SUPPORTING INFORMATION FOR

Over expression of *miRNA-100* is responsible for the low expression of ATM in the human glioma cell line: M059J

Sequence 5'-3'	Remark
CCTAAAGTCCACTGGATTTG	
CCAGTTACAAGAGATATGGG	
CTAGTAATATTTAAGTGAACTATTGTGGGTTTTT	Wild-type
AGCTAAAAACCCACAATAGTTCACTTAAATATTA	
CTAGTAAGTAGGGATTAATTTTTGAATGTTGG	Mutant
AGCTCCAACATTCAAAAATTAATCCCTACTTA	
CTAGTTCAGCAAGGCTTTATCTATGGGAATCT	Wild-type
AGCTAGATTCCCATAGATAAAGCCTTGCTGAA	
CTAGGTGAGTTTATTTTCTCTTGAGTGTCTGT	Mutant
AGCTACAGACACTCAAGAGAAAATAAACTCAC	
CTAGTCCCAAAGTGCTGGGATTACAGGTGTGA	Wild-type
AGCTTCACACCTGTAATCCCAGCACTTTGGGA	
CTAGCCTCCTCGGCCTCCTGAGCCACCGCGCC	Mutant
AGCTGGCGCGGTGGCTCAGGAGGCCGAGGAGG	
CGGTTAATACGACTCACTATAGGGAGACACAA	
AACCCGTAGATCCGAACTTGTGTCTCC	
CGGTTAATACGACTCACTATAGGGAGAGGTCAGA	
GGTCAGAGCGCTGCGGTGAT	
GATGACCCCAGGTAACTCTGAGTGTGT	
TGACCCAGATCATGTTTGAGACCT	Housekeeping
GACTCCATGCCCAGGAAGGAAG	50110
CAGCTTGATGAGGATCGAACAGAG	RT-PCR
TGTGCACCATTCAAGAACACCACT	
	Sequence 5'-3'CCTAAAGTCCACTGGATTTGCCAGTTACAAGAGATATGGGCTAGTAATATTTAAGTGAACTATTGTGGGTTTTTAGCTAAAAACCCACAATAGTTCACTTAAATATTACTAGTAAGTAGGGATTAATTTTGAATGTTGGAGCTCCAACATTCAAAAATTAATCCCTACTTACTAGTTCAGCAAGGCTTTATCTATGGGAATCTAGCTAGATTCCCATAGATAAAAGCCTTGCTGAACTAGGTGAGTTTATTTTCTCTTGAGTGTCTGTAGCTACAGACACTCAAGAGAAAATAAACTCACCTAGTCCCAAAGTGCTGGGATTACAGGTGTGAAGCTTCACACCTGTAATCCCAGCACTTTGGGACTAGCTCCCTCGGCCTCCTGAGCCACCGCGCCAGCTGGCGCGGTGGCTCAGGAGGCCGAGGAGGCGGTTAATACGACTCACTATAGGGAGACACAAAACCCGTAGATCCGACTTGTGTCTCCCGGTTAATACGACTCACTATAGGGAGAGGACACAAAGATCAGAGCGCTGCGGTGATGATGACCCCAGGTAACTCTGAGTGTGTTGACCCAGGTACATGTTTGAGACCTGACTCCATGCCCAGGAAGGAAGGCAGCTTGATGAGGATCGAACAGAGCAGCTTGATGAGGATCGAACGAAGACAGCTTGATGAGGATCGAACAAGAACCCCAGGTAACTCTGAGTGTGTTGACCCAGGTAACTCAAGAACACCACTGACTCCATGCCCAAGGAACGAAGACAGCTTGATGAGGATCGAACAACAACACACACAC

Table S1. Primers information



Fig. S1- Comparing the *ATM* mRNA level between M059J and M059K cells. Total RNAs were prepared from M059J or M059K cells. RT-PCR was performed with the proper primers (Table S1). Human β -Actin was used as an internal loading control.



Fig. S2- Comparing the effects of cycloheximide (CHX) on the ATM level changed between M059J and M059K cells. The cells were treated with 100 μ g/ml (CHX) (Sigma-Aldrich Inc, St. Louis, MO, USA). At different times the cells were collected and whole cell lyses were prepared. The ATM level was detected by Western blot. Considering the big difference of ATM levels in M059K and M059J cells, in order to observe the relative comparable image, we loaded 10 μ g/each point for M059K cells and 40 μ g/each point for M059J cells. Ku70 was used as the internal loading control. The quantity of ATM was analyzed by the ImageQuate.



Fig. S3- Description of lentivirus vector construction. To construct a plasmid expressing *miR-100*, we first amplified a DNA fragment carrying pri-*miR-100*, using genomic DNA from a healthy blood donor as a template. PCR reactions were performed using the high fidelity Phusion enzyme (New England Biolabs), and specific primers (Table S1). The amplified fragment was first cloned into a PCR cloning vector and subsequently cloned into pCDHCMV-MCS-EF1-copGFP at the *EcoR1* and *NotI* sites.



Fig. S4- The effects of *miR-100* on the cell radiosensitivity. (A) The effects of *miR-100* on the ATM level of U87MG cells. U87MG cells were purchased from the American Type Culture Collection (Manassas, VA, USA). The lung cancer cell lines, 95C and 95D, were obtained from Dr. Lu's laboratory. (B) The effects of *miR-100* on the sensitivity of U87MG cells to IR-induced killing. The data represent mean \pm SE of three independent experiments. **, *P* < 0.01, compared with cells transfected with the vector control. (C) The effects of *miR-100* on the ATM level of 95C cells. (D) The effects of *miR-100* on the sensitivity of 95C cells to IR-induced killing. The data represent mean \pm SE of three independent experiments. 95D cells had a similar radiosensitivity to 95C cells and the effects of *miR-100* on 95D cells were similar to that on 95C cells (data not shown).



Fig. S5- No influence on the ATM protein level and miR-100 expression after *PRKDC* siRNA (100 nM) treatment in U87MG cells. (A) Western blot analysis of DNA-PKcs, ATM and Ku70 (loading control). The cells were collected for Western blot after 48 hr siRNA treatment. (B) Comparison of the endogenous miR-100 levels in siRNA treated and control cells. Total RNA was isolated after 48 hr of siRNA treatment and qRT-PCR was used to detect the miR-100 expression with triplicate reactions. RNU48 was used as an internal loading control.



Fig. S6- No direct correlation between the protein level of DNA-PKcs and ATM or miR-100 in different glioma cell lines: 1. U87MG, 2. M059K, 3. M059J, 4. T98G. (A) Western blot analysis of DNA-PKcs, ATM and Ku70 in 4 glioma cell lines. (B)

Comparison of miR-100 endogenous level in 4 glioma cell lines. qRT-PCR was used to detect the miR-100 expression with triplicate reactions. RNU48 was used as an internal loading control.



Fig. S7- Comparing the mTOR levels between M059J and M059K cells, and detecting the effect of *miR-100* on the mTOR expression in M059K cells. Western blot was used to detect mTOR expression in these cells. Whole cell lyses were used for the experiments. Ku70 was used as an internal loading control.