

**Figure S1** Validation of the angiogenesis-related lncRNA signature. (A-D) Validation of the angiogenesis-related lncRNA signature in the external validation set. AUC, area under the curve; lncRNAs, long noncoding RNAs; ROC, receiver operating characteristic.



**Figure S2** The relationship between the lncRNA signature and the immune microenvironment of GBM. (A-C) The results analyzed in the "immunedeconv" package showed significant differences in macrophage M2, uncharacterized cells, and macrophage/monocyte cells between the high- and low-risk groups (P<0.05). (D) Online database xCell analysis showed the difference in immune/nonimmune cells between the high- and low-risk groups (P<0.05). (E) The leukocyte fraction was significantly higher in the high-risk group than in the low-risk group (P<0.05). \*, P<0.05; \*\*, P<0.01, aDC, activated DCs; CLP, common lymphoid progenitor; CMP, common myeloid progenitors; cDC, conventional dendritic cell; DC, dendritic cell; GBM, glioblastoma multiforme; GMP, granulocyte-monocyte progenitor; HSC, hepatic stellate cell; iDC, immature dendritic cells; lncRNAs, long noncoding RNAs; ly, lymphatic; MEP, megakaryocyte erythroid progenitor; MPP, multipotent blood progenitors; MSC, mesenchymal stem cell; mv, microvascular; NK, natural killer; NKT, natural killer T; ns, no significance; pDC, plasmacytoid dendritic cell; Tcm, central memory T cell; Tem, effector memory T cell; Tgd, γ/δ T cell; Treg, T regulator cell.

Table S1	The cli	nical infor	mation of	f TCGA-	GBM cohorts
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ID	fustat	futime	Vital	Age, year	Gender	Grade
TCGA-02-0047	1	448	Dead	78	Male	G4
TCGA-02-0055	1	76	Dead	62	Female	G4
TCGA-02-2483	0	466	Alive	43	Male	G4
TCGA-02-2485	0	470	Alive	53	Male	G4
TCGA-02-2486	1	618	Dead	64	Male	G4
TCGA-06-0125	1	1448	Dead	63	Female	G4
TCGA-06-0129	1	394	Dead	30 54	Male	G4 G4
TCGA-06-0132	1	771	Dead	49	Male	G4
TCGA-06-0138	1	737	Dead	43	Male	G4
TCGA-06-0139	1	362	NA	40	Male	NA
TCGA-06-0141	1	313	Dead	62	Male	G4
TCGA-06-0152	1	375	Dead	NA	NA	NA
TCGA-06-0156	1	178	Dead	57	Male	G4
TCGA-06-0157	1	97	Dead	63	Female	G4
TCGA-06-0158	1	329	Dead	73	Male	G4
TCGA-06-0171	1	398	Dead	59 NA	Female NA	G4 NA
TCGA-06-0174	1	98	Dead	54	Male	G4
TCGA-06-0178	1	2681	Dead	38	Male	G4
TCGA-06-0184	1	2126	Dead	63	Male	G4
TCGA-06-0187	1	828	Dead	69	Male	G4
TCGA-06-0190	1	317	Dead	NA	NA	NA
TCGA-06-0210	1	225	Dead	NA	NA	NA
TCGA-06-0211	1	360	Dead	NA 67	NA	NA
TCGA-06-0219	1	603	Dead	NA	NA	NA
TCGA-06-0238	1	405	Dead	46	Male	G4
TCGA-06-0644	1	384	Dead	71	Male	G4
TCGA-06-0645	1	175	Dead	55	Female	G4
TCGA-06-0646	1	175	Dead	60	Male	G4
TCGA-06-0649	1	64	Dead	73	Female	G4
TCGA-06-0543	1	432	Dead	53	Male	G4
TCGA-06-0743	1	1426	Dead	66	Male	G4 G4
TCGA-06-0745	1	239	Dead	59	Male	G4
TCGA-06-0747	1	82	Dead	53	Male	G4
TCGA-06-0749	1	82	Dead	50	Male	G4
TCGA-06-0750	1	28	Dead	43	Male	G4
TCGA-06-0878	0	218	Alive	74	Male	G4
TCGA-06-0882	1	632	Dead	30	Male	G4
TCGA-06-2557	1	33	Dead	76	Male	G4 G4
TCGA-06-2558	1	380	Dead	75	Female	G4
TCGA-06-2559	1	150	Dead	83	Male	G4
TCGA-06-2561	1	537	Dead	53	Female	G4
TCGA-06-2562	1	382	Dead	81	Male	G4
TCGA-06-2563	0	932	Alive	72	Female	G4
TCGA-06-2564	0	181	Alive	50	Male	G4
TCGA-06-2565	1 1	506 133	Dead	59 65	wale	G4
TCGA-06-2569	0	13	Alive	24	Female	G4
TCGA-06-2570	0	958	Alive	21	Female	G4
TCGA-06-5408	1	357	Dead	54	Female	G4
TCGA-06-5410	1	108	Dead	72	Female	G4
TCGA-06-5411	1	254	Dead	51	Male	G4
TCGA-06-5412	1	138	Dead	78	Female	G4
TCGA-06-5413	0	268	Alive	67	Male	G4
TCGA-06-5414	0	273	Alive	61 23	Male	G4
TCGA-06-5417	0	155	Alive	45	Female	G4
TCGA-06-5418	1	83	Dead	75	Female	G4
TCGA-06-5856	1	114	Dead	58	Male	G4
TCGA-06-5858	0	187	Alive	45	Female	G4
TCGA-06-5859	0	139	Alive	63	Male	G4
TCGA-08-0386	1	548	Dead	74	Male	G4
TCGA-12-0618	1	448	Dead	36	Female	G4
TCGA-12-0619	1	1062	Dead	49 60	Male	G4 G4
TCGA-12-0821	1	323	Dead	62	Male	G4
TCGA-12-1597	1	675	Dead	62	Female	G4
TCGA-12-3650	1	333	Dead	46	Male	G4
TCGA-12-3652	1	1062	Dead	60	Male	G4
TCGA-12-3653	1	442	Dead	34	Female	G4
TCGA-12-5295	1	454	Dead	60	Female	G4
TCGA-12-5299	1	98	Dead	56	Female	G4
TCGA-14-0781	1	29	Dead	49	Male	G4
TCGA-14-0787	1	68	Dead	69	Male	G4
TCGA-14-0789	1	342	Dead	54	Male	G4
TCGA-14-0790	1	419	Dead	64	Female	G4
TCGA-14-0817	1	164	Dead	69	Female	G4
TCGA-14-0871	1	880	Dead	74	Female	G4
TCGA-14-1034	1	485	Dead	NA	NA	NA
TCGA-14-1402	1	975	Dead	NA 59	NA	NA C4
TCGA-14-1823	1	543	Dead	58	Female	G4
TCGA-14-1829	0	232	Alive	57	Male	G4 G4
TCGA-14-2554	1	532	Dead	52	Female	G4
TCGA-15-0742	1	419	Dead	65	Male	G4
TCGA-15-1444	1	1537	Dead	21	Male	G4
TCGA-16-0846	1	119	Dead	85	Male	G4
TCGA-16-1045	1	883	Dead	49	Female	G4
TCGA-19-0957	1	666	Dead	NA	NA	NA
TCGA-19-1389	1	141	Dead	NA	NA	NA C4
TCGA-19-1390	1	385	Dead	48	Male	G4 G4
TCGA-19-2619	0	294	Alive	55	Female	G4
TCGA-19-2620	1	148	Dead	70	Male	G4
TCGA-19-2624	1	5	Dead	51	Male	G4
TCGA-19-2625	1	124	Dead	76	Female	G4
TCGA-19-2629	1	737	Dead	60	Male	G4
TCGA-19-4065	U 1	214 455	Alive	36	Male	G4
TCGA-26-1442	0	953	Alive	43	Male	G4
TCGA-26-5132	0	286	Alive	74	Male	G4
TCGA-26-5133	0	452	Alive	59	Male	G4
TCGA-26-5134	0	167	Alive	74	Male	G4
TCGA-26-5135	1	270	Dead	72	Female	G4
TCGA-26-5136	1 0	577 10	Dead	78 65	remale Female	G4
TCGA-20-5139	U 1	48 154	Alive	57	n emale Male	G4 G4
TCGA-27-1831	1	505	Dead	66	Male	G4
TCGA-27-1832	1	300	Dead	59	Female	G4
TCGA-27-1834	1	1233	Dead	56	Male	G4
TCGA-27-1835	1	648	Dead	53	Female	G4
TCGA-27-1837	1	427	Dead	36	Male	G4
TCGA-27-2519	1	550	Dead	48	Male	G4
TCGA-27-2521	1 1	510 489	Dead	34 63	iviale Male	G4
TCGA-27-2523	' 1	409 231	Dead	56	Male	G4
TCGA-27-2526	1	87	Dead	79	Female	G4
TCGA-27-2528	1	480	Dead	62	Male	G4
TCGA-28-1747	1	77	Dead	44	Male	G4
TCGA-28-1753	0	37	Alive	53	Male	G4
TCGA-28-2509	0	145	Alive	77	Female -	G4
TCGA-28-2513	0	222	Alive	69	Female	G4
TCGA-28-5204	U 1	454	Alive	45 72	wale	G4
TCGA-28-5207	1	343	Dead	71	Male	G4
TCGA-28-5208	1	544	Dead	52	Male	G4
TCGA-28-5209	0	442	Alive	66	Female	G4
TCGA-28-5215	1	335	Dead	62	Female	G4
TCGA-28-5216	0	415	Alive	52	Male	G4
TCGA-28-5218	1	157	Dead	63	Male	G4
TCGA-28-5220	1	388	Dead	67	Male	G4
TCGA 22-1970	1	468	Dead	59	Male	G4
TCGA-32-1980	1	36 140	Dead	72 76	Male Female	G4
TCGA-32-1982	ı 1	142 485	Dead	62	n ernale Male	G4
TCGA-32-2616	1	224	Dead	48	Female	G4
TCGA-32-2632	1	269	Dead	80	Male	G4
TCGA-32-2634	0	693	Alive	82	Male	G4
TCGA-32-2638	1	766	Dead	67	Male	G4
TCGA-32-4213	0	604	Alive	47	Female	G4
TCGA-32-5222	1	585	Dead	66	Male	G4
TCGA-41-2571	1	26 40e	Dead	89	Male	G4
TCGA-41-3915	' 1	400 360	Dead	48	Male	G4
TCGA-41-4097	' 1	6	Dead	63	Female	G4
TCGA-41-5651	1	460	Dead	59	Female	G4
TCGA-76-4925	1	146	Dead	76	Male	G4
TCGA-76-4926	1	138	Dead	68	Male	G4
TCGA-76-4927	1	535	Dead	58	Male	G4
TCGA-76-4928	1 1	94 111	Dead	ช5 76	remale Female	G4 G4
			-040		Smalt	JT

TCGA-76-4931	1	279	Dead	70	Female	G4	WT	Unmethylated	80	Classical	1.213032	High	Training	Treated	Treated
TCGA-76-4932	1	1458	Dead	50	Female	G4	WT	Methylated	80	Proneural	0.669549	Low	Training	Treated	Treated

GBM, glioblastoma multiforme; G-CIMP, glioma CpG island methylator phenotype; NA, not available; TCGA, The Cancer Genome Atlas; WT, wild type; IDH, isocitrate dehydrogenase.

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Table S2 The clinical information of CGGA cohorts

CGGA_ID	futime	fustat	Grade	Gender	Age, year	Radio_status	Chemo_status	IDH_mutation_status	1p19q_codeletion_status	MGMTp_methylation_status	riskScore	Risk
CGGA_139	694	1	WHO IV	Male	59	1	1	Mutant	Non-codel	Un-methylated	13700.63	High
CGGA_1017	768	1	WHO IV	Female	29	1	0	Wild type	Non-codel	Un-methylated	11912.59	High
CGGA_1420	364	0		Fomalo	43	1	1	Wild type	Non-codel	Methylated	4484.713	High
CGGA_1571	41Z 834	1		Male	43 65	1	1	Wild type	Non-codel	NA	4224.402	High
CGGA 1769	1854	0	WHO IV	Female	00 49	n N	1	Wild type	Non-codel	Methylated	1029 878	High
CGGA 1750	250	1	WHO IV	Female	49 52	1	1	Wild type	Non-codel	Methylated	418 5919	High
CGGA 1501	222	1	WHO IV	Male	58	1	1	NA	Non-codel	Methylated	132.9349	High
CGGA_1452	468	1	WHO IV	Male	53	1	1	Wild type	Non-codel	Methylated	72.22825	High
 CGGA_1840	1179	0	WHO IV	Female	58	1	1	Wild type	Non-codel	Methylated	69.06815	High
CGGA_1534	27	1	WHO IV	Female	58	0	0	Mutant	Non-codel	Un-methylated	63.15978	High
CGGA_1500	108	1	WHO IV	Female	45	1	1	Wild type	Non-codel	Un-methylated	57.82887	High
CGGA_1740	363	1	WHO IV	Female	50	0	0	Wild type	Non-codel	Methylated	47.16943	High
CGGA_1735	813	1	WHO IV	Male	54	1	1	Wild type	Non-codel	Un-methylated	41.02415	High
CGGA_P15	723	1	WHO IV	Male	49	1	1	NA	Non-codel	NA	38.15733	High
CGGA 1870	1556	0	WHO IV	Male	62	1	1	Mutant	Codel	Un-methylated	28,15274	High
CGGA P22	406	1	WHO IV	Male	62	1	1	Wild type	Non-codel	NA	20.47522	Hiah
CGGA 1041	3593	0	WHO IV	Male	58	1	1	Wild type	Non-codel	Un-methylated	20.21255	High
CGGA_1539	2462	0	WHO IV	Male	61	1	1	Mutant	Non-codel	Methylated	16.24608	High
CGGA_1690	592	1	WHO IV	Male	60	1	1	Wild type	Non-codel	Un-methylated	13.95259	High
CGGA_1472	1025	1	WHO IV	Male	34	0	0	NA	Non-codel	Methylated	13.74482	High
CGGA_1548	1054	1	WHO IV	Male	53	1	1	Wild type	Non-codel	Un-methylated	12.62223	High
CGGA_1326	322	1	WHO IV	Male	45	1	0	Mutant	Non-codel	Un-methylated	10.999	High
CGGA_1380	291	1	WHO IV	Male	46	1	1	Wild type	Non-codel	Methylated	9.251914	High
CGGA_P100	268	1	WHO IV	Male	67	NA	NA	Wild type	Non-codel	NA	8.716854	High
CGGA_1476	299	1	WHO IV	Female	53	0	0	Wild type	Non-codel	Methylated	8.392699	High
CGGA_1698	388	1	WHO IV	Female	55	0	0	Wild type	Non-codel	Methylated	8.193378	High
CGGA_1371	2791	0	WHO IV	Male	68	1	1	Wild type	Non-codel	Methylated	7.660351	High
CGGA_1727	1980	0	WHO IV	Male	48	1	1	Mutant	Non-codel	Un-methylated	7.116809	High
CGGA_1749	401	1	WHO IV	Female	44	1	1	Wild type	Non-codel	Un-methylated	7.100204	High
CGGA_1713	332	1	WHO IV	Male	62	1	1	Wild type	Non-codel	Methylated	7.097641	High
CGGA_1529	583	1	WHO IV	Male	63	NA	NA	Wild type	Non-codel	Un-methylated	6.668938	High
CGGA_1826	44	1	WHO IV	Female	70	0	0	Wild type	Non-codel	Methylated	5.82109	High
CGGA_1444	378	1	WHO IV	Female	68	1	1	Wild type	Non-codel	Methylated	5.733422	High
CGGA_1382	204 101	1		Fomalo	57	1	1	Wild type	Non-codel	Methylated	5.023735	High
CGGA 1521	205	1	WHO IV	Female	47 63	1	1	Wild type	Non-codel	Methylated	5 17/618	High
CGGA 500	623	י 1	WHO IV	Male	38	י 1	ı ۱	Wild type		Un-methylated	4.99 <u>4</u> 070	High
CGGA 1559	603	1	WHO IV	Male	63	, N	1	Mutant	Codel	Methylated	4.8888849	Hiah
CGGA 1728	917	1	WHO IV	Male	45	1	1	Mutant	Non-codel	Un-methylated	4.797313	Hiah
CGGA 1595	2363	0	WHO IV	Female	34	1	1	NA	Non-codel	Un-methylated	4.706975	Hiah
CGGA_1103	585	- 1	WHO IV	Female	35	1	1	Mutant	Non-codel	Methylated	4.328651	High
CGGA_1172	3131	0	WHO IV	Female	36	1	1	Mutant	Non-codel	Methylated	4.297041	High
CGGA_1256	2557	0	WHO IV	Female	52	1	1	NA	Non-codel	Methylated	4.012705	High
CGGA_1135	1244	1	WHO IV	Male	40	1	1	Wild type	Non-codel	Un-methylated	3.93855	High
CGGA_1433	394	1	WHO IV	Female	72	1	1	Wild type	Non-codel	Un-methylated	3.805769	High
CGGA_1596	205	1	WHO IV	Male	63	1	1	Wild type	Non-codel	Methylated	3.545952	High
CGGA_1812	780	1	WHO IV	Male	65	NA	NA	Wild type	Non-codel	Un-methylated	3.488737	High
CGGA_1807	247	1	WHO IV	Female	65	NA	NA	Wild type	Non-codel	Methylated	3.417393	High
CGGA_1694	624	1	WHO IV	Male	55	1	1	Wild type	Non-codel	Un-methylated	3.370004	High
CGGA_831	546	1	WHO IV	Female	55	1	1	Wild type	Non-codel	Un-methylated	3.303636	High
CGGA_1564	190	1	WHO IV	Male	48	1	1	Wild type	Non-codel	Un-methylated	3.265481	High
CGGA_1392	473	1	WHO IV	Male	62	1	1	Wild type	Non-codel	Un-methylated	3.045552	High
CGGA_1138	411	1	WHO IV	Male	54	1	1	Wild type	Non-codel	Un-methylated	2.848698	High
CGGA_1626	696	1	WHO IV	Male	66	1	1	Wild type	Non-codel	Un-methylated	2.770323	High
CGGA_1744	1936	0	WHO IV	Male	51	1	1	NA Mild to us a	Non-codel	Methylated	2.629381	High
CGGA_1546	223	1		Fomalo	50	1	1		Non-codel	Un-methylated	2.525209	High
CGGA 1543	723	1		Male	57	1	0	Mutant	Non-codel		2.402400	High
CGGA 1612	723	1	WHO IV	Male	68	1	1	Wild type	Non-codel		2.370904	High
CGGA 1075	398	1	WHO IV	Male	72	1	1	Wild type	Non-codel	Un-methylated	2 159129	High
CGGA 1601	710	1	WHO IV	Male	66	1	1	Wild type	Non-codel	Methylated	2.100128	High
CGGA 1391	426	0	WHO IV	Male	62	1	1	Wild type	Non-codel	Un-methylated	2.08978	High
CGGA_1764	710	1	WHO IV	Male	33	1	1	Mutant	Non-codel	Un-methylated	2.067779	High
CGGA_1833	494	1	WHO IV	Female	60	1	1	Wild type	Non-codel	Methylated	1.932302	High
CGGA_1901	540	1	WHO IV	Male	60	1	1	Wild type	Non-codel	Methylated	1.841542	High
CGGA_1817	399	1	WHO IV	Female	72	1	1	Wild type	Non-codel	Methylated	1.841531	Low
CGGA_1036	806	1	WHO IV	Male	41	1	1	Wild type	Non-codel	Methylated	1.840055	Low
CGGA_1537	97	1	WHO IV	Male	73	0	0	Wild type	Non-codel	Methylated	1.832147	Low
CGGA_1451	438	1	WHO IV	Female	45	1	1	Wild type	Non-codel	Un-methylated	1.768326	Low
CGGA_1134	59	1	WHO IV	Female	56	0	1	Wild type	Non-codel	Methylated	1.720361	Low
CGGA_1650	1283	1	WHO IV	Male	36	1	1	Mutant	Non-codel	Methylated	1.696587	Low
CGGA_1708	1122	1	WHO IV	Female	54	1	1	Wild type	Non-codel	Methylated	1.693432	Low
CGGA_1586	232	1	WHO IV	Female	55	1	1	Wild type	Non-codel	Un-methylated	1.619538	Low
CGGA_1354	530	1	WHO IV	Female	40	1	1	Wild type	Non-codel	Methylated	1.56303	Low
CGGA_1410	825	1	WHO IV	Female	27	1	1	Wild type	Non-codel	Methylated	1.554541	Low
CGGA_P609	726	0	WHO IV	Female	19	1	1	Wild type	Non-codel	Un-methylated	1.509591	Low
CGGA_1478	542	1	WHO IV	Female	72	1	1	Wild type	Non-codel	Methylated	1.490135	Low
CGGA_1441	1882	1	WHO IV	Male	70	1	1	Wild type	Non-codel	Methylated	1.488041	Low
CGGA_1758	414	1	WHO IV	Female	45	1	1	Wild type	Non-codel	Methylated	1.444681	Low
CGGA_PT02	1269	1		Mala	30	1	1	Wild type	Non-codel	NA	1.422524	LOW
CGGA_1699	2088	0		Female	55 /1	0	1	Mutant	NOT-COUEI		1 388717	Low
CGGA 1457	312	1	WHO IV	Male	60	1	1	Wild type	Non-codel	Methylated	1.306695	Low
CGGA 1644	173	1	WHO IV	Male	48	1	1	Wild type	Non-codel	Methylated	1.280691	Low
CGGA_1418	287	1	WHO IV	Female	73	1	1	Wild type	NA	Un-methylated	1.246618	Low
CGGA_1597	174	1	WHO IV	Male	58	1	0	Wild type	Non-codel	Methylated	1.234466	Low
 CGGA_1106	420	1	WHO IV	Male	37	1	0	Wild type	Non-codel	Methylated	1.233681	Low
CGGA_P178	1442	0	WHO IV	Female	52	1	1	Wild type	NA	Methylated	1.228416	Low
CGGA_P28	107	1	WHO IV	Male	61	0	0	Wild type	Non-codel	NA	1.223842	Low
CGGA_1462	174	1	WHO IV	Male	49	1	1	Wild type	Non-codel	Methylated	1.204831	Low
CGGA_1542	184	0	WHO IV	Male	26	1	1	Mutant	NA	Un-methylated	1.18985	Low
CGGA_1426	133	1	WHO IV	Female	50	1	1	Wild type	Non-codel	Un-methylated	1.160183	Low
CGGA_1706	2068	0	WHO IV	Male	60	1	1	Wild type	Non-codel	NA	1.155537	Low
CGGA_1681	346	1	WHO IV	Female	58	1	1	Wild type	Codel	Methylated	1.143278	Low
CGGA_1142	1005	1	WHO IV	Male	60	1	1	Wild type	Non-codel	Un-methylated	1.089902	LOW
CGGA 1400	00740	і 0		Mala	20	1 1	1	Wild type	Non-oodol	Methylated	1 02721	
CGGA 1736	038	1	WHO IV	Femalo	50	י 1	י 1	Wild type		Un-methylated	0. <u>99</u> 5717	
CGGA 1353	1022	' 1	WHO IV	Male	65	' 1	1	Wild type	Non-codel	Un-methylated	0.980293	Low
CGGA 1560	459	1	WHO IV	Female	35	1	1	Mutant	Non-codel	Methylated	0.967865	Low
CGGA_1365	253	1	WHO IV	Male	55	1	1	Wild type	NA	Methylated	0.950972	Low
CGGA_1866	127	1	WHO IV	Male	68	1	1	Wild type	Non-codel	Un-methylated	0.90668	Low
CGGA_1819	1005	1	WHO IV	Male	55	0	1	Wild type	Non-codel	Methylated	0.902441	Low
CGGA_P160	219	1	WHO IV	Female	72	1	1	Wild type	Non-codel	NA	0.898032	Low
CGGA_1467	866	1	WHO IV	Male	58	1	0	Mutant	NA	Un-methylated	0.865512	Low
CGGA_1767	86	1	WHO IV	Male	63	0	0	Wild type	NA	Methylated	0.863224	Low
CGGA_1687	2118	0	WHO IV	Male	14	1	1	Wild type	Non-codel	Un-methylated	0.859015	Low
CGGA_P143	261	1	WHO IV	Female	66	1	1	Wild type	Non-codel	NA	0.853727	Low
CGGA_1461	226	1	WHO IV	Female	60	1	1	Wild type	Non-codel	Un-methylated	0.832466	Low
CGGA_1666	249	1	WHO IV	Male	60	1	1	Wild type	NA	Methylated	0.816079	Low
CGGA_1282	1116	1	WHO IV	Female	33	1	1	Wild type	Non-codel	Un-methylated	0.813022	Low
CGGA_1086	1977	1	WHO IV	Female	65	1	1	Wild type	NA	Methylated	0.810788	Low
CGGA_1635	332	1	WHO IV	Female	43	1	1	Wild type	NA	Un-methylated	0.802611	Low
CGGA_1491	246	1	WHO IV	Male	29	1	1	Mutant	Non-codel	Un-methylated	0.786287	Low
CGGA_1709	415	1	WHO IV	Male	47	1	1	Wild type	Non-codel	Un-methylated	0.770231	Low
CGGA_1503	777	1	WHO IV	Male	47	1	1	Wild type	NA	Un-methylated	0.76868	Low
CGGA_1425	640	1	WHO IV	Female	22	1	1	Wild type	Codel	Methylated	0.713432	Low
CGGA_P116	305	1	WHO IV	Male	58	1	NA	Wild type	NA	NA	0.70161	Low
UGGA_1403	679	1		⊢emale	43	1 ₄	1	Wild type	Non-codel	Methylated	0.701189	LOW
CGCA 1790	842 1996	1		Female	41 57	1	1	Wild type	NA NA	NA	0.095196	LOW
CGGA 1624	1020	U 1		Female	01 26	U N		Wild type	Non-oodol	INA Mathylatod	0.004211 0.681255	
CGGA 1422	204	1	WHO IV	Male	20 76	1	1	Wild type	NA	Un-methylated	0.680169	
CGGA 1494	269	י 1	WHO IV	Male	21	' 1	1	Wild type	NA	Methylated	0.678442	Low
CGGA P205	583	1	WHO IV	Male	66	1	1	Wild type	NA	NA	0.639481	Low
CGGA_P180	260	1	WHO IV	Male	47	1	1	Mutant	NA	NA	0.63623	Low
CGGA_1481	131	1	WHO IV	Male	55	0	0	Wild type	NA	Methylated	0.63525	Low
CGGA_1486	184	1	WHO IV	Male	45	1	1	Wild type	NA	Methylated	0.631435	Low
CGGA_1378	378	1	WHO IV	Male	47	1	1	Wild type	NA	Un-methylated	0.61457	Low
CGGA_1722	349	1	WHO IV	Female	60	1	1	Wild type	NA	Un-methylated	0.610515	Low
CGGA_P25	147	1	WHO IV	Male	64	1	1	Wild type	NA	NA	0.599144	Low
CGGA_P164	1553	0	WHO IV	Male	27	1	1	Wild type	NA	NA	0.594725	Low

CGGA, Chinese Glioma Genome Atlas; Codel, codeletion; NA, not available; WHO, World Health Organization; IDH, isocitrate dehydrogenase.

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