SUPPLEMENTARY TABLE

Supplementary Table 1. Clinical and molecular characteristics of patients included in this study.

Cohort	**TCGA (*n* = 616)**	**CGGA (mRNAseq_325) (*n* = 309)**	**CGGA (array) (*n* = 282)**	**GSE16011 (*n* = 264)**
Database	TCGA	CGGA	CGGA	GEO
Platform	Illumina Hiseq 2000 RNAseq	Illumina Hiseq 2000 RNAseq	AgilentWholeHuman Genome (Array)	Affymetrix GeneChip Human Genome U133 Plus 2.0 Array
Age(year)				
Mean (range)	47.4 (14–89)	43.2 (8–79)	42.5 (12–70)	50.87 (14.38–81.18)
Gender				
Female	259	116	117	87
Male	357	193	165	177
WHO grade				
II	224	98	106	24
III	243	74	53	85
IV	149	137	123	155
TCGA subtype				
Classical	83	–	23	–
Mesenchymal	89	–	105	–
Neural	99	–	74	–
Proneural	218	–	80	–
Unavailable	127	309	0	264
IDH status				
Mutant	391	166	127	80
Wild-type	220	142	154	132
Unavailable	5	1	1	52
1p/19q status				
Codel	156	62	16	–
Non-codel	455	242	73	–
Unavailable	5	5	193	264
MGMT promoter methylation status				
Methylated	441	150	95	–
Unmethylated	144	141	177	–
Unavailable	31	18	10	264

Abbreviations: CGGA: Chinese Glioma Genome Atlas; TCGA: The Cancer Genome Atlas; WHO: World Health Organization; 1p19q Codel: 1p19q codeleted; 1p19qNon-codel: 1p19q non-codeleted.