

Table S1

Clinical characteristics of patients included in this study from four datasets

Dataset	TCGA RNA-Seq	CGGA RNA-Seq_325	CGGA microarray_301	REMBRANDT	GTEX RNA-Seq
Formation					
Glioma tissue	697	325	306	381	0
Non-tumor tissue	5	20	0	0	200
Gender					
Male	288	122	121	126	
Female	394	203	180	221	
Unavailable	15	0	5	34	
Age(years)					
Means	60	43	43	Unavailable	
Range	14-89	8-81	13-70	Unavailable	
Survival status					
Alive	414	99	100	65	
Dead	235	219	187	281	
Unavailable	48	7	14	35	
Overall survival(month)					
Median	48,6	37.37	27.47	19.93	
Histology					
LGG	512	114	124	200	
GBM	151	139	124	181	
Unavailable	45	4	3		
WHO grade					
II	254	109	122	92	
III	262	72	51	71	
IV	153	144	128	181	
Unavailable	28	0	5	38	

Table S2: The clinical information in the First Hospital of China Medical University

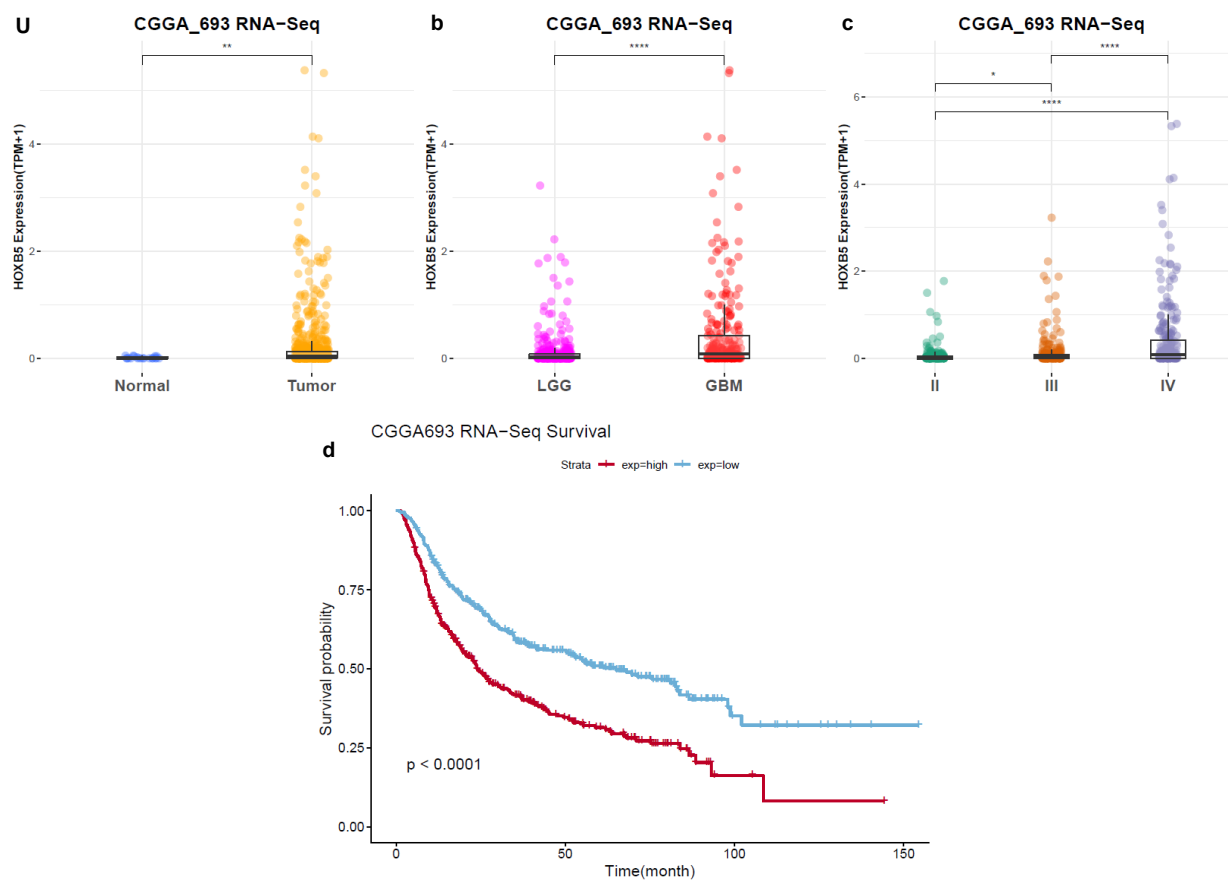
Sample	Gender	Age	WHO Grade
1	male	60	III
2	male	35	III
3	male	35	Peri-tumor (paired with sample 2)
4	female	55	II
5	female	49	II
6	male	56	IV
7	female	65	IV
8	female	33	IV

Table S3: Pearson correlation of angiogenesis genes with HOXB5 in four datasets

symbol	TCGA RNA-Seq		CGGA RNA-Seq_325		CGGA microarray_301		REMBRANDT	
	correlation	pvalue	correlation	pvalue	correlation	pvalue	correlation	pvalue
VCAN	-0.088	0.02017	0.063	0.255024	0.031	0.587202	0.012	0.819175
POSTN	0.511	1.01E-47	0.472	2.07E-19	0.483	5.87E-19	0.298	2.87E-09
FSTL1	0.487	9.76E-43	0.322	2.68E-09	0.449	2.26E-16	0.346	3.86E-12
LRPAP1	0.193	2.65E-07	0.139	0.012184	0.037	0.520382	0.107	0.036021
STC1	0.406	4.75E-29	0.321	3.33E-09	0.605	2.19E-31	0.351	1.78E-12
LPL	-0.091	0.016317	-0.025	0.658036	-0.048	0.40362	0.055	0.284115
VEGFA	0.353	6.75E-22	0.278	3.55E-07	0.391	1.90E-12	0.300	2.45E-09
PF4	0.047	0.219153	0.105	0.058305	0.219	0.000129	0.199	9.48E-05
THBD	0.319	6.64E-18	0.265	1.24E-06	0.359	1.34E-10	0.164	0.001303
FGFR1	0.319	6.10E-18	0.322	2.66E-09	0.263	3.63E-06	0.212	3.03E-05
TNFRSF21	-0.077	0.04218	-0.088	0.112865	-0.126	0.029199	0.047	0.364522
CCND2	0.028	0.454034	-0.014	0.807745	-0.082	0.158162	0.201	8.10E-05
COL5A2	0.467	4.99E-39	0.389	3.56E-13	0.527	5.96E-23	0.275	4.68E-08
ITGAV	0.096	0.011606	0.085	0.127844	-0.013	0.824622	0.011	0.82576
SERPINA5	0.386	4.03E-26	0.191	0.000548	0.317	1.89E-08	0.180	0.000403
KCNJ8	0.154	4.39E-05	0.195	0.000403	0.209	0.000269	0.123	0.016568
APP	0.028	0.468352	0.039	0.481724	-0.025	0.670518	-0.023	0.65071
COL3A1	0.455	7.51E-37	0.394	1.56E-13	0.510	2.72E-21	0.304	1.32E-09
SPP1	0.255	8.15E-12	0.158	0.004298	0.177	0.002089	0.086	0.092358
NRP1	0.393	3.92E-27	0.310	1.09E-08	0.431	4.99E-15	0.251	7.03E-07
OLR1	0.108	0.004217	0.018	0.752411	-0.059	0.306753	-0.067	0.189846
PDGFA	0.317	9.31E-18	0.248	5.83E-06	0.259	5.34E-06	0.296	3.96E-09
PTK2	-0.151	6.06E-05	-0.108	0.05172	-0.228	6.61E-05	-0.341	7.47E-12
SLCO2A1	0.309	7.77E-17	0.195	0.000402	0.158	0.005959	0.101	0.048105

PGLYRP1	0.093	0.013758	0.238	1.48E-05	0.439	1.31E-15	0.254	5.07E-07
VAV2	0.014	0.712234	0.090	0.10347	0.207	0.000292	0.259	3.04E-07
S100A4	0.413	4.72E-30	0.284	1.85E-07	0.403	3.51E-13	0.257	3.73E-07
MSX1	0.179	1.96E-06	0.221	5.96E-05	0.136	0.017897	0.229	6.23E-06
VTN	-0.155	4.03E-05	0.034	0.540261	0.144	0.01267	0.044	0.394748
TIMP1	0.475	1.58E-40	0.354	5.06E-11	0.358	1.66E-10	0.284	1.62E-08
JAG2	0.028	0.461569	0.043	0.436632	0.006	0.913523	-0.082	0.108443
LUM	0.437	7.08E-34	0.395	1.37E-13	0.435	2.44E-15	0.230	5.53E-06
CXCL6	0.290	5.53E-15	0.141	0.010688	0.366	5.85E-11	0.137	0.007377

Figure S1: Validation in CGGA_mRNA693 dataset



HOXB5 expression level between glioma and normal brain samples(a), LGG and GBM(b), and with different grades(c);(d) Kaplan–Meier survival plots for *HOXB5*. (Wilcoxon, *: $p < 0.05$; **: $p < 0.01$; ****: $p < 0.0001$)