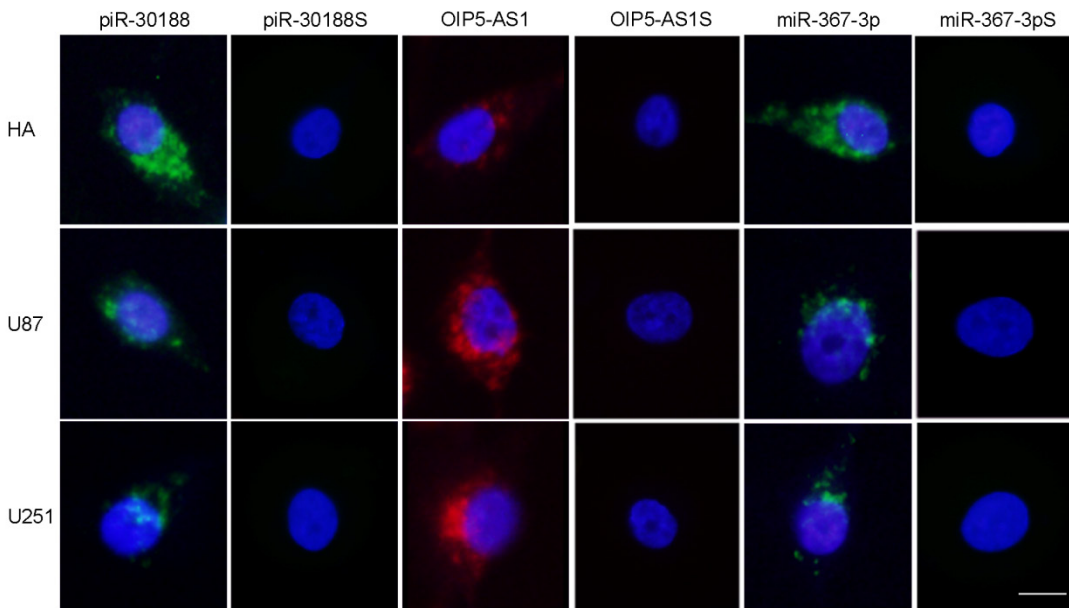


Supplementary Figure 1. piRNA, lncRNA and miRNA microarrays data in astrocytes, U87, and U251 cells. (A) PiRNA gene expression profiles as obtained from samples in three groups as indicated. Note: The piRNA ID is in Pubmed. (B) lncRNA gene expression profiles as obtained from samples in three groups as indicated. (C) miRNA gene expression profiles as obtained from samples in three groups as indicated. (D, E and F) qRT-PCR was performed to validate the selected molecules.



Supplementary Figure 2. Location and expression of piR-30188, OIP5-AS1, and miR-367-3p in normal human astrocytes (NHA), U87 and U251 cells. Left: FISH was used to determine expression and location of piR-30188 in NHA, U87 and U251 cells (green, piR-30188; blue, DAPI nuclear staining). Middle: FISH was used to determine expression and location of OIP5-AS1 in NHA, U87 and U251 cells (red, OIP5-AS1; blue, DAPI nuclear staining). Right: FISH was used to determine expression and location of miR-367-3p in NHA, U87 and U251 cells (green, miR-367-3p; blue, DAPI nuclear staining). Scale bars represent 20 μm . PiR-30188S, OIP5-AS1S, and miR-367-3pS represented negative controls (sense sequence probe).

Supplementary Table 1: Detailed information about the glioma patients.

Clinicalpathological parameters and molecular subtype					
Age (years)		Number			
≤45		16			
>45		21			
Gender					
Male		23			
Female		14			
WHO grade		IDH1/2 status		LOH on 1p/19q	
		Wt	Mut	Complete	Lack
I grade	3	0	3	2	1
II grade	5	1	4	4	1
III grade	12	5	7	7	5
IV grade	17	14	3	5	12

Supplementary Table 2 and Table 3: Primers used in ChIP assays.