-72,693,720	94382	q23	LOH	55	6	BC034424, BRUNOL6, CELF6, HEXA, TMEM202
chr15:76,891,782-76,892,117	335	q24.3	CNA Loss	58	1	SCAPER
chr16:32,180,795-32,291,662	110867	p11.2	LOH	58	3	AK300387, BC042588, TP53TG3b
chr16:32,305,355-32,501,659	196304	p11.2	LOH	58	2	BC041879, DQ578965
chr16:32,699,406-32,793,376	93970	p11.2	LOH	55	2	DQ574674, X69637
chr16:46,973,595-47,001,592	27997	q11.2	LOH	57	1	DNAJA2

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SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>Region</i>	<i>Region length (bp)</i>	<i>Cytoband</i>	<i>Event</i>	<i>Frequency %</i>	<i>Genes</i>	<i>Gene symbols (most relevant)</i>
chr16:67,006,431-67,079,578	73147	q22.1	LOH	72	6	CBFB, CES3, CES4A, CES8, UNQ440, UNQ869
chr16:67,521,501-67,579,786	58285	q22.1	LOH	73	1	FAM65A
chr16:67,923,177-68,036,074	112897	q22.1	LOH	58	9	DPEP2, KCC1, PSKH1, PSMB10, SLC12A4
chr17:18,365,394-18,384,217	18823	p11.2	CNA Loss	53	1	LGALS9C
chr17:37,851,743-37,855,170	3427	q12	LOH	35	2	ERBB2, c-ERBB-2
chr17:40,356,548-40,393,215	36667	q21.2	LOH	38	1	STAT5B
chr17:40,481,586-40,494,460	12874	q21.2	LOH	33	1	STAT3
chr17:41,168,047-41,231,960	63913	q21.31	LOH	22	3	BRCA1, RND2, VAT1
chr17:44,364,192-44,379,313	15121	q21.31	CNA Gain	58	5	ARL17A, ARL17B, ARL17P1, LRRC37A
chr17:58,044,185-58,115,499	71314	q23.1	LOH	65	3	AK097658, DHX40P, DHX40P1
chr17:58,213,981-58,282,621	68640	q23.1	LOH	77	2	CA4, USP32
chr17:58,479,880-58,521,096	41216	q23.2	LOH	82	3	APPBP2, AX746718, C17orf64
chr17:58,658,544-58,721,479	62935	q23.2	LOH	78	1	PPM1D
chr17:62,493,482-62,599,558	106076	q23.3	LOH	55	5	CCDC45, CEP95, DDX5, SMURF2
chr17:62,767,483-62,960,501	193018	q24.1	LOH	50	4	DKFZp313K107, LRRC37A3, PLEKHM1P
chr17:7,553,384-7,583,498	30114	p13.1	CNA Loss	13	3	ATP1B2, TP53, p53
chr20:34,026,177-34,048,140	21963	q11.22	LOH	53	3	C-NAP1, CEP250, GDF5
chr20:34,477,137-34,535,591	58454	q11.23	LOH	60	2	AX746620, PHF20
chr21:34,367,689-34,414,360	46671	q22.11	CNA Gain	10	1	OLIG2
chr21:36,877,378-36,889,274	11896	q22.12	CNA Gain	10	1	RUNX1
chr22:22,382,116-22,384,395	2279	q11.22	CNA Loss	70	2	AK131325
chr22:29,980,726-30,080,694	99968	q12.2	LOH	17	1	NF2
chr22:42,299,725-42,671,487	371762	q13.2	CNA Loss	12	20	CYP2D6, NAGA, SEPT3, SHISA8, SREBF2