SUPPLEMENTARY TABLES

Sample ID#	Sex (M, F)	Age at diagnosis (yr)	Glioma Subtype (original path)	Interval diagnosis to LP (days)	# prior tumor resections	Prior RT (0=no, 1=yes)	Lines of Prior Systemic therapy
Patient--01	M	36	OD, IDH-mutant and 1p/19q-codeleted	5745	3	1	5
Patient--02	M	33	AO, IDH-mutant and 1p/19q-codeleted	3876	2	1	5
Patient--03	M	31	AO, IDH-mutant and 1p/19q-codeleted	2038	3	1	3
Patient--04	M	30	Astrocytoma, IDH-mutant	1911	2	1	2
Patient--05	M	31	AA, IDH-mutant	828	1	1	3
Patient--06	F	38	AA, IDH-mutant	172	2	1	0
Patient--07	F	28	AA, IDH-mutant	2167	4	1	5
Patient--08	M	26	Astrocytoma, IDH-wildtype	1749	4	1	5
Patient--09	M	51	AA, IDH-wildtype	273	2	1	2
Patient--10	M	40	AA, IDH-wildtype	350	1	1	1
Patient--11	M	29	GBM, IDH-mutant	176	1	1	1
Patient--12	M	22	GBM, IDH-wildtype	389	2	1	4
Patient--13	F	26	GBM, IDH-wildtype	392	1	1	1
Patient--14	M	54	GBM, IDH-wildtype	277	1	1	2
Patient--15	M	59	GBM, IDH-wildtype	82	1	1	0
Patient--16	M	23	GBM, IDH-wildtype	334	1	1	2
Patient--17	M	66	GBM, IDH-wildtype	272	2	1	2
Patient--18	M	33	GBM, IDH-wildtype	1014	3	1	3
Patient--19	F	72	GBM, IDH-wildtype	189	1	1	2
Patient--20	M	47	GBM, IDH-wildtype	373	2	1	3
Patient--21	M	42	GBM, IDH-wildtype	466	2	1	3
Patient--22	M	75	GBM, IDH-wildtype	336	1	1	1

Patient--23	M	27	GBM, IDH-wildtype	611	1	1	2
Patient--24	F	60	GBM, IDH-wildtype	502	2	1	3
Patient--25	M	54	GBM, IDH-wildtype	528	1	1	2
Patient--26	M	69	GBM, IDH-wildtype	528	2	1	2
Patient--27	M	41	GBM, IDH-wildtype	460	1	1	3
Patient--28	M	50	GBM, IDH-wildtype	1279	4	1	5
Patient--29	F	77	GBM, IDH-wildtype	62	1	1	1
Patient--30	M	49	GBM, IDH-wildtype	1025	1	1	1
Patient--31	F	43	OD, IDH-mutant and 1p/19q-codeleted	4776	5	1	2
Patient--32	M	47	OD, IDH-mutant and 1p/19q-codeleted	4803	2	1	2
Patient--33	M	38	AA, IDH-mutant	1395	2	1	2
Patient--34	F	31	AA, IDH-mutant	1685	3	1	3
Patient--35	F	61	GBM, IDH-wildtype	671	2	1	3
Patient--36	M	56	GBM, IDH-wildtype	834	2	1	4
Patient--37	F	53	GBM, IDH-wildtype	263	1	1	1
Patient--38	F	64	GBM, IDH-wildtype	163	1	1	1
Patient--39	M	68	GBM, IDH-wildtype	77	1	1	1
Patient--40	M	65	GBM, IDH-wildtype	146	1	1	1
Patient--41	F	34	AA, IDH-wildtype (Spinal cord)	234	1	1	2
Patient--42	M	59	GBM, IDH-wildtype	101	1	1	1
Patient--43	M	56	OD, IDH-mutant and 1p/19q-codeleted	3296	2	1	1
Patient--44	F	64	GBM, IDH-wildtype	801	2	1	3
Patient--45	M	42	GBM, IDH-wildtype	485	1	1	4
Patient--46	F	67	GBM, IDH-wildtype	487	1	1	1
Patient--47	F	27	Astrocytoma, IDH-mutant	2969	2	1	3
Patient--48	M	57	GBM, IDH-wildtype	279	1	1	1

Patient--49	M	41	AA, IDH-wildtype	379	1	1	1
Patient--50	M	32	OD, IDH-mutant and 1p/19q-codeleted	7351	2	1	2
Patient--51	F	53	AA, IDH-mutant	548	2	1	3
Patient--52	F	45	GBM, IDH-wildtype	296	1	1	2
Patient--53	M	31	Astrocytoma, IDH-mutant	2195	3	0	2
Patient--54	F	68	GBM, IDH-mutant	621	1	1	1
Patient--55	M	78	GBM, IDH-wildtype	102	1	1	1
Patient--56	F	55	Astrocytoma, NOS	3738	1	1	1
Patient--57	M	71	GBM, IDH-wildtype	1606	2	1	2
Patient--58	M	65	GBM, IDH-wildtype	165	1	1	1
Patient--59	F	38	OD, NOS	3032	2	1	4
Patient--60	F	45	AO, IDH-mutant and 1p/19q-codeleted	1710	1	1	3
Patient--61	M	62	GBM, IDH-wildtype	1020	2	1	5
Patient--62	F	39	OD, NOS	9122	2	1	1
Patient--63	F	44	GBM, IDH-wildtype	263	1	1	2
Patient--64	M	51	AA, IDH-wildtype	1076	1	1	2
Patient--65	F	57	AA, IDH-wildtype	824	2	1	3
Patient--66	F	57	AA, IDH-wildtype	436	2	1	3
Patient--67	M	64	GBM, IDH-wildtype	914	1	1	5
Patient--68	M	59	GBM, IDH-wildtype	383	2	1	3
Patient--69	M	54	GBM, IDH-wildtype	209	1	1	0
Patient--70	M	90	GBM, IDH-wildtype	296	1	1	2
Patient--71	F	72	AA, IDH-wildtype	2982	3	1	4
Patient--72	F	44	AA, IDH-mutant	1052	1	1	2
Patient--73	M	69	GBM, IDH-wildtype	112	1	1	1
Patient--74	F	22	AA, IDH-wildtype	79	1	1	1

Patient--75	M	47	GBM, IDH-wildtype	204	3	1	1
Patient--76	M	35	AA, IDH-mutant	1088	1	1	1
Patient--77	F	44	GBM, IDH-wildtype	123	1	1	2
Patient--78	F	43	AA, IDH-mutant	401	1	1	1
Patient--79	F	79	AA, IDH-wildtype	591	3	1	2
Patient--80	M	39	GBM, IDH-wildtype	410	1	1	3
Patient--81	M	74	AA, IDH-wildtype	510	1	1	1
Patient--82	M	35	AA, IDH-mutant	63	1	1	1
Patient--83	M	44	AO, IDH-mutant and 1p/19q-codeleted	7669	4	1	3
Patient--84	M	26	AA, IDH-mutant	2116	1	1	0
Patient--85	M	29	OD, IDH-mutant and 1p/19q-codeleted	4406	5	1	1

Supplementary Information Table 1. Demographic data for all patients included in our glioma cohort (N=85). OD=oligodendroglioma; AO=anaplastic oligodendroglioma; AA=anaplastic astrocytoma; GBM=glioblastoma

Sample ID#	Vital Status (0=alive, 1=dead)	Survival from CSF collection to Death/LFU	Tumor volume (initial Preop) (cm3)	Tumor volume (initial Postop) (cm3)	% extent of resection	Tumor burden @ LP (mm2)	IDH status	CSF ctDNA status
02	0	774	28.6	0	100%	1371.6	mutant	positive
03	1	812	113	21.9	81%	0.0	mutant	positive
05	1	192	73.5	58.3	21%	10322.6	mutant	positive
06	0	781	11.5	1.5	87%	730.8	mutant	positive
07	1	141	90.9	0	100%	1728.5	mutant	positive
10	1	71	1.4	0	100%	404.2	WT	positive
11	1	945	30.7	3.8	88%	676.9	mutant	positive
12	1	56	25.7	10.5	59%	870.0	WT	positive
15	1	255	68	67.3	1%	3648.9	WT	positive
16	1	64	7.4	1.3	82%	498.5	WT	positive
17	1	47	69.4	3.1	96%	4031.8	WT	positive
18	1	311	3	0	100%	452.1	WT	positive
19	1	115	26.2	17	35%	1817.1	WT	positive
20	1	26	104	9.1	91%	1318.1	WT	positive
21	1	30	15.6	0.4	97%	8001.1	WT	positive
22	1	60	98.8	19.3	80%	1928.08	WT	positive
23	1	555	53.3	17.9	66%	822.3	WT	positive
24	1	17	19.7	0	100%	649.2	WT	positive
25	1	44	65	6.4	90%	2511.0	WT	positive
26	1	80	44.8	7.5	83%	1238.3	WT	positive
27	1	115	3.1	0	100%	2527.8	WT	positive
28	1	102	7.3	0	100%	1582.7	WT	positive
29	1	150	79.3	4.2	95%	2306.4	WT	positive
30	1	119	0.9	0	100%	2831.8	WT	positive

33	1	96	59.7	0	100%	932.5	mutant	positive
35	1	26	45.8	7.6	83%	2447	WT	positive
36	1	22	89.4	3.5	96%	982.6	WT	positive
37	1	14	0.5	0	100%	104.9	WT	positive
38	1	131	69.8	0.8	99%	369.9	WT	positive
39	1	16	85.9	45.9	47%	6941.8	WT	positive
40	1	21	84.4	14.8	82%	1825.2	WT	positive
41	1	235	5	4.8	4%	0.0	WT	positive
42	1	30	57.3	32.3	44%	2564.6	WT	positive
43	0	1130	23.9	20	16%	0.0	mutant	negative
44	1	938	7.9	0	100%	250.9	WT	negative
45	1	377	20	0	100%	284.0	WT	negative
46	0	1265	104	0	100%	992.6	WT	negative
49	1	613	90.7	90.1	1%	4501.8	WT	negative
52	1	169	25.7	25.4	1%	1339.9	WT	negative
53	0	655	9.9	0	100%	1256.6	mutant	negative
54	0	954	82.8	0	100%	192.2	mutant	negative
55	1	65	67.1	12.7	81%	1566.7	WT	negative
58	1	219	44.8	33.2	26%	588.1	WT	negative
60	0	850	77.2	0	100%	1019.5	mutant	negative
61	1	263	20.4	0	100%	184.1	WT	negative
63	1	51	20.3	0	100%	341.4	WT	negative
64	1	101	5.1	0	100%	1128.1	WT	negative
65	1	194	36.9	36.5	1%	1888.1	WT	negative
66	1	216	24.5	24.3	1%	1392.9	WT	negative
67	1	49	6.1	5.6	8%	915.8	WT	negative
68	1	313	2.8	0	100%	0.0	WT	negative
69	1	256	7.3	0	100%	202.0	WT	negative

70	1	328	17.5	0	100%	288.0	WT	negative
73	1	496	11.8	0	100%	0.0	WT	negative
74	1	619	7.39	7.39	0%	370.6	WT	negative
75	0	734	25.4	22.9	10%	0.0	WT	negative
76	0	717	40.1	13.9	65%	413.4	mutant	negative
77	1	430	40.2	3.6	91%	487.2	WT	negative
78	0	630	77	0	100%	373.4	mutant	negative
80	1	289	14.6	14.4	1%	950.2	WT	negative
81	0	255	587	575.8	2%	0.0	WT	negative
82	0	597	81.2	0	100%	443.9	mutant	negative
84	0	1178	61.9	0	100%	0.0	mutant	negative

Supplementary Information Table 2. Source data for multivariate model for overall survival (see Extended Data Fig. 5) from the time of CSF collection. LP=Lumbar Puncture CSF=Cerebral Spinal Fluid.

Patient #	CSF ctDNA	Plasma ctDNA	Plasma coverage
Patient-02	Positive	Negative	1070x
Patient-21	Positive	Negative	1253x
Patient-28	Positive	Negative	1010x
Patient-33	Positive	Negative	957x
Patient-37	Positive	Negative	1228x
Patient-38	Positive	Negative	930x
Patient-34	Positive	**Positive**	1047x
Patient-01	Positive	Negative	908x
Patient-03	Positive	Negative	294x
Patient-05	Positive	Negative	1094x
Patient-06	Positive	Negative	1227x
Patient-10	Positive	Negative	1005x
Patient-11	Positive	**Positive**	857x
Patient-20	Positive	Negative	1557x
Patient-22	Positive	Negative	743x
Patient-23	Positive	**Positive**	1388x
Patient-25	Positive	Negative	650x
Patient-26	Positive	Negative	1017x
Patient-40	Positive	Negative	1253x

Supplementary Information Table 3. Comparison of CSF and plasma cfDNA for 19 patients. 211/896 of the mutations previously detected in CSF ctDNA from these 19 patients were contained within the targets of a custom high-sensitivity capture-based plasma NGS assay. cfDNA samples were sequenced to an average raw sequence coverage of >18,000x (range 9676x-32194x raw sequencing coverage not shown) and collapsed using unique molecular indexes (UMIs) to create consensus sequences representing individual DNA molecules. The average unique sequence coverage after collapsing is shown. Mutations from the CSF were considered to be present in the plasma if they were detected in two or more independent cfDNA molecules, or approximately 0.2% mutant allele fraction.

Sample #	Chr	Pos	Ref	Alt	Gene	cDNAchange	AAchange	Total Depth(DP)	Variant Allele Depth(AD)	**PLASMA** Variant Allele Frequency(VAF)	**CSF** Variant Allele Frequency(VAF)
Patient-11	17	7578271	T	C	TP53	c.578A>G	p.H193R	896	4	0.004	0.983
Patient-23	17	7578406	C	T	TP53	c.524G>A	p.R175H	828	5	0.005	0.493
Patient-23	17	7574003	G	A	TP53	c.1024C>T	p.R342*	844	3	0.006	0.444
Patient-34	5	112155017	G	A	APC	c.1288G>A	p.G430S	1226	4	0.003	0.137
Patient-34	1	27101201	G	A	ARID1A	c.4483G>A	p.G1495S	913	5	0.005	0.134
Patient-34	1	27097808	C	T	ARID1A	c.3397C>T	p.P1133S	833	5	0.006	0.165
Patient-34	X	66766250	G	A	AR	c.1262G>A	p.G421E	830	4	0.004	0.126
Patient-34	X	66765436	C	T	AR	c.448C>T	p.P150S	1400	4	0.006	0.159
Patient-34	11	108137982	G	A	ATM	c.2551G>A	p.D851N	1259	6	0.005	0.058
Patient-34	13	32914196	G	A	BRCA2	c.5704G>A	p.D1902N	1192	3	0.007	0.100
Patient-34	16	3786740	G	A	CREBBP	c.4471C>T	p.Q1491*	1146	3	0.003	0.041
Patient-34	14	38061670	C	T	FOXA1	c.319G>A	p.A107T	1266	2	0.002	0.143
Patient-34	14	38061768	C	T	FOXA1	c.221G>A	p.G74E	1216	16	0.011	0.405
Patient-34	14	38061812	C	T	FOXA1	c.177G>A	p.M59I	1220	2	0.002	0.048
Patient-34	3	138665527	C	T	FOXL2	c.38G>A	p.G13E	1078	3	0.003	0.091
Patient-34	2	209113112	C	T	IDH1	c.395G>A	p.R132H	591	3	0.011	0.448
Patient-34	12	25378670	G	A	KRAS	c.328C>T	p.P110S	1011	2	0.003	0.117
Patient-34	15	66774162	G	A	MAP2K1	c.638G>A	p.G213E	1208	5	0.005	0.101
Patient-34	3	37038114	G	A	MLH1	c.121G>A	p.D41N	658	5	0.008	0.431
Patient-34	2	48026579	C	T	MSH6	c.1457C>T	p.T486I	1153	4	0.003	0.096
Patient-34	8	128751158	C	T	MYC	c.695C>T	p.S232F	1054	14	0.020	0.263
Patient-34	17	29654667	G	A	NF1	c.5419G>A	p.G1807S	1142	3	0.003	0.051
Patient-34	1	115256578	C	T	NRAS	c.133G>A	p.V45I	919	2	0.002	0.045
Patient-34	1	156845911	G	A	NTRK1	c.1541G>A	p.W514*	1597	9	0.007	0.151
Patient-34	20	9561565	C	T	PAK7	c.217G>A	p.G73R	1120	4	0.003	0.145
Patient-34	13	48941735	G	A	RB1	c.1045G>A	p.D349N	896	11	0.014	0.463
Patient-34	18	48575056	G	A	SMAD4	c.250G>A	p.V84M	897	2	0.002	0.126
Patient-34	5	1295243	G	A	TERT_			599	3	0.010	0.300
Patient-34	17	7578475	G	T	TP53	c.455C>A	p.P152Q	1066	10	0.008	0.453
Patient-34	17	7577538	C	T	TP53	c.743G>A	p.R248Q	871	7	0.012	0.478
Patient-34	9	135772593	C	T	TSC1	c.2953G>A	p.A985T	1002	2	0.002	0.041
Patient-34	16	2098680	G	A	TSC2	c.64G>A	p.G22R	952	2	0.002	0.114
Patient-34	16	2122981	A	C	TSC2	c.2352A>C	p.K784N	1222	18	0.011	0.476
Patient-34	3	10183848	G	A	VHL	c.317G>A	p.G106D	675	20	0.022	0.433
Patient-34	3	10191515	G	A	VHL	c.508G>A	p.V170I	1179	2	0.002	0.058

Supplementary Information Table 4. Sequence variants detected in plasma cfDNA using a high-sensitivity capture-based NGS assay. Allele counts represent individual distinct cfDNA molecules after UMI-based collapsing.

Supplementary Information Table 5. Matched pair analysis complete mutation list (see excel file for table). SNVs detected in tumor and CSF from 36 glioma patients with positive CSF ctDNA and available tumor tissue for comparison.