Supplementary data

Table S1. Primer sets for RT-PCR and quantitative PCR

Gene ID	Forward (5'-3')	Reverse (5'-3')
ID 2 (AGPAT2)	TGTACTGCGCGCTGTGCTTC	ACCTGCACTGTGACTGTTCCTG
ID45 (ADORA2B)	CTTTGGCATCGGATTGACTC	CCACTCTTGACATCTGCTTG
ID259 (CAV1)	CTCGGAGGGACATCTCTACACCGTT	GCAAGTTGATGCGGACATTGCTGA
ID287 (CD44s)	AACCGTGATGGCACCCGCTATG	TGGCCTCTCCGTTGAGTCCACTT
ID314 (TXNDC14)	GTGCGGCGACTTTCACGATG	GGGTGATGTGCTCACTTTGTACC
ID339 (CMTM6)	GTGTACAGCCCCACTACGGA	GCTCAGGCACCACAATGCAG
ID428 (CNIH)	GCGGCCTTCTGCTACATGCT	CAGATTCCACAGGCTACTCTTGGAC
ID910 (LEPROTL1)	TCTTACAACGGGCATTGTCG	CTTGACCAGTAATAGAGCCG
ID998 (M11S1)	GCAGAACACTGGATTTCCACGTAG	GGCTCAAGATGACGCTTAGGACA
ID1012 (MET)	ACAGCTGAATCTGCAACTCC	CTCTTGCATCGTAGCGAACT
ID1282 (PTPRS)	GCCCTATATTGCAGCTCGCTT	GAGAGCTTGAGGCTGTCGTT
ID1286 (PLP2)	CATAGCGGCAATCCTCTACCTG	AACCTAGGGCCTGGACTCTG
ID1389 (RECK)	GTGTGCTTCTGTCAAGTGTC	AACCAGCAGTCCTGAATGTC
EGFR	TCCCTCAGCCACCCATATGTAC	GTCTCGGGCCATTTTGGAGAATTC
GAPDH	CCCTTCATTGACCTCAACTAC	CCACCTTCTTGATGTCATCAT

Figure S1: Extraction of focused genes with feature. Each gene was plotted by nine glioma cell lines vs normal adult brain (A) and vs fetal brain (B) according to $|A - G|$ in horizontal axis and V in vertical axis. The border is lined by $V = |A - G|$. The area around where $|A - G| - V > 0$ is circled with red.

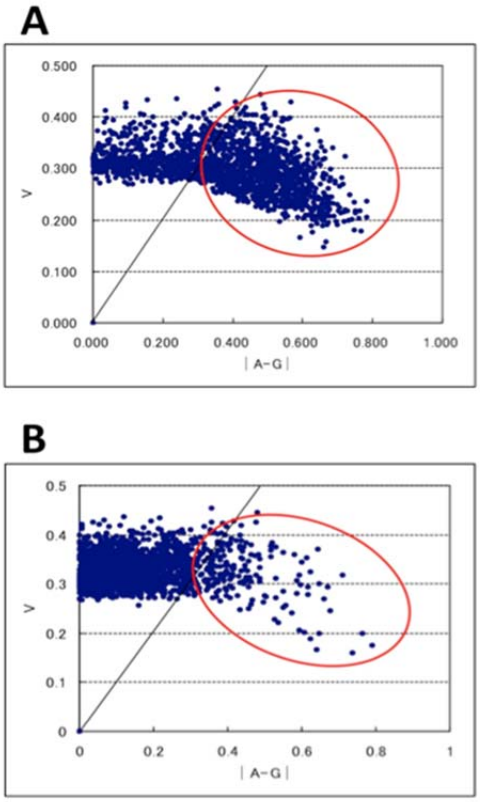

Figure S2: Gene expression levels of CD44 (A) and caveolin-1 (B). The relative expression levels of each cell line were confirmed by quantitative PCR. The graph shows the average levels of cell lines compared to adult brain.

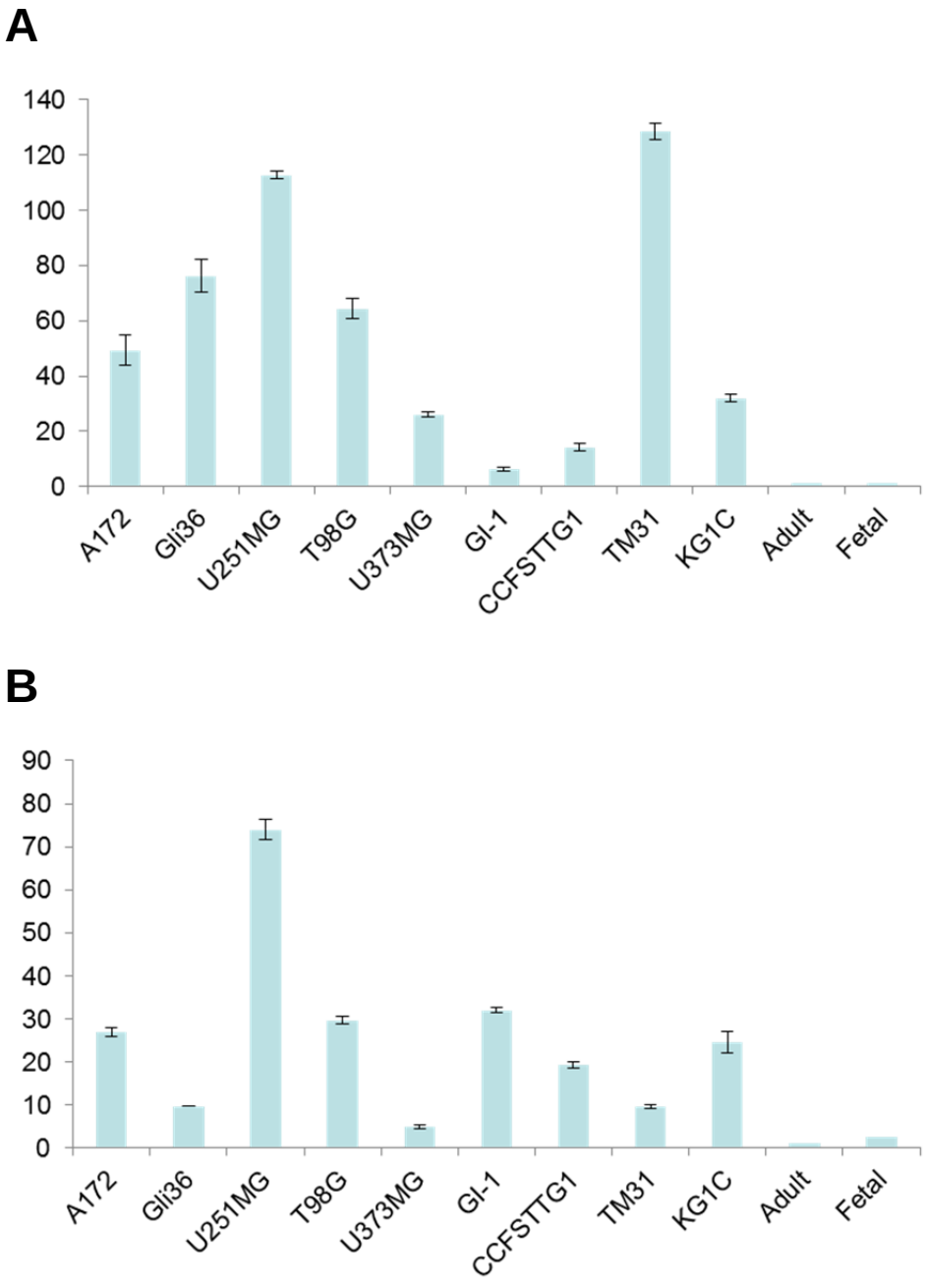

Figure S3: Evaluation of the variable forms of CD44 in glioma cell lines. CD44 is known to be variable due to the alternative splicing. Primers were designed to amplify the variable region. RT-PCR was performed and the fragment of 500 bp, which corresponds to the shortest form, was only amplified in each glioma cell line. M; size marker.