

Figure S1. Pearson's correlation coefficient analysis demonstrated that THBS1 expression was positively correlated with mesenchymal biomarkers in The Cancer Genome Atlas-glioblastoma dataset. THBS1, thrombospondin-1.

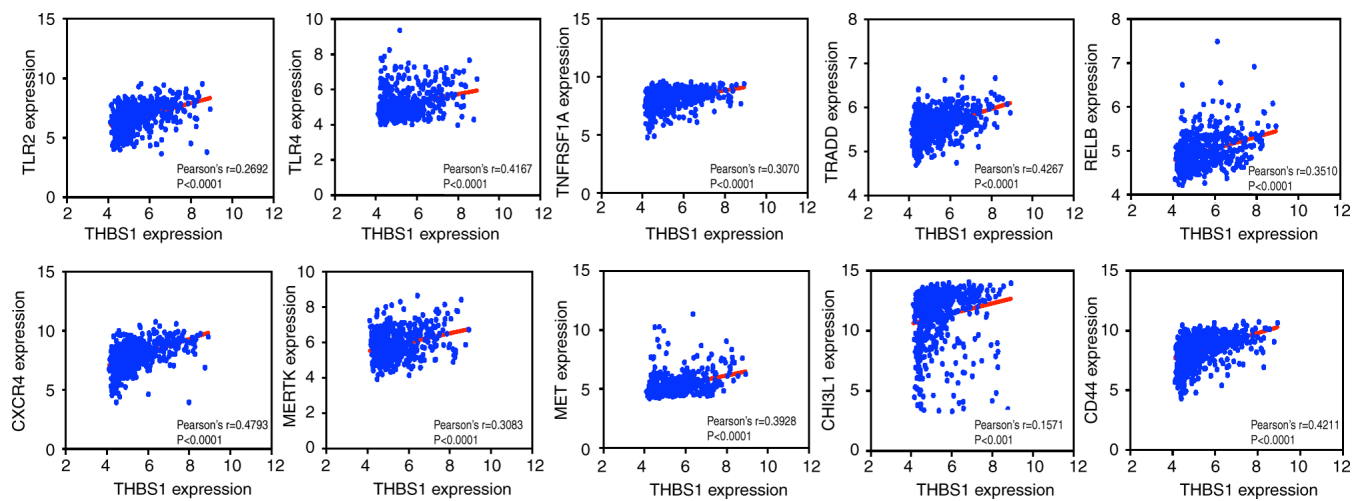


Figure S2. DNA hypomethylation level predicts higher THBS1 expression and IDH-1 wt GBM. (A-D) Four CpG sites were negatively correlated with THBS1 expression as evidenced by the Pearson's correlation coefficient. (E-H) IDH-1 mt GBM was associated with high THBS1 DNA methylation levels. **** $P < 0.0001$. THBS1, thrombospondin-1; IDH-1, isocitrate dehydrogenase-1; wt, wild-type; GBM, glioblastoma; mt, mutation type.

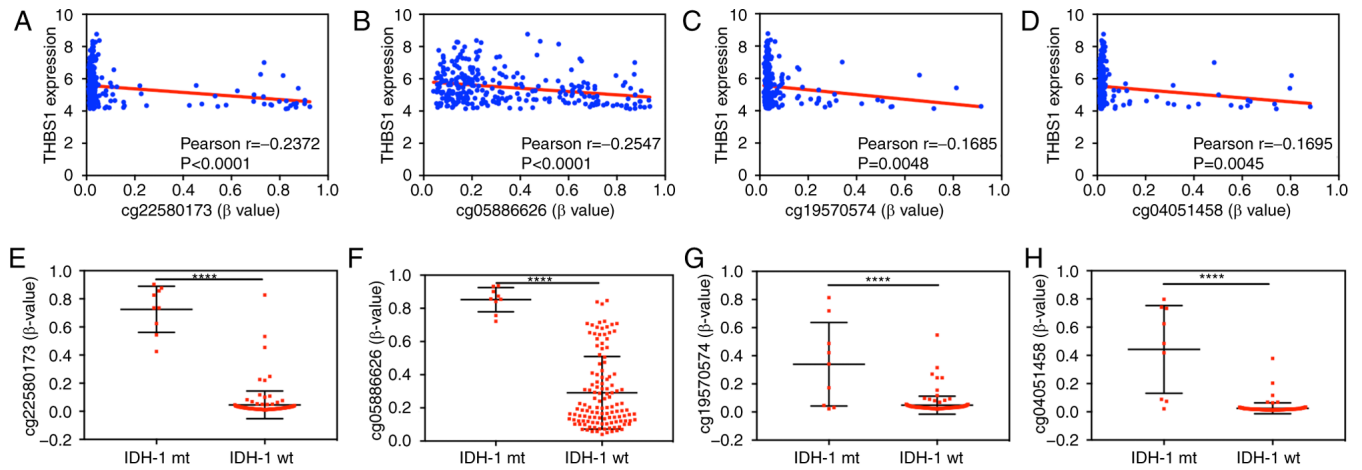


Table SI. Clinical data of the three transcriptome datasets.

	TCGA-GBM ^a	CGGA ^b	GSE16011 ^a
Sex			
Female	205	122	92
Male	320	203	184
NA	14	0	8
Age			
≤50	147	233	132
>50	378	92	144
NA	14	0	8
WHO grade			
Control	10	0	8
LGG	0	181	117
GBM	529	144	159
NA	0	0	0
IDH-1 status			
MT	13	162	83
WT	239	163	143
NA	287	0	58
Total	539	325	284

^aMicroarray data. ^bRNA sequencing data. NA, not acquired; WHO, World Health Organization; LGG, low-grade glioma; GBM, glioblastoma; IDH-1, isocitrate dehydrogenase-1; MT, mutation type; WT, wild-type; TCGA, The Cancer Genome Atlas; CCGA, Chinese Cancer Genome Atlas.